

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE
PATENT APPLICATION TRANSMITTAL UNDER 37 CFR 1.53

BOX PATENT APPLICATION
Assistant Commissioner for Patents
Washington, D.C. 20231

Sir:

Transmitted herewith for filing is the patent application of

Inventor(s): Y. Tom Tang, Ping Zhou, Ryle Goodrich, Chenghua Liu, Vinod Asundi,
Feiyan Ren, Jie Zhang, Qing A. Zhao, Aidong J. Xue, Yonghong Yang,
Tom Wehrman, Radoje T. Drmanac

Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

1. Type of application

- x This is a new application for a
x Utility patent.
☐ Design patent.
x Applicants claim small entity status (See 37 CFR 1.27)

2. Application Papers Enclosed

- 1 Title Page
142 Pages of Specification (excluding Claims, Abstract, Drawings & Sequence Listing)
4 Page(s) of Claims
1 Page(s) of Abstract
0 Sheet(s) of Drawings (Figs. X-X) ☐ Formal ☐ Informal
723 Page(s) of Sequence Listing

CERTIFICATION UNDER 37 CFR 1.10

I hereby certify that this Patent Application Transmittal and the documents referred to as enclosed therewith are being deposited with the United States Postal Service on November 17, 2000, in an envelope addressed to the Assistant Commissioner for Patents, Washington, D.C. 20231 utilizing the "Express Mail Post Office to Addressee" service of the United States Postal Service under Mailing Label No. EK415382545US


Sandy Fong

3. Oath or Declaration

- ☐ Enclosed
- ☐ Executed by (check all applicable boxes)
- ☐ Inventor(s)
- ☐ Legal representative of inventors(s) (37 CFR 1.42 or 1.43)
- ☐ Joint inventor or person showing a proprietary interest on behalf of inventor who refused to sign or cannot be reached
- ☐ The petition required by 37 CFR 1.47 and the statement required by 37 CFR 1.47 are enclosed. See Item 5D below for fee.
- x Unexecuted – the undersigned attorney or agent is authorized to file this application on behalf of the applicant(s). An executed declaration will follow.

4. Additional Papers Enclosed

- ☐ Preliminary Amendment
- ☐ Information Disclosure Statement
- ☐ Declaration of Biological Deposit
- x Computer readable copy of sequence listing containing nucleotide and/or amino acid sequence
- x Statement Under 37 CFR § 1.821
- x Paper copy of sequence listing identical to computer copy (723 pages)
- ☐ Microfiche computer program
- ☐ Associate Power of Attorney
- ☐ Verified translation of a non-English patent application
- x Return receipt postcard
- ☐ Other _____

5. Priority Applications Under 35 USC 119

Certified copies of applications from which priority under 35 USC 119 is claimed are listed below and

- ☐ are attached.
- ☐ will follow.

6. **Filing Fee Calculation (37 CFR 1.16)**

A. ☒ **Utility Application**

CLAIMS AS FILED – INCLUDING PRELIMINARY AMENDMENT (IF ANY)						
			SMALL ENTITY		OTHER THAN A SMALL ENTITY	
	NO. FILED	NO. EXTRA	RATE	FEE	RATE	FEE
BASIC FEE				\$355.00		\$710.00
TOTAL	30-20	= 10	X 9 =	\$90.00	X 18 =	\$0.00
INDEP.	3-3	= 0	X 40 =	\$00.00	X 80 =	\$0.00
Γ First Presentation of Multiple Dependent Claim			+ 135 =	\$135.00	+ 270 =	\$0.00
FILING FEE:				\$580.00	OR	\$0.00

B. ☐ **Design Application (\$160.00/\$320.00)** Filing Fee: \$ _____

C. ☐ **Plant Application (\$245.00/\$490.00)** Filing Fee: \$ _____

D. **Other fees**

☐ Recording Assignment [Fee -- \$40.00 per assignment] \$ _____

☐ Petition fee for filing by other than all the inventors or person on behalf of the inventor where inventor refused to sign or cannot be reached [Fee -- \$130.00] \$ _____

☐ Other \$ _____

TOTAL FEES ENCLOSED \$ 580.00

7. Method of Payments of Fees

- ☐ Enclosed check
- ☒ Charge Deposit Account No. 501169. A duplicate copy of this transmittal is enclosed
- ☐ Not enclosed

8. Deposit Account and Refund Authorization

The Commissioner is hereby authorized to charge payment of any additional fees due or credit any overpayment to Deposit Account No. 501169. A duplicate copy of this transmittal is enclosed.

Please refund any overpayment to Hyseq, Inc. at the address below.

Please direct all future correspondence to Leslie A. Mooi at the address below.

Respectfully submitted,

Date: November 17, 2000

By: Leslie Mooi
Leslie A. Mooi
Attorney for Applicants
Registration No.: 37,047
HYSEQ, INC.
670 Almanor Avenue
Sunnyvale, CA 94085
(408) 524-8100
(408) 524-8145 (Telefacsimile)

Our Ref. No.: 797

NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

Express Mail Label No.: EF415382545US

NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

1. BACKGROUND OF THE INVENTION

5 1.1 TECHNICAL FIELD

The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with uses for these polynucleotides and proteins, for example in therapeutic, diagnostic and research methods.

10 1.2 BACKGROUND

Technology aimed at the discovery of protein factors (including e.g., cytokines, such as lymphokines, interferons, CSFs, chemokines, and interleukins) has matured rapidly over the past decade. The now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (i.e., partial DNA/amino acid sequence of the protein in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization-based cloning techniques, have advanced the state of the art by making available large numbers of DNA/amino acid sequences for proteins that are known to have biological activity, for example, by virtue of their secreted nature in the case of leader sequence cloning, by virtue of their cell or tissue source in the case of PCR-based techniques, or by virtue of structural similarity to other genes of known biological activity.

Identified polynucleotide and polypeptide sequences have numerous applications in, for example, diagnostics, forensics, gene mapping; identification of mutations responsible for genetic disorders or other traits, to assess biodiversity, and to produce many other types of data and products dependent on DNA and amino acid sequences.

30 2. SUMMARY OF THE INVENTION

The compositions of the present invention include novel isolated polypeptides, novel isolated polynucleotides encoding such polypeptides, including recombinant DNA molecules, cloned genes or degenerate variants thereof, especially naturally occurring variants such as allelic variants, antisense polynucleotide molecules, and antibodies that specifically recognize one or more epitopes present on such polypeptides, as well as hybridomas producing such antibodies.

The compositions of the present invention additionally include vectors, including expression vectors, containing the polynucleotides of the invention, cells genetically engineered to contain such polynucleotides and cells genetically engineered to express such polynucleotides.

The present invention relates to a collection or library of at least one novel nucleic acid sequence assembled from expressed sequence tags (ESTs) isolated mainly by sequencing by hybridization (SBH), and in some cases, sequences obtained from one or more public databases. The invention relates also to the proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins. These nucleic acid sequences are designated as SEQ ID NO: 1 – 362 and are provided in the Sequence Listing. In the nucleic acids provided in the Sequence Listing, A is adenosine; C is cytosine; G is guanine; T is thymine; and N is any of the four bases. In the amino acids provided in the Sequence Listing, * corresponds to the stop codon.

The nucleic acid sequences of the present invention also include, nucleic acid sequences that hybridize to the complement of SEQ ID NO: 1 – 362 under stringent hybridization conditions; nucleic acid sequences which are allelic variants or species homologues of any of the nucleic acid sequences recited above, or nucleic acid sequences that encode a peptide comprising a specific domain or truncation of the peptides encoded by SEQ ID NO: 1 – 362. A polynucleotide comprising a nucleotide sequence having at least 90% identity to an identifying sequence of SEQ ID NO: 1 – 362 or a degenerate variant or fragment thereof. The identifying sequence can be 100 base pairs in length.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO: 1 – 362. The sequence

information can be a segment of any one of SEQ ID NO: 1 – 362 that uniquely identifies or represents the sequence information of SEQ ID NO: 1 – 362.

A collection as used in this application can be a collection of only one polynucleotide. The collection of sequence information or identifying information of each sequence can be provided on a nucleic acid array. In one embodiment, segments of sequence information is provided on a nucleic acid array to detect the polynucleotide that contains the segment. The array can be designed to detect full-match or mismatch to the polynucleotide that contains the segment. The collection can also be provided in a computer-readable format.

This invention also includes the reverse or direct complement of any of the nucleic acid sequences recited above; cloning or expression vectors containing the nucleic acid sequences; and host cells or organisms transformed with these expression vectors. Nucleic acid sequences (or their reverse or direct complements) according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology, such as use as hybridization probes, use as primers for PCR, use in an array, use in computer-readable media, use in sequencing full-length genes, use for chromosome and gene mapping, use in the recombinant production of protein, and use in the generation of anti-sense DNA or RNA, their chemical analogs and the like.

In a preferred embodiment, the nucleic acid sequences of SEQ ID NO: 1-362 or novel segments or parts of the nucleic acids of the invention are used as primers in expression assays that are well known in the art. In a particularly preferred embodiment, the nucleic acid sequences of SEQ ID NO: 1-362 or novel segments or parts of the nucleic acids provided herein are used in diagnostics for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., *Science* 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The isolated polynucleotides of the invention include, but are not limited to, a polynucleotide comprising any one of the nucleotide sequences set forth in SEQ ID NO: 1–362; a polynucleotide comprising any of the full length protein coding sequences of SEQ ID NO: 1–362; and a polynucleotide comprising any of the nucleotide sequences of the mature protein coding sequences of SEQ ID NO: 1–362. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under

stringent hybridization conditions to (a) the complement of any one of the nucleotide sequences set forth in SEQ ID NO: 1-362; (b) a nucleotide sequence encoding any one of the amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotides recited above; (d) a polynucleotide which encodes a species homolog (e.g. orthologs) of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of any of the polypeptides comprising an amino acid sequence set forth in the Sequence Listing.

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising any of the amino acid sequences set forth in the Sequence Listing; or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides with biological activity that are encoded by (a) any of the polynucleotides having a nucleotide sequence set forth in SEQ ID NO: 1-362; or (b) polynucleotides that hybridize to the complement of the polynucleotides of (a) under stringent hybridization conditions. Biologically or immunologically active variants of any of the polypeptide sequences in the Sequence Listing, and "substantial equivalents" thereof (e.g., with at least about 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or 99% amino acid sequence identity) that preferably retain biological activity are also contemplated. The polypeptides of the invention may be wholly or partially chemically synthesized but are preferably produced by recombinant means using the genetically engineered cells (e.g. host cells) of the invention.

The invention also provides compositions comprising a polypeptide of the invention. Polypeptide compositions of the invention may further comprise an acceptable carrier, such as a hydrophilic, e.g., pharmaceutically acceptable, carrier.

The invention also provides host cells transformed or transfected with a polynucleotide of the invention.

The invention also relates to methods for producing a polypeptide of the invention comprising growing a culture of the host cells of the invention in a suitable culture medium under conditions permitting expression of the desired polypeptide, and purifying the polypeptide from the culture or from the host cells. Preferred embodiments include those in which the protein produced by such process is a mature form of the protein.

Polynucleotides according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology. These

techniques include use as hybridization probes, use as oligomers, or primers, for PCR, use for chromosome and gene mapping, use in the recombinant production of protein, and use in generation of anti-sense DNA or RNA, their chemical analogs and the like. For example, when the expression of an mRNA is largely restricted to a particular cell or tissue type, polynucleotides of the invention can be used as hybridization probes to detect the presence of the particular cell or tissue mRNA in a sample using, *e.g.*, *in situ* hybridization.

In other exemplary embodiments, the polynucleotides are used in diagnostics as expressed sequence tags for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The polypeptides according to the invention can be used in a variety of conventional procedures and methods that are currently applied to other proteins. For example, a polypeptide of the invention can be used to generate an antibody that specifically binds the polypeptide. Such antibodies, particularly monoclonal antibodies, are useful for detecting or quantitating the polypeptide in tissue. The polypeptides of the invention can also be used as molecular weight markers, and as a food supplement.

Methods are also provided for preventing, treating, or ameliorating a medical condition which comprises the step of administering to a mammalian subject a therapeutically effective amount of a composition comprising a polypeptide of the present invention and a pharmaceutically acceptable carrier.

In particular, the polypeptides and polynucleotides of the invention can be utilized, for example, in methods for the prevention and/or treatment of disorders involving aberrant protein expression or biological activity.

The present invention further relates to methods for detecting the presence of the polynucleotides or polypeptides of the invention in a sample. Such methods can, for example, be utilized as part of prognostic and diagnostic evaluation of disorders as recited herein and for the identification of subjects exhibiting a predisposition to such conditions. The invention provides a method for detecting the polynucleotides of the invention in a sample, comprising contacting the sample with a compound that binds to and forms a complex with the polynucleotide of interest for a period sufficient to form

the complex and under conditions sufficient to form a complex and detecting the complex such that if a complex is detected, the polynucleotide of interest is detected. The invention also provides a method for detecting the polypeptides of the invention in a sample comprising contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex and detecting the formation of the complex such that if a complex is formed, the polypeptide is detected.

The invention also provides kits comprising polynucleotide probes and/or monoclonal antibodies, and optionally quantitative standards, for carrying out methods of the invention. Furthermore, the invention provides methods for evaluating the efficacy of drugs, and monitoring the progress of patients, involved in clinical trials for the treatment of disorders as recited above.

The invention also provides methods for the identification of compounds that modulate (i.e., increase or decrease) the expression or activity of the polynucleotides and/or polypeptides of the invention. Such methods can be utilized, for example, for the identification of compounds that can ameliorate symptoms of disorders as recited herein. Such methods can include, but are not limited to, assays for identifying compounds and other substances that interact with (e.g., bind to) the polypeptides of the invention. The invention provides a method for identifying a compound that binds to the polypeptides of the invention comprising contacting the compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and detecting the complex by detecting the reporter gene sequence expression such that if expression of the reporter gene is detected the compound the binds to a polypeptide of the invention is identified.

The methods of the invention also provides methods for treatment which involve the administration of the polynucleotides or polypeptides of the invention to individuals exhibiting symptoms or tendencies. In addition, the invention encompasses methods for treating diseases or disorders as recited herein comprising administering compounds and other substances that modulate the overall activity of the target gene products.

Compounds and other substances can effect such modulation either on the level of target gene/protein expression or target protein activity.

The polypeptides of the present invention and the polynucleotides encoding them are also useful for the same functions known to one of skill in the art as the polypeptides and polynucleotides to which they have homology (set forth in Table 1); for which they have a signature region (as set forth in Table 3); or for which they have homology to a gene family (as set forth in Table 4). If no homology is set forth for a sequence, then the polypeptides and polynucleotides of the present invention are useful for a variety of applications, as described herein, including use in arrays for detection.

3. DETAILED DESCRIPTION OF THE INVENTION

3.1 DEFINITIONS

It must be noted that as used herein and in the appended claims, the singular forms "a", "an" and "the" include plural references unless the context clearly dictates otherwise.

The term "active" refers to those forms of the polypeptide which retain the biologic and/or immunologic activities of any naturally occurring polypeptide. According to the invention, the terms "biologically active" or "biological activity" refer to a protein or peptide having structural, regulatory or biochemical functions of a naturally occurring molecule. Likewise "immunologically active" or "immunological activity" refers to the capability of the natural, recombinant or synthetic polypeptide to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

The term "activated cells" as used in this application are those cells which are engaged in extracellular or intracellular membrane trafficking, including the export of secretory or enzymatic molecules as part of a normal or disease process.

The terms "complementary" or "complementarity" refer to the natural binding of polynucleotides by base pairing. For example, the sequence 5'-AGT-3' binds to the complementary sequence 3'-TCA-5'. Complementarity between two single-stranded molecules may be "partial" such that only some of the nucleic acids bind or it may be "complete" such that total complementarity exists between the single stranded molecules.

The degree of complementarity between the nucleic acid strands has significant effects on the efficiency and strength of the hybridization between the nucleic acid strands.

The term "embryonic stem cells (ES)" refers to a cell that can give rise to many differentiated cell types in an embryo or an adult, including the germ cells. The term "germ line stem cells (GSCs)" refers to stem cells derived from primordial stem cells that provide a steady and continuous source of germ cells for the production of gametes. The term "primordial germ cells (PGCs)" refers to a small population of cells set aside from other cell lineages particularly from the yolk sac, mesenteries, or gonadal ridges during embryogenesis that have the potential to differentiate into germ cells and other cells.

PGCs are the source from which GSCs and ES cells are derived. The PGCs, the GSCs and the ES cells are capable of self-renewal. Thus these cells not only populate the germ line and give rise to a plurality of terminally differentiated cells that comprise the adult specialized organs, but are able to regenerate themselves.

The term "expression modulating fragment," EMF, means a series of nucleotides which modulates the expression of an operably linked ORF or another EMF.

As used herein, a sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are nucleic acid fragments which induce the expression of an operably linked ORF in response to a specific regulatory factor or physiological event.

The terms "nucleotide sequence" or "nucleic acid" or "polynucleotide" or "oligonucleotide" are used interchangeably and refer to a heteropolymer of nucleotides or the sequence of these nucleotides. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA) or to any DNA-like or RNA-like material. In the sequences herein A is adenine, C is cytosine, T is thymine, G is guanine and N is A, C, G or T (U). It is contemplated that where the polynucleotide is RNA, the T (thymine) in the sequences provided herein is substituted with U (uracil).

Generally, nucleic acid segments provided by this invention may be assembled from fragments of the genome and short oligonucleotide linkers, or from a series of

oligonucleotides, or from individual nucleotides, to provide a synthetic nucleic acid which is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon, or a eukaryotic gene.

The terms "oligonucleotide fragment" or a "polynucleotide fragment", "portion," or "segment" or "probe" or "primer" are used interchangeably and refer to a sequence of nucleotide residues which are at least about 5 nucleotides, more preferably at least about 7 nucleotides, more preferably at least about 9 nucleotides, more preferably at least about 11 nucleotides and most preferably at least about 17 nucleotides. The fragment is preferably less than about 500 nucleotides, preferably less than about 200 nucleotides, more preferably less than about 100 nucleotides, more preferably less than about 50 nucleotides and most preferably less than 30 nucleotides. Preferably the probe is from about 6 nucleotides to about 200 nucleotides, preferably from about 15 to about 50 nucleotides, more preferably from about 17 to 30 nucleotides and most preferably from about 20 to 25 nucleotides. Preferably the fragments can be used in polymerase chain reaction (PCR), various hybridization procedures or microarray procedures to identify or amplify identical or related parts of mRNA or DNA molecules. A fragment or segment may uniquely identify each polynucleotide sequence of the present invention. Preferably the fragment comprises a sequence substantially similar to any one of SEQ ID NOs:1-362.

Probes may, for example, be used to determine whether specific mRNA molecules are present in a cell or tissue or to isolate similar nucleic acid sequences from chromosomal DNA as described by Walsh et al. (Walsh, P.S. et al., 1992, PCR Methods Appl 1:241-250). They may be labeled by nick translation, Klenow fill-in reaction, PCR, or other methods well known in the art. Probes of the present invention, their preparation and/or labeling are elaborated in Sambrook, J. et al., 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY; or Ausubel, F.M. et al., 1989, Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, both of which are incorporated herein by reference in their entirety.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NOs: 1-362. The sequence information can be a segment of any one of SEQ ID NOs: 1-362 that uniquely identifies

or represents the sequence information of that sequence of SEQ ID NO: 1-362. One such segment can be a twenty-mer nucleic acid sequence because the probability that a twenty-mer is fully matched in the human genome is 1 in 300. In the human genome, there are three billion base pairs in one set of chromosomes. Because 4^{20} possible twenty-mers exist, there are 300 times more twenty-mers than there are base pairs in a set of human chromosomes. Using the same analysis, the probability for a seventeen-mer to be fully matched in the human genome is approximately 1 in 5. When these segments are used in arrays for expression studies, fifteen-mer segments can be used. The probability that the fifteen-mer is fully matched in the expressed sequences is also approximately one in five because expressed sequences comprise less than approximately 5% of the entire genome sequence.

Similarly, when using sequence information for detecting a single mismatch, a segment can be a twenty-five mer. The probability that the twenty-five mer would appear in a human genome with a single mismatch is calculated by multiplying the probability for a full match ($1/4^{25}$) times the increased probability for mismatch at each nucleotide position (3×25). The probability that an eighteen mer with a single mismatch can be detected in an array for expression studies is approximately one in five. The probability that a twenty-mer with a single mismatch can be detected in a human genome is approximately one in five.

The term "open reading frame," ORF, means a series of nucleotide triplets coding for amino acids without any termination codons and is a sequence translatable into protein.

The terms "operably linked" or "operably associated" refer to functionally related nucleic acid sequences. For example, a promoter is operably associated or operably linked with a coding sequence if the promoter controls the transcription of the coding sequence. While operably linked nucleic acid sequences can be contiguous and in the same reading frame, certain genetic elements e.g. repressor genes are not contiguously linked to the coding sequence but still control transcription/translation of the coding sequence.

The term "pluripotent" refers to the capability of a cell to differentiate into a number of differentiated cell types that are present in an adult organism. A pluripotent cell is restricted in its differentiation capability in comparison to a totipotent cell.

The terms "polypeptide" or "peptide" or "amino acid sequence" refer to an oligopeptide, peptide, polypeptide or protein sequence or fragment thereof and to naturally occurring or synthetic molecules. A polypeptide "fragment," "portion," or "segment" is a stretch of amino acid residues of at least about 5 amino acids, preferably at least about 7 amino acids, more preferably at least about 9 amino acids and most preferably at least about 17 or more amino acids. The peptide preferably is not greater than about 200 amino acids, more preferably less than 150 amino acids and most preferably less than 100 amino acids. Preferably the peptide is from about 5 to about 200 amino acids. To be active, any polypeptide must have sufficient length to display biological and/or immunological activity.

The term "naturally occurring polypeptide" refers to polypeptides produced by cells that have not been genetically engineered and specifically contemplates various polypeptides arising from post-translational modifications of the polypeptide including, but not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation and acylation.

The term "translated protein coding portion" means a sequence which encodes for the full length protein which may include any leader sequence or any processing sequence.

The term "mature protein coding sequence" means a sequence which encodes a peptide or protein without a signal or leader sequence. The "mature protein portion" means that portion of the protein which does not include a signal or leader sequence. The peptide may have been produced by processing in the cell which removes any leader/signal sequence. The mature protein portion may or may not include the initial methionine residue. The methionine residue may be removed from the protein during processing in the cell. The peptide may be produced synthetically or the protein may have been produced using a polynucleotide only encoding for the mature protein coding sequence.

The term "derivative" refers to polypeptides chemically modified by such techniques as ubiquitination, labeling (e.g., with radionuclides or various enzymes), covalent polymer attachment such as pegylation (derivatization with polyethylene glycol)

and insertion or substitution by chemical synthesis of amino acids such as ornithine, which do not normally occur in human proteins.

The term "variant"(or "analog") refers to any polypeptide differing from naturally occurring polypeptides by amino acid insertions, deletions, and substitutions, created using, *e g.*, recombinant DNA techniques. Guidance in determining which amino acid residues may be replaced, added or deleted without abolishing activities of interest, may be found by comparing the sequence of the particular polypeptide with that of homologous peptides and minimizing the number of amino acid sequence changes made in regions of high homology (conserved regions) or by replacing amino acids with consensus sequence.

Alternatively, recombinant variants encoding these same or similar polypeptides may be synthesized or selected by making use of the "redundancy" in the genetic code. Various codon substitutions, such as the silent changes which produce various restriction sites, may be introduced to optimize cloning into a plasmid or viral vector or expression in a particular prokaryotic or eukaryotic system. Mutations in the polynucleotide sequence may be reflected in the polypeptide or domains of other peptides added to the polypeptide to modify the properties of any part of the polypeptide, to change characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate.

Preferably, amino acid "substitutions" are the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, *i.e.*, conservative amino acid replacements. "Conservative" amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved. For example, nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; positively charged (basic) amino acids include arginine, lysine, and histidine; and negatively charged (acidic) amino acids include aspartic acid and glutamic acid. "Insertions" or "deletions" are preferably in the range of about 1 to 20 amino acids, more preferably 1 to 10 amino acids. The variation allowed may be experimentally determined by systematically making insertions,

deletions, or substitutions of amino acids in a polypeptide molecule using recombinant DNA techniques and assaying the resulting recombinant variants for activity.

Alternatively, where alteration of function is desired, insertions, deletions or non-conservative alterations can be engineered to produce altered polypeptides. Such alterations can, for example, alter one or more of the biological functions or biochemical characteristics of the polypeptides of the invention. For example, such alterations may change polypeptide characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate. Further, such alterations can be selected so as to generate polypeptides that are better suited for expression, scale up and the like in the host cells chosen for expression. For example, cysteine residues can be deleted or substituted with another amino acid residue in order to eliminate disulfide bridges.

The terms "purified" or "substantially purified" as used herein denotes that the indicated nucleic acid or polypeptide is present in the substantial absence of other biological macromolecules, *e.g.*, polynucleotides, proteins, and the like. In one embodiment, the polynucleotide or polypeptide is purified such that it constitutes at least 95% by weight, more preferably at least 99% by weight, of the indicated biological macromolecules present (but water, buffers, and other small molecules, especially molecules having a molecular weight of less than 1000 daltons, can be present).

The term "isolated" as used herein refers to a nucleic acid or polypeptide separated from at least one other component (*e.g.*, nucleic acid or polypeptide) present with the nucleic acid or polypeptide in its natural source. In one embodiment, the nucleic acid or polypeptide is found in the presence of (if anything) only a solvent, buffer, ion, or other component normally present in a solution of the same. The terms "isolated" and "purified" do not encompass nucleic acids or polypeptides present in their natural source.

The term "recombinant," when used herein to refer to a polypeptide or protein, means that a polypeptide or protein is derived from recombinant (*e.g.*, microbial, insect, or mammalian) expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (*e.g.*, yeast) expression systems. As a product, "recombinant microbial" defines a polypeptide or protein essentially free of native endogenous substances and unaccompanied by associated native glycosylation. Polypeptides or proteins expressed in most bacterial cultures, *e.g.*, *E. coli*, will be free of

glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern in general different from those expressed in mammalian cells.

The term "recombinant expression vehicle or vector" refers to a plasmid or phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence. An expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers, (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate transcription initiation and termination sequences. Structural units intended for use in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include an amino terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

The term "recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit extrachromosomally. Recombinant expression systems as defined herein will express heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed. This term also means host cells which have stably integrated a recombinant genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers. Recombinant expression systems as defined herein will express polypeptides or proteins endogenous to the cell upon induction of the regulatory elements linked to the endogenous DNA segment or gene to be expressed. The cells can be prokaryotic or eukaryotic.

The term "secreted" includes a protein that is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence when it is expressed in a suitable host cell. "Secreted" proteins include without limitation proteins secreted wholly (*e.g.*, soluble proteins) or partially (*e.g.*, receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins that are transported across the membrane of the endoplasmic reticulum. "Secreted"

proteins are also intended to include proteins containing non-typical signal sequences (e.g. Interleukin-1 Beta, see Krasney, P.A. and Young, P.R. (1992) Cytokine 4(2):134-143) and factors released from damaged cells (e.g. Interleukin-1 Receptor Antagonist, see Arend, W.P. et. al. (1998) Annu. Rev. Immunol. 16:27-55)

5 Where desired, an expression vector may be designed to contain a "signal or leader sequence" which will direct the polypeptide through the membrane of a cell. Such a sequence may be naturally present on the polypeptides of the present invention or provided from heterologous protein sources by recombinant DNA techniques.

10 The term "stringent" is used to refer to conditions that are commonly understood in the art as stringent. Stringent conditions can include highly stringent conditions (i.e., hybridization to filter-bound DNA in 0.5 M NaHPO₄, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65°C, and washing in 0.1X SSC/0.1% SDS at 68°C), and moderately stringent conditions (i.e., washing in 0.2X SSC/0.1% SDS at 42°C). Other exemplary hybridization conditions are described herein in the examples.

15 In instances of hybridization of deoxyoligonucleotides, additional exemplary stringent hybridization conditions include washing in 6X SSC/0.05% sodium pyrophosphate at 37°C (for 14-base oligonucleotides), 48°C (for 17-base oligos), 55°C (for 20-base oligonucleotides), and 60°C (for 23-base oligonucleotides).

20 As used herein, "substantially equivalent" can refer both to nucleotide and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which does not result in an adverse functional dissimilarity between the reference and subject sequences.

Typically, such a substantially equivalent sequence varies from one of those listed herein by no more than about 35% (i.e., the number of individual residue substitutions, additions, and/or deletions in a substantially equivalent sequence, as compared to the corresponding reference sequence, divided by the total number of residues in the substantially equivalent sequence is about 0.35 or less). Such a sequence is said to have 65% sequence identity to the listed sequence. In one embodiment, a substantially equivalent, e.g., mutant, sequence of the invention varies from a listed sequence by no more than 30% (70% sequence identity); in a variation of this embodiment, by no more than 25% (75% sequence identity); and in a further variation of this embodiment, by no

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more than 20% (80% sequence identity) and in a further variation of this embodiment, by no more than 10% (90% sequence identity) and in a further variation of this embodiment, by no more than 5% (95% sequence identity). Substantially equivalent, *e.g.*, mutant, amino acid sequences according to the invention preferably have at least 80% sequence identity with a listed amino acid sequence, more preferably at least 90% sequence identity. Substantially equivalent nucleotide sequences of the invention can have lower percent sequence identities, taking into account, for example, the redundancy or degeneracy of the genetic code. Preferably, nucleotide sequence has at least about 65% identity, more preferably at least about 75% identity, and most preferably at least about 95% identity. For the purposes of the present invention, sequences having substantially equivalent biological activity and substantially equivalent expression characteristics are considered substantially equivalent. For the purposes of determining equivalence, truncation of the mature sequence (*e.g.*, via a mutation which creates a spurious stop codon) should be disregarded. Sequence identity may be determined, *e.g.*, using the Jotun Hein method (Hein, J. (1990) *Methods Enzymol.* 183:626-645). Identity between sequences can also be determined by other methods known in the art, *e.g.* by varying hybridization conditions.

The term "totipotent" refers to the capability of a cell to differentiate into all of the cell types of an adult organism.

The term "transformation" means introducing DNA into a suitable host cell so that the DNA is replicable, either as an extrachromosomal element, or by chromosomal integration. The term "transfection" refers to the taking up of an expression vector by a suitable host cell, whether or not any coding sequences are in fact expressed. The term "infection" refers to the introduction of nucleic acids into a suitable host cell by use of a virus or viral vector.

As used herein, an "uptake modulating fragment," UMF, means a series of nucleotides which mediate the uptake of a linked DNA fragment into a cell. UMFs can be readily identified using known UMFs as a target sequence or target motif with the computer-based systems described below. The presence and activity of a UMF can be confirmed by attaching the suspected UMF to a marker sequence. The resulting nucleic acid molecule is then incubated with an appropriate host under appropriate conditions and

the uptake of the marker sequence is determined. As described above, a UMF will increase the frequency of uptake of a linked marker sequence.

Each of the above terms is meant to encompass all that is described for each, unless the context dictates otherwise.

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3.2 NUCLEIC ACIDS OF THE INVENTION

Nucleotide sequences of the invention are set forth in the Sequence Listing.

10 The isolated polynucleotides of the invention include a polynucleotide comprising the nucleotide sequences of SEQ ID NO: 1 – 362; a polynucleotide encoding any one of the peptide sequences of SEQ ID NO:1 – 362; and a polynucleotide comprising the nucleotide sequence encoding the mature protein coding sequence of the polynucleotides of any one of SEQ ID NO: 1 - 362. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent conditions to (a) the complement of any of the nucleotides sequences of SEQ ID NO: 1 – 362; (b) 15 nucleotide sequences encoding any one of the amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotide recited above; (d) a polynucleotide which encodes a species homolog of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of the polypeptides of SEQ ID NO: 1- 362. Domains of 20 interest may depend on the nature of the encoded polypeptide; e.g., domains in receptor-like polypeptides include ligand-binding, extracellular, transmembrane, or cytoplasmic domains, or combinations thereof; domains in immunoglobulin-like proteins include the variable immunoglobulin-like domains; domains in enzyme-like polypeptides include catalytic and substrate binding domains; and domains in ligand polypeptides include 25 receptor-binding domains.

The polynucleotides of the invention include naturally occurring or wholly or partially synthetic DNA, e.g., cDNA and genomic DNA, and RNA, e.g., mRNA. The polynucleotides may include all of the coding region of the cDNA or may represent a portion of the coding region of the cDNA.

30 The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known

methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. Further 5' and 3' sequence can be obtained using methods known in the art. For example, full length cDNA or genomic DNA that corresponds to any of the polynucleotides of SEQ ID NO: 1 - 362 can be obtained by screening appropriate cDNA or genomic DNA libraries under suitable hybridization conditions using any of the polynucleotides of SEQ ID NO: 1 - 362 or a portion thereof as a probe. Alternatively, the polynucleotides of SEQ ID NO: 1 - 362 may be used as the basis for suitable primer(s) that allow identification and/or amplification of genes in appropriate genomic DNA or cDNA libraries.

The nucleic acid sequences of the invention can be assembled from ESTs and sequences (including cDNA and genomic sequences) obtained from one or more public databases, such as dbEST, gbpr, and UniGene. The EST sequences can provide identifying sequence information, representative fragment or segment information, or novel segment information for the full-length gene.

The polynucleotides of the invention also provide polynucleotides including nucleotide sequences that are substantially equivalent to the polynucleotides recited above. Polynucleotides according to the invention can have, *e.g.*, at least about 65%, at least about 70%, at least about 75%, at least about 80%, more typically at least about 90%, and even more typically at least about 95%, sequence identity to a polynucleotide recited above.

Included within the scope of the nucleic acid sequences of the invention are nucleic acid sequence fragments that hybridize under stringent conditions to any of the nucleotide sequences of SEQ ID NO: 1 - 362, or complements thereof, which fragment is greater than about 5 nucleotides, preferably 7 nucleotides, more preferably greater than 9 nucleotides and most preferably greater than 17 nucleotides. Fragments of, *e.g.* 15, 17, or 20 nucleotides or more that are selective for (*i.e.* specifically hybridize to any one of the polynucleotides of the invention) are contemplated. Probes capable of specifically hybridizing to a polynucleotide can differentiate polynucleotide sequences of the invention from other polynucleotide sequences in the same family of genes or can

differentiate human genes from genes of other species, and are preferably based on unique nucleotide sequences.

The sequences falling within the scope of the present invention are not limited to these specific sequences, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequence provided in SEQ ID NO: 1 - 362, a representative fragment thereof, or a nucleotide sequence at least 90% identical, preferably 95% identical, to SEQ ID NOs: 1 - 362 with a sequence from another isolate of the same species. Furthermore, to accommodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the specific ORFs disclosed herein. In other words, in the coding region of an ORF, substitution of one codon for another codon that encodes the same amino acid is expressly contemplated.

The nearest neighbor or homology result for the nucleic acids of the present invention, including SEQ ID NOs: 1 - 362, can be obtained by searching a database using an algorithm or a program. Preferably, a BLAST which stands for Basic Local Alignment Search Tool is used to search for local sequence alignments (Altshul, S.F. J Mol. Evol. 36 290-300 (1993) and Altschul S.F. et al. J. Mol. Biol. 21:403-410 (1990)). Alternatively a FASTA version 3 search against Genpept, using Fastxy algorithm.

Species homologs (or orthologs) of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the polynucleotides.

The nucleic acid sequences of the invention are further directed to sequences which encode variants of the described nucleic acids. These amino acid sequence variants may be prepared by methods known in the art by introducing appropriate nucleotide changes into a native or variant polynucleotide. There are two variables in the construction of amino acid sequence variants: the location of the mutation and the nature of the mutation. Nucleic acids encoding the amino acid sequence variants are preferably

constructed by mutating the polynucleotide to encode an amino acid sequence that does not occur in nature. These nucleic acid alterations can be made at sites that differ in the nucleic acids from different species (variable positions) or in highly conserved regions (constant regions). Sites at such locations will typically be modified in series, *e.g.*, by substituting first with conservative choices (*e.g.*, hydrophobic amino acid to a different hydrophobic amino acid) and then with more distant choices (*e.g.*, hydrophobic amino acid to a charged amino acid), and then deletions or insertions may be made at the target site. Amino acid sequence deletions generally range from about 1 to 30 residues, preferably about 1 to 10 residues, and are typically contiguous. Amino acid insertions include amino- and/or carboxyl-terminal fusions ranging in length from one to one hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. Intrasequence insertions may range generally from about 1 to 10 amino residues, preferably from 1 to 5 residues. Examples of terminal insertions include the heterologous signal sequences necessary for secretion or for intracellular targeting in different host cells and sequences such as FLAG or poly-histidine sequences useful for purifying the expressed protein.

In a preferred method, polynucleotides encoding the novel amino acid sequences are changed via site-directed mutagenesis. This method uses oligonucleotide sequences to alter a polynucleotide to encode the desired amino acid variant, as well as sufficient adjacent nucleotides on both sides of the changed amino acid to form a stable duplex on either side of the site of being changed. In general, the techniques of site-directed mutagenesis are well known to those of skill in the art and this technique is exemplified by publications such as, Edelman et al., *DNA* 2:183 (1983). A versatile and efficient method for producing site-specific changes in a polynucleotide sequence was published by Zoller and Smith, *Nucleic Acids Res.* 10:6487-6500 (1982). PCR may also be used to create amino acid sequence variants of the novel nucleic acids. When small amounts of template DNA are used as starting material, primer(s) that differs slightly in sequence from the corresponding region in the template DNA can generate the desired amino acid variant. PCR amplification results in a population of product DNA fragments that differ from the polynucleotide template encoding the polypeptide at the position specified by

the primer. The product DNA fragments replace the corresponding region in the plasmid and this gives a polynucleotide encoding the desired amino acid variant.

A further technique for generating amino acid variants is the cassette mutagenesis technique described in Wells et al., *Gene* 34:315 (1985); and other mutagenesis

5 techniques well known in the art, such as, for example, the techniques in Sambrook et al., supra, and *Current Protocols in Molecular Biology*, Ausubel et al. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be used in the practice of the invention for the cloning and expression of these novel nucleic acids. Such DNA
10 sequences include those which are capable of hybridizing to the appropriate novel nucleic acid sequence under stringent conditions.

Polynucleotides encoding preferred polypeptide truncations of the invention can be used to generate polynucleotides encoding chimeric or fusion proteins comprising one or more domains of the invention and heterologous protein sequences.

15 The polynucleotides of the invention additionally include the complement of any of the polynucleotides recited above. The polynucleotide can be DNA (genomic, cDNA, amplified, or synthetic) or RNA. Methods and algorithms for obtaining such polynucleotides are well known to those of skill in the art and can include, for example, methods for determining hybridization conditions that can routinely isolate
20 polynucleotides of the desired sequence identities.

In accordance with the invention, polynucleotide sequences comprising the mature protein coding sequences corresponding to any one of SEQ ID NO: 1-362, or functional equivalents thereof, may be used to generate recombinant DNA molecules that direct the expression of that nucleic acid, or a functional equivalent thereof, in
25 appropriate host cells. Also included are the cDNA inserts of any of the clones identified herein.

A polynucleotide according to the invention can be joined to any of a variety of other nucleotide sequences by well-established recombinant DNA techniques (see Sambrook J et al. (1989) *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor
30 Laboratory, NY). Useful nucleotide sequences for joining to polynucleotides include an assortment of vectors, e.g., plasmids, cosmids, lambda phage derivatives, phagemids, and

the like, that are well known in the art. Accordingly, the invention also provides a vector including a polynucleotide of the invention and a host cell containing the polynucleotide. In general, the vector contains an origin of replication functional in at least one organism, convenient restriction endonuclease sites, and a selectable marker for the host cell.

- 5 Vectors according to the invention include expression vectors, replication vectors, probe generation vectors, and sequencing vectors. A host cell according to the invention can be a prokaryotic or eukaryotic cell and can be a unicellular organism or part of a multicellular organism.

The present invention further provides recombinant constructs comprising a
10 nucleic acid having any of the nucleotide sequences of SEQ ID NOs: 1 - 362 or a fragment thereof or any other polynucleotides of the invention. In one embodiment, the recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a nucleic acid having any of the nucleotide sequences of SEQ ID NOs: 1 - 362 or a fragment thereof is inserted, in a forward or reverse orientation. In the
15 case of a vector comprising one of the ORFs of the present invention, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the ORF. Large numbers of suitable vectors and promoters are known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following vectors are provided by way of
20 example. Bacterial: pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia). Eukaryotic: pWLneo, pSV2cat, pOG44, PXTI, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia).

The isolated polynucleotide of the invention may be operably linked to an
25 expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman et al., *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods in Enzymology* 185, 537-566 (1990). As defined herein
30 "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the

protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

Promoter regions can be selected from any desired gene using CAT

(chloramphenicol transferase) vectors or other vectors with selectable markers. Two

5 appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda PR, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art. Generally, recombinant expression vectors will

10 include origins of replication and selectable markers permitting transformation of the host cell, *e.g.*, the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), a-factor, acid phosphatase, or heat

15 shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an amino terminal identification peptide imparting desired

20 characteristics, *e.g.*, stabilization or simplified purification of expressed recombinant product. Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or more phenotypic selectable markers and an origin of

25 replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may also be employed as a matter of choice.

30 As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived

from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (Promega Biotech, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced or derepressed by appropriate means (*e.g.*, temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Polynucleotides of the invention can also be used to induce immune responses. For example, as described in Fan et al., *Nat. Biotech.* 17:870-872 (1999), incorporated herein by reference, nucleic acid sequences encoding a polypeptide may be used to generate antibodies against the encoded polypeptide following topical administration of naked plasmid DNA or following injection, and preferably intramuscular injection of the DNA. The nucleic acid sequences are preferably inserted in a recombinant expression vector and may be in the form of naked DNA.

3.3 HOSTS

The present invention further provides host cells genetically engineered to contain the polynucleotides of the invention. For example, such host cells may contain nucleic acids of the invention introduced into the host cell using known transformation, transfection or infection methods. The present invention still further provides host cells genetically engineered to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell.

Knowledge of nucleic acid sequences allows for modification of cells to permit, or increase, expression of endogenous polypeptide. Cells can be modified (*e.g.*, by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the polypeptide at higher levels. The heterologous

promoter is inserted in such a manner that it is operatively linked to the encoding sequences. See, for example, PCT International Publication No. WO94/12650, PCT International Publication No. WO92/20808, and PCT International Publication No. WO91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., *ada*, *dhfr*, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected by calcium phosphate transfection, DEAE, dextran mediated transfection, or electroporation (Davis, L. et al., *Basic Methods in Molecular Biology* (1986)). The host cells containing one of the polynucleotides of the invention, can be used in conventional manners to produce the gene product encoded by the isolated fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF.

Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, Cv-1 cell, COS cells, 293 cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or protein at low natural level. Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, et al., in *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7

lines of monkey kidney fibroblasts, described by Gluzman, Cell 23:175 (1981). Other cell lines capable of expressing a compatible vector are, for example, the C127, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed
5 primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking
10 nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements. Recombinant polypeptides and proteins produced in bacterial culture are usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion
15 chromatography steps. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

20 Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or insects or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella*
25 *typhimurium*, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

30 In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the

invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequence include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the host cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this

purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No.

5 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

10 3.4 POLYPEPTIDES OF THE INVENTION

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising: the amino acid sequences set forth as any one of SEQ ID NO: 1-362 or an amino acid sequence encoded by any one of the nucleotide sequences SEQ ID NOs: 1 - 362 or the corresponding full length or mature protein. Polypeptides of the
15 invention also include polypeptides preferably with biological or immunological activity that are encoded by: (a) a polynucleotide having any one of the nucleotide sequences set forth in SEQ ID NOs: 1 – 362 or (b) polynucleotides encoding any one of the amino acid sequences set forth as SEQ ID NO: 1-362 or (c) polynucleotides that hybridize to the complement of the polynucleotides of either (a) or (b) under stringent hybridization
20 conditions. The invention also provides biologically active or immunologically active variants of any of the amino acid sequences set forth as SEQ ID NO: 1-362 or the corresponding full length or mature protein; and “substantial equivalents” thereof (e.g., with at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, typically at least about 95%, more typically at least
25 about 98%, or most typically at least about 99% amino acid identity) that retain biological activity. Polypeptides encoded by allelic variants may have a similar, increased, or decreased activity compared to polypeptides comprising SEQ ID NO: 1-362.

Fragments of the proteins of the present invention which are capable of exhibiting
30 biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for

example, as described in H. U. Saragovi, et al., Bio/Technology 10, 773-778 (1992) and in R. S. McDowell, et al., J. Amer. Chem. Soc. 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites.

The present invention also provides both full-length and mature forms (for example, without a signal sequence or precursor sequence) of the disclosed proteins. The protein coding sequence is identified in the sequence listing by translation of the disclosed nucleotide sequences. The mature form of such protein may be obtained by expression of a full-length polynucleotide in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein is also determinable from the amino acid sequence of the full-length form. Where proteins of the present invention are membrane bound, soluble forms of the proteins are also provided. In such forms, part or all of the regions causing the proteins to be membrane bound are deleted so that the proteins are fully secreted from the cell in which they are expressed.

Protein compositions of the present invention may further comprise an acceptable carrier, such as a hydrophilic, *e.g.*, pharmaceutically acceptable, carrier.

The present invention further provides isolated polypeptides encoded by the nucleic acid fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments which differ from a nucleic acid fragment of the present invention (*e.g.*, an ORF) by nucleotide sequence but, due to the degeneracy of the genetic code, encode an identical polypeptide sequence. Preferred nucleic acid fragments of the present invention are the ORFs that encode proteins.

A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. This technique is particularly useful in producing small peptides and fragments

of larger polypeptides. Fragments are useful, for example, in generating antibodies against the native polypeptide. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

5 The polypeptides and proteins of the present invention can alternatively be purified from cells which have been altered to express the desired polypeptide or protein. As used herein, a cell is said to be altered to express a desired polypeptide or protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein which it normally does not produce or which the cell normally produces at a lower level.

10 One skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic sequences into eukaryotic or prokaryotic cells in order to generate a cell which produces one of the polypeptides or proteins of the present invention.

 The invention also relates to methods for producing a polypeptide comprising
15 growing a culture of host cells of the invention in a suitable culture medium, and purifying the protein from the cells or the culture in which the cells are grown. For example, the methods of the invention include a process for producing a polypeptide in which a host cell containing a suitable expression vector that includes a polynucleotide of the invention is cultured under conditions that allow expression of the encoded
20 polypeptide. The polypeptide can be recovered from the culture, conveniently from the culture medium, or from a lysate prepared from the host cells and further purified. Preferred embodiments include those in which the protein produced by such process is a full length or mature form of the protein.

 In an alternative method, the polypeptide or protein is purified from bacterial
25 cells which naturally produce the polypeptide or protein. One skilled in the art can readily follow known methods for isolating polypeptides and proteins in order to obtain one of the isolated polypeptides or proteins of the present invention. These include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography, and immuno-affinity chromatography. See, *e.g.*, Scopes,
30 *Protein Purification: Principles and Practice*, Springer-Verlag (1994); Sambrook, et al., in *Molecular Cloning: A Laboratory Manual*; Ausubel et al., *Current Protocols in*

Molecular Biology. Polypeptide fragments that retain biological/immunological activity include fragments comprising greater than about 100 amino acids, or greater than about 200 amino acids, and fragments that encode specific protein domains.

The purified polypeptides can be used in *in vitro* binding assays which are well known in the art to identify molecules which bind to the polypeptides. These molecules include but are not limited to, for e.g., small molecules, molecules from combinatorial libraries, antibodies or other proteins. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

In addition, the peptides of the invention or molecules capable of binding to the peptides may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for SEQ ID NO: 1-362.

The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications, in the peptide or DNA sequence, can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Pat. No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein. Regions of the protein that are important for the protein function can be determined by various methods known in

the art including the alanine-scanning method which involved systematic substitution of single or strings of amino acids with alanine, followed by testing the resulting alanine-containing variant for biological activity. This type of analysis determines the importance of the substituted amino acid(s) in biological activity. Regions of the protein that are important for protein function may be determined by the eMATRIX program.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and are useful for screening or other immunological methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are encompassed by the present invention.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *e.g.*, Invitrogen, San Diego, Calif., U.S.A. (the MaxBat™ kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (*i.e.*, from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl™ or Cibacrom blue 3GA Sepharose™; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin

(TRX), or as a His tag. Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, Mass.), Pharmacia (Piscataway, N.J.) and Invitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope.

- 5 One such epitope ("FLAG®") is commercially available from Kodak (New Haven, Conn.).

Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, *e.g.*, silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or
10 all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The polypeptides of the invention include analogs (variants). This embraces
15 fragments, as well as peptides in which one or more amino acids has been deleted, inserted, or substituted. Also, analogs of the polypeptides of the invention embrace fusions of the polypeptides or modifications of the polypeptides of the invention, wherein the polypeptide or analog is fused to another moiety or moieties, *e.g.*, targeting moiety or another therapeutic agent. Such analogs may exhibit improved properties such as activity
20 and/or stability. Examples of moieties which may be fused to the polypeptide or an analog include, for example, targeting moieties which provide for the delivery of polypeptide to pancreatic cells, *e.g.*, antibodies to pancreatic cells, antibodies to immune cells such as T-cells, monocytes, dendritic cells, granulocytes, etc., as well as receptor and ligands expressed on pancreatic or immune cells. Other moieties which may be
25 fused to the polypeptide include therapeutic agents which are used for treatment, for example, immunosuppressive drugs such as cyclosporin, SK506, azathioprine, CD3 antibodies and steroids. Also, polypeptides may be fused to immune modulators, and other cytokines such as alpha or beta interferon.

30 **3.4.1 DETERMINING POLYPEPTIDE AND POLYNUCLEOTIDE IDENTITY AND SIMILARITY**

Preferred identity and/or similarity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in computer programs including, but are not limited to, the GCG program package, including GAP (Devereux, J., et al., Nucleic Acids Research 12(1):387 (1984); Genetics Computer Group, University of Wisconsin, Madison, WI), BLASTP, BLASTN, BLASTX, FASTA (Altschul, S.F. et al., J. Molec. Biol. 215:403-410 (1990), PSI-BLAST (Altschul S.F. et al., Nucleic Acids Res. vol. 25, pp. 3389-3402, herein incorporated by reference), eMatrix software (Wu et al., J. Comp. Biol., Vol. 6, pp. 219-235 (1999), herein incorporated by reference), eMotif software (Nevill-Manning et al, ISMB-97, Vol. 4, pp. 202-209, herein incorporated by reference), pFam software (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1), pp. 320-322 (1998), herein incorporated by reference) and the Kyte-Doolittle hydrophobicity prediction algorithm (J. Mol Biol, 157, pp. 105-31 (1982), incorporated herein by reference). The BLAST programs are publicly available from the National Center for Biotechnology Information (NCBI) and other sources (BLAST Manual, Altschul, S., et al. NCB NLM NIH Bethesda, MD 20894; Altschul, S., et al., J. Mol. Biol. 215:403-410 (1990).

3.5 GENE THERAPY

Mutations in the polynucleotides of the invention gene may result in loss of normal function of the encoded protein. The invention thus provides gene therapy to restore normal activity of the polypeptides of the invention; or to treat disease states involving polypeptides of the invention. Delivery of a functional gene encoding polypeptides of the invention to appropriate cells is effected *ex vivo*, *in situ*, or *in vivo* by use of vectors, and more particularly viral vectors (e.g., adenovirus, adeno-associated virus, or a retrovirus), or *ex vivo* by use of physical DNA transfer methods (e.g., liposomes or chemical treatments). See, for example, Anderson, Nature, supplement to vol. 392, no. 6679, pp.25-20 (1998). For additional reviews of gene therapy technology see Friedmann, Science, 244: 1275-1281 (1989); Verma, Scientific American: 68-84 (1990); and Miller, Nature, 357: 455-460 (1992). Introduction of any one of the nucleotides of the present invention or a gene encoding the polypeptides of the present invention can also be accomplished with extrachromosomal substrates (transient

expression) or artificial chromosomes (stable expression). Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes. Alternatively, it is contemplated that in other human

5 disease states, preventing the expression of or inhibiting the activity of polypeptides of the invention will be useful in treating the disease states. It is contemplated that antisense therapy or gene therapy could be applied to negatively regulate the expression of polypeptides of the invention.

Other methods inhibiting expression of a protein include the introduction of

10 antisense molecules to the nucleic acids of the present invention, their complements, or their translated RNA sequences, by methods known in the art. Further, the polypeptides of the present invention can be inhibited by using targeted deletion methods, or the insertion of a negative regulatory element such as a silencer, which is tissue specific.

The present invention still further provides cells genetically engineered *in vivo* to

15 express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell. These methods can be used to increase or decrease the expression of the polynucleotides of the present invention.

Knowledge of DNA sequences provided by the invention allows for modification of

20 cells to permit, increase, or decrease, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the protein at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the desired protein

25 encoding sequences. See, for example, PCT International Publication No. WO 94/12650, PCT International Publication No. WO 92/20808, and PCT International Publication No. WO 91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., *ada*, *dhfr*, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron

30 DNA may be inserted along with the heterologous promoter DNA. If linked to the desired

protein coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequences include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting

sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

5 The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by
10 reference herein in its entirety.

3.6 TRANSGENIC ANIMALS

In preferred methods to determine biological functions of the polypeptides of the invention in vivo, one or more genes provided by the invention are either over expressed
15 or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals,
20 preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals,
25 are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of a promoter of the polynucleotides of the invention is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using
30 homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased

protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

The polynucleotides of the present invention also make possible the development, through, e.g., homologous recombination or knock out strategies, of animals that fail to express polypeptides of the invention or that express a variant polypeptide. Such animals are useful as models for studying the *in vivo* activities of polypeptide as well as for studying modulators of the polypeptides of the invention.

In preferred methods to determine biological functions of the polypeptides of the invention *in vivo*, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of the polynucleotides of the invention promoter is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

3.7 USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified herein. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or of

5 polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA). The mechanism underlying the particular condition or pathology will dictate whether the polypeptides of the invention, the polynucleotides of the invention or modulators (activators or inhibitors) thereof would be beneficial to the subject in need of treatment. Thus, "therapeutic compositions of the
10 invention" include compositions comprising isolated polynucleotides (including recombinant DNA molecules, cloned genes and degenerate variants thereof) or polypeptides of the invention (including full length protein, mature protein and truncations or domains thereof), or compounds and other substances that modulate the overall activity of the target gene products, either at the level of target gene/protein
15 expression or target protein activity. Such modulators include polypeptides, analogs, (variants), including fragments and fusion proteins, antibodies and other binding proteins; chemical compounds that directly or indirectly activate or inhibit the polypeptides of the invention (identified, e.g., via drug screening assays as described herein); antisense polynucleotides and polynucleotides suitable for triple helix formation; and in particular
20 antibodies or other binding partners that specifically recognize one or more epitopes of the polypeptides of the invention.

The polypeptides of the present invention may likewise be involved in cellular activation or in one of the other physiological pathways described herein.

25 3.7.1 RESEARCH USES AND UTILITIES

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either
30 constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on gels; as chromosome markers or tags (when

labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The polypeptides provided by the present invention can similarly be used in assays to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding polypeptide is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E. F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology:

Guide to Molecular Cloning Techniques", Academic Press, Berger, S. L. and A. R. Kimmel eds., 1987.

3.7.2 NUTRITIONAL USES

Polynucleotides and polypeptides of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the polypeptide or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the polypeptide or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

3.7.3 CYTOKINE AND CELL PROLIFERATION/DIFFERENTIATION

ACTIVITY

A polypeptide of the present invention may exhibit activity relating to cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of therapeutic compositions of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+(preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e, CMK, HUVEC, and Caco. Therapeutic compositions of the invention can be used in the following:

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19;

Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., I. Immunol. 149:3778-3783, 1992; Bowman et al., I. Immunol. 152:1756-1761, 1994.

- 5 Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A. M. and Shevach, E. M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human interleukin- γ , Schreiber, R. D. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

- 15 Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L. S. and Lipsky, P. E. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6--Nordan, R. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Aced. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11--Bennett, F., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9--Ciarletta, A., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

- 25 Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function; Chapter
- 30

6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

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3.7.4 STEM CELL GROWTH FACTOR ACTIVITY

A polypeptide of the present invention may exhibit stem cell growth factor activity and be involved in the proliferation, differentiation and survival of pluripotent and totipotent stem cells including primordial germ cells, embryonic stem cells, hematopoietic stem cells and/or germ line stem cells. Administration of the polypeptide of the invention to stem cells *in vivo* or *ex vivo* is expected to maintain and expand cell populations in a totipotent or pluripotent state which would be useful for re-engineering damaged or diseased tissues, transplantation, manufacture of bio-pharmaceuticals and the development of bio-sensors. The ability to produce large quantities of human cells has important working applications for the production of human proteins which currently must be obtained from non-human sources or donors, implantation of cells to treat diseases such as Parkinson's, Alzheimer's and other neurodegenerative diseases; tissues for grafting such as bone marrow, skin, cartilage, tendons, bone, muscle (including cardiac muscle), blood vessels, cornea, neural cells, gastrointestinal cells and others; and organs for transplantation such as kidney, liver, pancreas (including islet cells), heart and lung.

It is contemplated that multiple different exogenous growth factors and/or cytokines may be administered in combination with the polypeptide of the invention to achieve the desired effect, including any of the growth factors listed herein, other stem cell maintenance factors, and specifically including stem cell factor (SCF), leukemia inhibitory factor (LIF), Flt-3 ligand (Flt-3L), any of the interleukins, recombinant soluble IL-6 receptor fused to IL-6, macrophage inflammatory protein 1-alpha (MIP-1-alpha), G-CSF, GM-CSF, thrombopoietin (TPO), platelet factor 4 (PF-4), platelet-derived growth factor (PDGF), neural growth factors and basic fibroblast growth factor (bFGF).

Since totipotent stem cells can give rise to virtually any mature cell type, expansion of these cells in culture will facilitate the production of large quantities of

specific differentiated cell type from undifferentiated stem cell populations involves the use of a cell-type specific promoter driving a selectable marker. The selectable marker allows only cells of the desired type to survive. For example, stem cells can be induced to differentiate into cardiomyocytes (Wobus et al., Differentiation, 48: 173-182, (1991); Klug et al., J. Clin. Invest., 98(1): 216-224, (1998)) or skeletal muscle cells (Browder, L. W. In: *Principles of Tissue Engineering* eds. Lanza et al., Academic Press (1997)).

Alternatively, directed differentiation of stem cells can be accomplished by culturing the stem cells in the presence of a differentiation factor such as retinoic acid and an antagonist of the polypeptide of the invention which would inhibit the effects of endogenous stem cell factor activity and allow differentiation to proceed.

In vitro cultures of stem cells can be used to determine if the polypeptide of the invention exhibits stem cell growth factor activity. Stem cells are isolated from any one of various cell sources (including hematopoietic stem cells and embryonic stem cells) and cultured on a feeder layer, as described by Thompson et al. Proc. Natl. Acad. Sci, U.S.A., 92: 7844-7848 (1995), in the presence of the polypeptide of the invention alone or in combination with other growth factors or cytokines. The ability of the polypeptide of the invention to induce stem cells proliferation is determined by colony formation on semi-solid support e.g. as described by Bernstein et al., Blood, 77: 2316-2321 (1991).

3.7.5 HEMATOPOIESIS REGULATING ACTIVITY

A polypeptide of the present invention may be involved in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell disorders. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation

of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

Therapeutic compositions of the invention can be used in the following:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M. G. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I. K. and Briddell, R. A. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R. E. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R. I.

Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Long term culture initiating cell assay, Sutherland, H. J. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

5 **3.7.6 TISSUE GROWTH ACTIVITY**

A polypeptide of the present invention also may be involved in bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as in wound healing and tissue repair and replacement, and in healing of burns, incisions and ulcers.

10 A polypeptide of the present invention which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Compositions of a polypeptide, antibody, binding partner, or other modulator of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an
15 osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

20 A polypeptide of this invention may also be involved in attracting bone-forming cells, stimulating growth of bone-forming cells, or inducing differentiation of progenitors of bone-forming cells. Treatment of osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes may also be possible using the composition of the invention.

25 Another category of tissue regeneration activity that may involve the polypeptide of the present invention is tendon/ligament formation. Induction of tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing
30 damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue.

De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The compositions of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a composition may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a composition of the invention.

Compositions of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

Compositions of the present invention may also be involved in the generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising

such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring may allow normal tissue to regenerate. A polypeptide of the present invention may also exhibit angiogenic activity.

A composition of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A composition of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

Therapeutic compositions of the invention can be used in the following:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, H. I. and Rovee, D. T., eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

3.7.7 IMMUNE STIMULATING OR SUPPRESSING ACTIVITY

A polypeptide of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A polynucleotide of the invention can encode a polypeptide exhibiting such activities. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpes

viruses, mycobacteria, *Leishmania* spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, proteins of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease.

Such a protein (or antagonists thereof, including antibodies) of the present invention may also to be useful in the treatment of allergic reactions and conditions (*e.g.*, anaphylaxis, serum sickness, drug reactions, food allergies, insect venom allergies, mastocytosis, allergic rhinitis, hypersensitivity pneumonitis, urticaria, angioedema, eczema, atopic dermatitis, allergic contact dermatitis, erythema multiforme, Stevens-Johnson syndrome, allergic conjunctivitis, atopic keratoconjunctivitis, venereal keratoconjunctivitis, giant papillary conjunctivitis and contact allergies), such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein (or antagonists thereof) of the present invention. The therapeutic effects of the polypeptides or antagonists thereof on allergic reactions can be evaluated by *in vivo* animals models such as the cumulative contact enhancement test (Lastbom et al., Toxicology 125: 59-66, 1998), skin prick test (Hoffmann et al., Allergy 54: 446-54, 1999), guinea pig skin sensitization test (Vohr et al., Arch. Toxicol. 73: 501-9), and murine local lymph node assay (Kimber et al., J. Toxicol. Environ. Health 53: 563-79).

Using the proteins of the invention it may also be possible to modulate immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both.

Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent.

Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a therapeutic composition of the invention may prevent cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, a lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular therapeutic compositions in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., *Science* 257:789-792 (1992) and Turka et al., *Proc. Natl. Acad. Sci USA*, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., *Fundamental Immunology*, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of therapeutic compositions of the invention on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms.

Administration of reagents which block stimulation of T cells can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythematosus in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., *Fundamental Immunology*, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (e.g., a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response may be useful in cases of viral infection, including systemic viral diseases such as influenza, the common cold, and encephalitis.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected

cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

A polypeptide of the present invention may provide the necessary stimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient mounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I alpha chain protein and β_2 microglobulin protein or an MHC class II alpha chain protein and an MHC class II beta chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., I. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bowman et al., J. Virology 61:1992-1998; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. *Immunol.* 144:3028-3033, 1990; and Assays for B cell function: In vitro antibody production, Mond, J. J. and Brunswick, M. In *Current Protocols in Immunology*. J. E. e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., *J. Immunol.* 137:3494-3500, 1986; Takai et al., *J. Immunol.* 140:508-512, 1988; Bertagnolli et al., *J. Immunol.* 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., *J. Immunol.* 134:536-544, 1995; Inaba et al., *Journal of Experimental Medicine* 173:549-559, 1991; Macatonia et al., *Journal of Immunology* 154:5071-5079, 1995; Porgador et al., *Journal of Experimental Medicine* 182:255-260, 1995; Nair et al., *Journal of Virology* 67:4062-4069, 1993; Huang et al., *Science* 264:961-965, 1994; Macatonia et al., *Journal of Experimental Medicine* 169:1255-1264, 1989; Bhardwaj et al., *Journal of Clinical Investigation* 94:797-807, 1994; and Inaba et al., *Journal of Experimental Medicine* 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., *Cytometry* 13:795-808, 1992; Gorczyca et al., *Leukemia* 7:659-670, 1993; Gorczyca et al., *Cancer Research* 53:1945-1951, 1993; Itoh et al., *Cell* 66:233-243, 1991; Zacharchuk, *Journal of Immunology* 145:4037-4045, 1990; Zamai et al., *Cytometry* 14:891-897, 1993; Gorczyca et al., *International Journal of Oncology* 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

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3.7.8 ACTIVIN/INHIBIN ACTIVITY

A polypeptide of the present invention may also exhibit activin- or inhibin-related activities. A polynucleotide of the invention may encode a polypeptide exhibiting such characteristics. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a polypeptide of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the polypeptide of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A polypeptide of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as, but not limited to, cows, sheep and pigs.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods.

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

3.7.9 CHEMOTACTIC/CHEMOKINETIC ACTIVITY

A polypeptide of the present invention may be involved in chemotactic or chemokinetic activity for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Chemotactic and chemokinetic receptor activation can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic compositions (e.g. proteins, antibodies, binding partners, or modulators of the invention) provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

Therapeutic compositions of the invention can be used in the following:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Marguiles, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25:1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153:1762-1768, 1994.

3.7.10 HEMOSTATIC AND THROMBOLYTIC ACTIVITY

A polypeptide of the invention may also be involved in hemostasis or thrombolysis or thrombosis. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Compositions may be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A composition of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

Therapeutic compositions of the invention can be used in the following:

Assays for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., *J. Clin. Pharmacol.* 26:131-140, 1986; Burdick et al., *Thrombosis Res.* 45:413-419, 1987; Humphrey et al., *Fibrinolysis* 5:71-79 (1991); Schaub, *Prostaglandins* 35:467-474, 1988.

3.7.11 CANCER DIAGNOSIS AND THERAPY

Polypeptides of the invention may be involved in cancer cell generation, proliferation or metastasis. Detection of the presence or amount of polynucleotides or polypeptides of the invention may be useful for the diagnosis and/or prognosis of one or more types of cancer. For example, the presence or increased expression of a polynucleotide/polypeptide of the invention may indicate a hereditary risk of cancer, a precancerous condition, or an ongoing malignancy. Conversely, a defect in the gene or absence of the polypeptide may be associated with a cancer condition. Identification of single nucleotide polymorphisms associated with cancer or a predisposition to cancer may also be useful for diagnosis or prognosis.

Cancer treatments promote tumor regression by inhibiting tumor cell proliferation, inhibiting angiogenesis (growth of new blood vessels that is necessary to support tumor growth) and/or prohibiting metastasis by reducing tumor cell motility or invasiveness. Therapeutic compositions of the invention may be effective in adult and pediatric oncology including in solid phase tumors/malignancies, locally advanced tumors, human soft tissue sarcomas, metastatic cancer, including lymphatic metastases,

blood cell malignancies including multiple myeloma, acute and chronic leukemias, and lymphomas, head and neck cancers including mouth cancer, larynx cancer and thyroid cancer, lung cancers including small cell carcinoma and non-small cell cancers, breast cancers including small cell carcinoma and ductal carcinoma, gastrointestinal cancers including esophageal cancer, stomach cancer, colon cancer, colorectal cancer and polyps associated with colorectal neoplasia, pancreatic cancers, liver cancer, urologic cancers including bladder cancer and prostate cancer, malignancies of the female genital tract including ovarian carcinoma, uterine (including endometrial) cancers, and solid tumor in the ovarian follicle, kidney cancers including renal cell carcinoma, brain cancers including intrinsic brain tumors, neuroblastoma, astrocytic brain tumors, gliomas, metastatic tumor cell invasion in the central nervous system, bone cancers including osteomas, skin cancers including malignant melanoma, tumor progression of human skin keratinocytes, squamous cell carcinoma, basal cell carcinoma, hemangiopericytoma and Kaposi's sarcoma.

Polypeptides, polynucleotides, or modulators of polypeptides of the invention (including inhibitors and stimulators of the biological activity of the polypeptide of the invention) may be administered to treat cancer. Therapeutic compositions can be administered in therapeutically effective dosages alone or in combination with adjuvant cancer therapy such as surgery, chemotherapy, radiotherapy, thermotherapy, and laser therapy, and may provide a beneficial effect, e.g. reducing tumor size, slowing rate of tumor growth, inhibiting metastasis, or otherwise improving overall clinical condition, without necessarily eradicating the cancer.

The composition can also be administered in therapeutically effective amounts as a portion of an anti-cancer cocktail. An anti-cancer cocktail is a mixture of the polypeptide or modulator of the invention with one or more anti-cancer drugs in addition to a pharmaceutically acceptable carrier for delivery. The use of anti-cancer cocktails as a cancer treatment is routine. Anti-cancer drugs that are well known in the art and can be used as a treatment in combination with the polypeptide or modulator of the invention include: Actinomycin D, Aminoglutethimide, Asparaginase, Bleomycin, Busulfan, Carboplatin, Carmustine, Chlorambucil, Cisplatin (cis-DDP), Cyclophosphamide, Cytarabine HCl (Cytosine arabinoside), Dacarbazine, Dactinomycin, Daunorubicin HCl,

Doxorubicin HCl, Estramustine phosphate sodium, Etoposide (V16-213), Floxuridine, 5-Fluorouracil (5-Fu), Flutamide, Hydroxyurea (hydroxycarbamide), Ifosfamide, Interferon Alpha-2a, Interferon Alpha-2b, Leuprolide acetate (LHRH-releasing factor analog), Lomustine, Mechlorethamine HCl (nitrogen mustard), Melphalan, Mercaptopurine, Mesna, Methotrexate (MTX), Mitomycin, Mitoxantrone HCl, Octreotide, Plicamycin, Procarbazine HCl, Streptozocin, Tamoxifen citrate, Thioguanine, Thiotepa, Vinblastine sulfate, Vincristine sulfate, Amsacrine, Azacitidine, Hexamethylmelamine, Interleukin-2, Mitoguazone, Pentostatin, Semustine, Teniposide, and Vindesine sulfate.

In addition, therapeutic compositions of the invention may be used for prophylactic treatment of cancer. There are hereditary conditions and/or environmental situations (e.g. exposure to carcinogens) known in the art that predispose an individual to developing cancers. Under these circumstances, it may be beneficial to treat these individuals with therapeutically effective doses of the polypeptide of the invention to reduce the risk of developing cancers.

In vitro models can be used to determine the effective doses of the polypeptide of the invention as a potential cancer treatment. These *in vitro* models include proliferation assays of cultured tumor cells, growth of cultured tumor cells in soft agar (see Freshney, (1987) Culture of Animal Cells: A Manual of Basic Technique, Wiley-Liss, New York, NY Ch 18 and Ch 21), tumor systems in nude mice as described in Giovanella et al., J. Natl. Can. Inst., 52: 921-30 (1974), mobility and invasive potential of tumor cells in Boyden Chamber assays as described in Pilkington et al., Anticancer Res., 17: 4107-9 (1997), and angiogenesis assays such as induction of vascularization of the chick chorioallantoic membrane or induction of vascular endothelial cell migration as described in Ribatta et al., Intl. J. Dev. Biol., 40: 1189-97 (1999) and Li et al., Clin. Exp. Metastasis, 17:423-9 (1999), respectively. Suitable tumor cells lines are available, e.g. from American Type Tissue Culture Collection catalogs.

3.7.12 RECEPTOR/LIGAND ACTIVITY

A polypeptide of the present invention may also demonstrate activity as receptor, receptor ligand or inhibitor or agonist of receptor/ligand interactions. A polynucleotide of the invention can encode a polypeptide exhibiting such characteristics. Examples of

such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and

5 receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses. Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of

10 receptor/ligand interactions.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek,

15 D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley- Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1- 7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al.,

20 Cell 80:661-670, 1995.

By way of example, the polypeptides of the invention may be used as a receptor for a ligand(s) thereby transmitting the biological activity of that ligand(s). Ligands may be identified through binding assays, affinity chromatography, dihybrid screening assays, BIAcore assays, gel overlay assays, or other methods known in the art.

25 Studies characterizing drugs or proteins as agonist or antagonist or partial agonists or a partial antagonist require the use of other proteins as competing ligands. The polypeptides of the present invention or ligand(s) thereof may be labeled by being coupled to radioisotopes, colorimetric molecules or a toxin molecules by conventional methods. ("Guide to Protein Purification" Murray P. Deutscher (ed) Methods in

30 Enzymology Vol. 182 (1990) Academic Press, Inc. San Diego). Examples of radioisotopes include, but are not limited to, tritium and carbon-14 . Examples of

colorimetric molecules include, but are not limited to, fluorescent molecules such as fluorescamine, or rhodamine or other colorimetric molecules. Examples of toxins include, but are not limited, to ricin.

5 **3.7.13 DRUG SCREENING**

This invention is particularly useful for screening chemical compounds by using the novel polypeptides or binding fragments thereof in any of a variety of drug screening techniques. The polypeptides or fragments employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface or located intracellularly. One
10 method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the polypeptide or a fragment thereof. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One
15 invention or fragments and the agent being tested or examine the diminution in complex formation between the novel polypeptides and an appropriate cell line, which are well known in the art.

Sources for test compounds that may be screened for ability to bind to or modulate (i.e., increase or decrease) the activity of polypeptides of the invention include
20 (1) inorganic and organic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of either random or mimetic peptides, oligonucleotides or organic molecules.

Chemical libraries may be readily synthesized or purchased from a number of commercial sources, and may include structural analogs of known compounds or
25 compounds that are identified as "hits" or "leads" via natural product screening.

The sources of natural product libraries are microorganisms (including bacteria and fungi), animals, plants or other vegetation, or marine organisms, and libraries of mixtures for screening may be created by: (1) fermentation and extraction of broths from soil, plant or marine microorganisms or (2) extraction of the organisms themselves.
30 Natural product libraries include polyketides, non-ribosomal peptides, and (non-naturally occurring) variants thereof. For a review, see *Science* 282:63-68 (1998).

Combinatorial libraries are composed of large numbers of peptides, oligonucleotides or organic compounds and can be readily prepared by traditional automated synthesis methods, PCR, cloning or proprietary synthetic methods. Of particular interest are peptide and oligonucleotide combinatorial libraries. Still other libraries of interest include peptide, protein, peptidomimetic, multiparallel synthetic collection, recombinatorial, and polypeptide libraries. For a review of combinatorial chemistry and libraries created therefrom, see Myers, *Curr. Opin. Biotechnol.* 8:701-707 (1997). For reviews and examples of peptidomimetic libraries, see Al-Obeidi et al., *Mol. Biotechnol.* 9(3):205-23 (1998); Hruby et al., *Curr Opin Chem Biol*, 1(1):114-19 (1997); Dorner et al., *Bioorg Med Chem*, 4(5):709-15 (1996) (alkylated dipeptides).

Identification of modulators through use of the various libraries described herein permits modification of the candidate "hit" (or "lead") to optimize the capacity of the "hit" to bind a polypeptide of the invention. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

The binding molecules thus identified may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells such as radioisotopes. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for a polypeptide of the invention. Alternatively, the binding molecules may be complexed with imaging agents for targeting and imaging purposes.

3.7.14 ASSAY FOR RECEPTOR ACTIVITY

The invention also provides methods to detect specific binding of a polypeptide e.g. a ligand or a receptor. The art provides numerous assays particularly useful for identifying previously unknown binding partners for receptor polypeptides of the invention. For example, expression cloning using mammalian or bacterial cells, or dihybrid screening assays can be used to identify polynucleotides encoding binding partners. As another example, affinity chromatography with the appropriate immobilized polypeptide of the invention can be used to isolate polypeptides that recognize and bind

polypeptides of the invention. There are a number of different libraries used for the identification of compounds, and in particular small molecules, that modulate (*i.e.*, increase or decrease) biological activity of a polypeptide of the invention. Ligands for receptor polypeptides of the invention can also be identified by adding exogenous ligands, or cocktails of ligands to two cells populations that are genetically identical except for the expression of the receptor of the invention: one cell population expresses the receptor of the invention whereas the other does not. The response of the two cell populations to the addition of ligands(s) are then compared. Alternatively, an expression library can be co-expressed with the polypeptide of the invention in cells and assayed for an autocrine response to identify potential ligand(s). As still another example, BIAcore assays, gel overlay assays, or other methods known in the art can be used to identify binding partner polypeptides, including, (1) organic and inorganic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of random peptides, oligonucleotides or organic molecules.

The role of downstream intracellular signaling molecules in the signaling cascade of the polypeptide of the invention can be determined. For example, a chimeric protein in which the cytoplasmic domain of the polypeptide of the invention is fused to the extracellular portion of a protein, whose ligand has been identified, is produced in a host cell. The cell is then incubated with the ligand specific for the extracellular portion of the chimeric protein, thereby activating the chimeric receptor. Known downstream proteins involved in intracellular signaling can then be assayed for expected modifications *i.e.* phosphorylation. Other methods known to those in the art can also be used to identify signaling molecules involved in receptor activity.

3.7.15 ANTI-INFLAMMATORY ACTIVITY

Compositions of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or

promote an inflammatory response. Compositions with such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation intimation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Compositions of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material. Compositions of this invention may be utilized to prevent or treat conditions such as, but not limited to, sepsis, acute pancreatitis, endotoxin shock, cytokine induced shock, rheumatoid arthritis, chronic inflammatory arthritis, pancreatic cell damage from diabetes mellitus type 1, graft versus host disease, inflammatory bowel disease, inflammation associated with pulmonary disease, other autoimmune disease or inflammatory disease, an antiproliferative agent such as for acute or chronic myelogenous leukemia or in the prevention of premature labor secondary to intrauterine infections.

3.7.16 LEUKEMIAS

Leukemias and related disorders may be treated or prevented by administration of a therapeutic that promotes or inhibits function of the polynucleotides and/or polypeptides of the invention. Such leukemias and related disorders include but are not limited to acute leukemia, acute lymphocytic leukemia, acute myelocytic leukemia, myeloblastic, promyelocytic, myelomonocytic, monocytic, erythroleukemia, chronic leukemia, chronic myelocytic (granulocytic) leukemia and chronic lymphocytic leukemia (for a review of such disorders, see Fishman et al., 1985, Medicine, 2d Ed., J.B. Lippincott Co., Philadelphia).

3.7.17 NERVOUS SYSTEM DISORDERS

Nervous system disorders, involving cell types which can be tested for efficacy of intervention with compounds that modulate the activity of the polynucleotides and/or polypeptides of the invention, and which can be treated upon thus observing an indication of therapeutic utility, include but are not limited to nervous system injuries, and diseases

or disorders which result in either a disconnection of axons, a diminution or degeneration of neurons, or demyelination. Nervous system lesions which may be treated in a patient (including human and non-human mammalian patients) according to the invention include but are not limited to the following lesions of either the central (including spinal cord, brain) or peripheral nervous systems:

(i) traumatic lesions, including lesions caused by physical injury or associated with surgery, for example, lesions which sever a portion of the nervous system, or compression injuries;

(ii) ischemic lesions, in which a lack of oxygen in a portion of the nervous system results in neuronal injury or death, including cerebral infarction or ischemia, or spinal cord infarction or ischemia;

(iii) infectious lesions, in which a portion of the nervous system is destroyed or injured as a result of infection, for example, by an abscess or associated with infection by human immunodeficiency virus, herpes zoster, or herpes simplex virus or with Lyme disease, tuberculosis, syphilis;

(iv) degenerative lesions, in which a portion of the nervous system is destroyed or injured as a result of a degenerative process including but not limited to degeneration associated with Parkinson's disease, Alzheimer's disease, Huntington's chorea, or amyotrophic lateral sclerosis;

(v) lesions associated with nutritional diseases or disorders, in which a portion of the nervous system is destroyed or injured by a nutritional disorder or disorder of metabolism including but not limited to, vitamin B12 deficiency, folic acid deficiency, Wernicke disease, tobacco-alcohol amblyopia, Marchiafava-Bignami disease (primary degeneration of the corpus callosum), and alcoholic cerebellar degeneration;

(vi) neurological lesions associated with systemic diseases including but not limited to diabetes (diabetic neuropathy, Bell's palsy), systemic lupus erythematosus, carcinoma, or sarcoidosis;

(vii) lesions caused by toxic substances including alcohol, lead, or particular neurotoxins; and

(viii) demyelinated lesions in which a portion of the nervous system is destroyed or injured by a demyelinating disease including but not limited to multiple

sclerosis, human immunodeficiency virus-associated myelopathy, transverse myelopathy or various etiologies, progressive multifocal leukoencephalopathy, and central pontine myelinolysis.

Therapeutics which are useful according to the invention for treatment of a nervous system disorder may be selected by testing for biological activity in promoting the survival or differentiation of neurons. For example, and not by way of limitation, therapeutics which elicit any of the following effects may be useful according to the invention:

- (i) increased survival time of neurons in culture;
- (ii) increased sprouting of neurons in culture or *in vivo*;
- (iii) increased production of a neuron-associated molecule in culture or *in vivo*, *e.g.*, choline acetyltransferase or acetylcholinesterase with respect to motor neurons; or
- (iv) decreased symptoms of neuron dysfunction *in vivo*.

Such effects may be measured by any method known in the art. In preferred, non-limiting embodiments, increased survival of neurons may be measured by the method set forth in Arakawa et al. (1990, J. Neurosci. 10:3507-3515); increased sprouting of neurons may be detected by methods set forth in Pestronk et al. (1980, Exp. Neurol. 70:65-82) or Brown et al. (1981, Ann. Rev. Neurosci. 4:17-42); increased production of neuron-associated molecules may be measured by bioassay, enzymatic assay, antibody binding, Northern blot assay, *etc.*, depending on the molecule to be measured; and motor neuron dysfunction may be measured by assessing the physical manifestation of motor neuron disorder, *e.g.*, weakness, motor neuron conduction velocity, or functional disability.

In specific embodiments, motor neuron disorders that may be treated according to the invention include but are not limited to disorders such as infarction, infection, exposure to toxin, trauma, surgical damage, degenerative disease or malignancy that may affect motor neurons as well as other components of the nervous system, as well as disorders that selectively affect neurons such as amyotrophic lateral sclerosis, and including but not limited to progressive spinal muscular atrophy, progressive bulbar palsy, primary lateral sclerosis, infantile and juvenile muscular atrophy, progressive

bulbar paralysis of childhood (Fazio-Londe syndrome), poliomyelitis and the post polio syndrome, and Hereditary Motorsensory Neuropathy (Charcot-Marie-Tooth Disease).

3.7.18 OTHER ACTIVITIES

5 A polypeptide of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue
10 pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, co-factors or other nutritional
15 factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case
20 of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is
25 cross-reactive with such protein.

3.7.19 IDENTIFICATION OF POLYMORPHISMS

The demonstration of polymorphisms makes possible the identification of such polymorphisms in human subjects and the pharmacogenetic use of this information for
30 diagnosis and treatment. Such polymorphisms may be associated with, e.g., differential predisposition or susceptibility to various disease states (such as disorders involving

inflammation or immune response) or a differential response to drug administration, and this genetic information can be used to tailor preventive or therapeutic treatment appropriately. For example, the existence of a polymorphism associated with a predisposition to inflammation or autoimmune disease makes possible the diagnosis of this condition in humans by identifying the presence of the polymorphism.

Polymorphisms can be identified in a variety of ways known in the art which all generally involve obtaining a sample from a patient, analyzing DNA from the sample, optionally involving isolation or amplification of the DNA, and identifying the presence of the polymorphism in the DNA. For example, PCR may be used to amplify an appropriate fragment of genomic DNA which may then be sequenced. Alternatively, the DNA may be subjected to allele-specific oligonucleotide hybridization (in which appropriate oligonucleotides are hybridized to the DNA under conditions permitting detection of a single base mismatch) or to a single nucleotide extension assay (in which an oligonucleotide that hybridizes immediately adjacent to the position of the polymorphism is extended with one or more labeled nucleotides). In addition, traditional restriction fragment length polymorphism analysis (using restriction enzymes that provide differential digestion of the genomic DNA depending on the presence or absence of the polymorphism) may be performed. Arrays with nucleotide sequences of the present invention can be used to detect polymorphisms. The array can comprise modified nucleotide sequences of the present invention in order to detect the nucleotide sequences of the present invention. In the alternative, any one of the nucleotide sequences of the present invention can be placed on the array to detect changes from those sequences.

Alternatively a polymorphism resulting in a change in the amino acid sequence could also be detected by detecting a corresponding change in amino acid sequence of the protein, e.g., by an antibody specific to the variant sequence.

3.7.20 ARTHRITIS AND INFLAMMATION

The immunosuppressive effects of the compositions of the invention against rheumatoid arthritis is determined in an experimental animal model system. The experimental model system is adjuvant induced arthritis in rats, and the protocol is described by J. Holoshitz, et al., 1983, Science, 219:56, or by B. Waksman et al., 1963,

Int. Arch. Allergy Appl. Immunol., 23:129. Induction of the disease can be caused by a single injection, generally intradermally, of a suspension of killed Mycobacterium tuberculosis in complete Freund's adjuvant (CFA). The route of injection can vary, but rats may be injected at the base of the tail with an adjuvant mixture. The polypeptide is administered in phosphate buffered solution (PBS) at a dose of about 1-5 mg/kg. The control consists of administering PBS only.

The procedure for testing the effects of the test compound would consist of intradermally injecting killed Mycobacterium tuberculosis in CFA followed by immediately administering the test compound and subsequent treatment every other day until day 24. At 14, 15, 18, 20, 22, and 24 days after injection of Mycobacterium CFA, an overall arthritis score may be obtained as described by J. Holoskitz above. An analysis of the data would reveal that the test compound would have a dramatic affect on the swelling of the joints as measured by a decrease of the arthritis score.

3.8 THERAPEUTIC METHODS

The compositions (including polypeptide fragments, analogs, variants and antibodies or other binding partners or modulators including antisense polynucleotides) of the invention have numerous applications in a variety of therapeutic methods.

Examples of therapeutic applications include, but are not limited to, those exemplified herein.

3.8.1 EXAMPLE

One embodiment of the invention is the administration of an effective amount of the polypeptides or other composition of the invention to individuals affected by a disease or disorder that can be modulated by regulating the peptides of the invention. While the mode of administration is not particularly important, parenteral administration is preferred. An exemplary mode of administration is to deliver an intravenous bolus. The dosage of the polypeptides or other composition of the invention will normally be determined by the prescribing physician. It is to be expected that the dosage will vary according to the age, weight, condition and response of the individual patient. Typically,

the amount of polypeptide administered per dose will be in the range of about 0.01µg/kg to 100 mg/kg of body weight, with the preferred dose being about 0.1µg/kg to 10 mg/kg of patient body weight. For parenteral administration, polypeptides of the invention will be formulated in an injectable form combined with a pharmaceutically acceptable

5 parenteral vehicle. Such vehicles are well known in the art and examples include water, saline, Ringer's solution, dextrose solution, and solutions consisting of small amounts of the human serum albumin. The vehicle may contain minor amounts of additives that maintain the isotonicity and stability of the polypeptide or other active ingredient. The preparation of such solutions is within the skill of the art.

3.9 PHARMACEUTICAL FORMULATIONS AND ROUTES OF ADMINISTRATION

A protein or other composition of the present invention (from whatever source
15 derived, including without limitation from recombinant and non-recombinant sources and including antibodies and other binding partners of the polypeptides of the invention) may be administered to a patient in need, by itself, or in pharmaceutical compositions where it is mixed with suitable carriers or excipient(s) at doses to treat or ameliorate a variety of disorders. Such a composition may optionally contain (in addition to protein or other
20 active ingredient and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain
25 cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the disease or disorder in question. These
30 agents include various growth factors such as epidermal growth factor (EGF),

platelet-derived growth factor (PDGF), transforming growth factors (TGF- α and TGF- β), insulin-like growth factor (IGF), as well as cytokines described herein.

The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or other active ingredient or complement its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein or other active ingredient of the invention, or to minimize side effects. Conversely, protein or other active ingredient of the present invention may be included in formulations of the particular clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent (such as IL-1Ra, IL-1 Hy1, IL-1 Hy2, anti-TNF, corticosteroids, immunosuppressive agents). A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

As an alternative to being included in a pharmaceutical composition of the invention including a first protein, a second protein or a therapeutic agent may be concurrently administered with the first protein (e.g., at the same time, or at differing times provided that therapeutic concentrations of the combination of agents is achieved at the treatment site). Techniques for formulation and administration of the compounds of the instant application may be found in "Remington's Pharmaceutical Sciences," Mack Publishing Co., Easton, PA, latest edition. A therapeutically effective dose further refers to that amount of the compound sufficient to result in amelioration of symptoms, *e.g.*, treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, a therapeutically effective dose refers to that ingredient alone. When applied to a combination, a therapeutically effective dose refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein or other active ingredient of the present invention is administered to a mammal having a condition to be treated. Protein or other active ingredient of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein or other active ingredient of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein or other active ingredient of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

3.9.1 ROUTES OF ADMINISTRATION

Suitable routes of administration may, for example, include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as intrathecal, direct intraventricular, intravenous, intraperitoneal, intranasal, or intraocular injections. Administration of protein or other active ingredient of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

Alternately, one may administer the compound in a local rather than systemic manner, for example, via injection of the compound directly into a arthritic joints or in fibrotic tissue, often in a depot or sustained release formulation. In order to prevent the scarring process frequently occurring as complication of glaucoma surgery, the compounds may be administered topically, for example, as eye drops. Furthermore, one may administer the drug in a targeted drug delivery system, for example, in a liposome

coated with a specific antibody, targeting, for example, arthritic or fibrotic tissue. The liposomes will be targeted to and taken up selectively by the afflicted tissue.

The polypeptides of the invention are administered by any route that delivers an effective dosage to the desired site of action. The determination of a suitable route of administration and an effective dosage for a particular indication is within the level of skill in the art. Preferably for wound treatment, one administers the therapeutic compound directly to the site. Suitable dosage ranges for the polypeptides of the invention can be extrapolated from these dosages or from similar studies in appropriate animal models. Dosages can then be adjusted as necessary by the clinician to provide maximal therapeutic benefit.

3.9.2 COMPOSITIONS/FORMULATIONS

Pharmaceutical compositions for use in accordance with the present invention thus may be formulated in a conventional manner using one or more physiologically acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. These pharmaceutical compositions may be manufactured in a manner that is itself known, *e.g.*, by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes. Proper formulation is dependent upon the route of administration chosen. When a therapeutically effective amount of protein or other active ingredient of the present invention is administered orally, protein or other active ingredient of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein or other active ingredient of the present invention, and preferably from about 25 to 90% protein or other active ingredient of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol,

propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein or other active ingredient of the present invention, and preferably from about 1 to 50% protein or other active ingredient of the present invention.

5 When a therapeutically effective amount of protein or other active ingredient of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein or other active ingredient of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein or other active ingredient solutions, having due regard to
10 pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein or other active ingredient of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other
15 vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art. For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiological saline buffer. For transmucosal
20 administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

For oral administration, the compounds can be formulated readily by combining the active compounds with pharmaceutically acceptable carriers well known in the art. Such carriers enable the compounds of the invention to be formulated as tablets, pills,
25 dragees, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral ingestion by a patient to be treated. Pharmaceutical preparations for oral use can be obtained from a solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including
30 lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose,

hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate. Dragee cores are provided with suitable coatings. For this purpose,

5 concentrated sugar solutions may be used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

10 Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds
15 may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added. All formulations for oral administration should be in dosages suitable for such administration. For buccal administration, the compositions may take the form of tablets or lozenges formulated in conventional manner.

20 For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, *e.g.*, dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be
25 determined by providing a valve to deliver a metered amount. Capsules and cartridges of, *e.g.*, gelatin for use in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch. The compounds may be formulated for parenteral administration by injection, *e.g.*, by bolus injection or continuous infusion. Formulations for injection may be presented in unit
30 dosage form, *e.g.*, in ampules or in multi-dose containers, with an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or

aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, *e.g.*, sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, *e.g.*, containing conventional suppository bases such as cocoa butter or other glycerides. In addition to the formulations described previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

A pharmaceutical carrier for the hydrophobic compounds of the invention is a co-solvent system comprising benzyl alcohol, a nonpolar surfactant, a water-miscible organic polymer, and an aqueous phase. The co-solvent system may be the VPD co-solvent system. VPD is a solution of 3% w/v benzyl alcohol, 8% w/v of the nonpolar surfactant polysorbate 80, and 65% w/v polyethylene glycol 300, made up to volume in absolute ethanol. The VPD co-solvent system (VPD:5W) consists of VPD diluted 1:1 with a 5% dextrose in water solution. This co-solvent system dissolves hydrophobic compounds well, and itself produces low toxicity upon systemic administration. Naturally, the proportions of a co-solvent system may be varied considerably without

destroying its solubility and toxicity characteristics. Furthermore, the identity of the co-solvent components may be varied: for example, other low-toxicity nonpolar surfactants may be used instead of polysorbate 80; the fraction size of polyethylene glycol may be varied; other biocompatible polymers may replace polyethylene glycol, e.g. polyvinyl pyrrolidone; and other sugars or polysaccharides may substitute for dextrose. Alternatively, other delivery systems for hydrophobic pharmaceutical compounds may be employed. Liposomes and emulsions are well known examples of delivery vehicles or carriers for hydrophobic drugs. Certain organic solvents such as dimethylsulfoxide also may be employed, although usually at the cost of greater toxicity. Additionally, the compounds may be delivered using a sustained-release system, such as semipermeable matrices of solid hydrophobic polymers containing the therapeutic agent. Various types of sustained-release materials have been established and are well known by those skilled in the art. Sustained-release capsules may, depending on their chemical nature, release the compounds for a few weeks up to over 100 days. Depending on the chemical nature and the biological stability of the therapeutic reagent, additional strategies for protein or other active ingredient stabilization may be employed.

The pharmaceutical compositions also may comprise suitable solid or gel phase carriers or excipients. Examples of such carriers or excipients include but are not limited to calcium carbonate, calcium phosphate, various sugars, starches, cellulose derivatives, gelatin, and polymers such as polyethylene glycols. Many of the active ingredients of the invention may be provided as salts with pharmaceutically compatible counter ions. Such pharmaceutically acceptable base addition salts are those salts which retain the biological effectiveness and properties of the free acids and which are obtained by reaction with inorganic or organic bases such as sodium hydroxide, magnesium hydroxide, ammonia, trialkylamine, dialkylamine, monoalkylamine, dibasic amino acids, sodium acetate, potassium benzoate, triethanol amine and the like.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) or other active ingredient(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T

cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with
5 co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a
10 liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithins, phospholipids, saponin, bile acids,
15 and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent Nos. 4,235,871; 4,501,728; 4,837,028; and 4,737,323, all of which are incorporated herein by reference.

The amount of protein or other active ingredient of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and
20 severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein or other active ingredient of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein or other active ingredient of the present invention and observe the patient's response.

25 Larger doses of protein or other active ingredient of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 μ g to about 100 mg (preferably about 0.1 μ g to about 10 mg, more
30 preferably about 0.1 μ g to about 1 mg) of protein or other active ingredient of the present invention per kg body weight. For compositions of the present invention which are

useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein or other active ingredient of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing or other active ingredient-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalcium phosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxyapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalcium phosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability. Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering

agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt %, preferably 1-10 wt % based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells. In further compositions, proteins or other active ingredients of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF- α and TGF- β), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins or other active ingredients of the present invention. The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, *e.g.*, amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (*e.g.*, bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final

composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either in vivo or ex vivo into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA). Cells may also be cultured ex vivo in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced in vivo for therapeutic purposes.

3.9.3 EFFECTIVE DOSAGE

Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective amount to achieve its intended purpose. More specifically, a therapeutically effective amount means an amount effective to prevent development of or to alleviate the existing symptoms of the subject being treated. Determination of the effective amount is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from appropriate in vitro assays. For example, a dose can be formulated in animal models to achieve a circulating concentration range that can be used to more accurately determine useful doses in humans. For example, a dose can be formulated in animal models to achieve a circulating concentration range that includes the IC_{50} as determined in cell culture (*i.e.*, the concentration of the test compound which achieves a half-maximal inhibition of the protein's biological activity). Such information can be used to more accurately determine useful doses in humans.

A therapeutically effective dose refers to that amount of the compound that results in amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical

procedures in cell cultures or experimental animals, *e.g.*, for determining the LD₅₀ (the dose lethal to 50% of the population) and the ED₅₀ (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio between LD₅₀ and ED₅₀.

5 Compounds which exhibit high therapeutic indices are preferred. The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in human. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED₅₀ with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. See, *e.g.*, Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p.1. Dosage amount and interval may be adjusted individually to provide plasma levels of the active moiety which are sufficient to maintain the desired effects, or minimal effective concentration (MEC). The MEC will vary for each compound but can be estimated from *in vitro* data. Dosages necessary to achieve the MEC will depend on individual characteristics and route of administration. However, HPLC assays or bioassays can be used to determine plasma concentrations.

Dosage intervals can also be determined using MEC value. Compounds should be administered using a regimen which maintains plasma levels above the MEC for 10-90% of the time, preferably between 30-90% and most preferably between 50-90%. In cases of local administration or selective uptake, the effective local concentration of the drug may not be related to plasma concentration.

An exemplary dosage regimen for polypeptides or other compositions of the invention will be in the range of about 0.01 µg/kg to 100 mg/kg of body weight daily, with the preferred dose being about 0.1 µg/kg to 25 mg/kg of patient body weight daily, varying in adults and children. Dosing may be once daily, or equivalent doses may be delivered at longer or shorter intervals.

The amount of composition administered will, of course, be dependent on the subject being treated, on the subject's age and weight, the severity of the affliction, the manner of administration and the judgment of the prescribing physician.

3.9.4 PACKAGING

The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may, for example, comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration. Compositions comprising a compound of the invention formulated in a compatible pharmaceutical carrier may also be prepared, placed in an appropriate container, and labeled for treatment of an indicated condition.

3.10 ANTIBODIES

Another aspect of the invention is an antibody that specifically binds the polypeptide of the invention. Such antibodies include monoclonal and polyclonal antibodies, single chain antibodies, chimeric antibodies, bifunctional/bispecific antibodies, humanized antibodies, human antibodies, and complementary determining region (CDR)-grafted antibodies, including compounds which include CDR and/or antigen-binding sequences, which specifically recognize a polypeptide of the invention. Preferred antibodies of the invention are human antibodies which are produced and identified according to methods described in WO93/11236, published June 20, 1993, which is incorporated herein by reference in its entirety. Antibody fragments, including Fab, Fab', F(ab')₂, and F_v, are also provided by the invention. The term "specific for" indicates that the variable regions of the antibodies of the invention recognize and bind polypeptides of the invention exclusively (*i.e.*, able to distinguish the polypeptide of the invention from other similar polypeptides despite sequence identity, homology, or similarity found in the family of polypeptides), but may also interact with other proteins (for example, *S. aureus* protein A or other antibodies in ELISA techniques) through interactions with sequences outside the variable region of the antibodies, and in particular, in the constant region of the molecule. Screening assays to determine binding specificity of an antibody of the invention are well known and routinely practiced in the art. For a comprehensive discussion of such assays, see Harlow et al. (Eds), *Antibodies A Laboratory Manual*; Cold Spring Harbor Laboratory; Cold Spring Harbor, NY (1988),

Chapter 6. Antibodies that recognize and bind fragments of the polypeptides of the invention are also contemplated, provided that the antibodies are first and foremost specific for, as defined above, full length polypeptides of the invention. As with antibodies that are specific for full length polypeptides of the invention, antibodies of the invention that recognize fragments are those which can distinguish polypeptides from the same family of polypeptides despite inherent sequence identity, homology, or similarity found in the family of proteins. Antibodies of the invention can be produced using any method well known and routinely practiced in the art.

Non-human antibodies may be humanized by any methods known in the art. In one method, the non-human CDRs are inserted into a human antibody or consensus antibody framework sequence. Further changes can then be introduced into the antibody framework to modulate affinity or immunogenicity.

Antibodies of the invention are useful for, for example, therapeutic purposes (by modulating activity of a polypeptide of the invention), diagnostic purposes to detect or quantitate a polypeptide of the invention, as well as purification of a polypeptide of the invention. Kits comprising an antibody of the invention for any of the purposes described herein are also comprehended. In general, a kit of the invention also includes a control antigen for which the antibody is immunospecific. The invention further provides a hybridoma that produces an antibody according to the invention. Antibodies of the invention are useful for detection and/or purification of the polypeptides of the invention.

Polypeptides of the invention may also be used to immunize animals to obtain polyclonal and monoclonal antibodies which specifically react with the protein. Such antibodies may be obtained using either the entire protein or fragments thereof as an immunogen. The peptide immunogens additionally may contain a cysteine residue at the carboxyl terminus, and are conjugated to a hapten such as keyhole limpet hemocyanin (KLH). Methods for synthesizing such peptides are known in the art, for example, as in R. P. Merrifield, J. Amer. Chem. Soc. 85, 2149-2154 (1963); J. L. Krstenansky, et al., FEBS Lett. 211, 10 (1987).

Monoclonal antibodies binding to the protein of the invention may be useful diagnostic agents for the immunodetection of the protein. Neutralizing monoclonal antibodies binding to the protein may also be useful therapeutics for both conditions

associated with the protein and also in the treatment of some forms of cancer where abnormal expression of the protein is involved. In the case of cancerous cells or leukemic cells, neutralizing monoclonal antibodies against the protein may be useful in detecting and preventing the metastatic spread of the cancerous cells, which may be mediated by the protein. In general, techniques for preparing polyclonal and monoclonal antibodies as well as hybridomas capable of producing the desired antibody are well known in the art (Campbell, A.M., Monoclonal Antibodies Technology: Laboratory Techniques in Biochemistry and Molecular Biology, Elsevier Science Publishers, Amsterdam, The Netherlands (1984); St. Groth et al., J. Immunol. 35:1-21 (1990); Kohler and Milstein, Nature 256:495-497 (1975)), the trioma technique, the human B-cell hybridoma technique (Kozbor et al., Immunology Today 4:72 (1983); Cole et al., in Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, Inc. (1985), pp. 77-96).

Any animal (mouse, rabbit, *etc.*) which is known to produce antibodies can be immunized with a peptide or polypeptide of the invention. Methods for immunization are well known in the art. Such methods include subcutaneous or intraperitoneal injection of the polypeptide. One skilled in the art will recognize that the amount of the protein encoded by the ORF of the present invention used for immunization will vary based on the animal which is immunized, the antigenicity of the peptide and the site of injection. The protein that is used as an immunogen may be modified or administered in an adjuvant in order to increase the protein's antigenicity. Methods of increasing the antigenicity of a protein are well known in the art and include, but are not limited to, coupling the antigen with a heterologous protein (such as globulin or β -galactosidase) or through the inclusion of an adjuvant during immunization.

For monoclonal antibodies, spleen cells from the immunized animals are removed, fused with myeloma cells, such as SP2/0-Ag14 myeloma cells, and allowed to become monoclonal antibody producing hybridoma cells. Any one of a number of methods well known in the art can be used to identify the hybridoma cell which produces an antibody with the desired characteristics. These include screening the hybridomas with an ELISA assay, Western blot analysis, or radioimmunoassay (Lutz et al., Exp. Cell Research. 175:109-124 (1988)). Hybridomas secreting the desired antibodies are cloned and the class and subclass is determined using procedures known in the art (Campbell,

A.M., Monoclonal Antibody Technology: Laboratory Techniques in Biochemistry and Molecular Biology, Elsevier Science Publishers, Amsterdam, The Netherlands (1984)).

Techniques described for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce single chain antibodies to proteins of the present invention.

For polyclonal antibodies, antibody-containing antiserum is isolated from the immunized animal and is screened for the presence of antibodies with the desired specificity using one of the above-described procedures. The present invention further provides the above-described antibodies in detectably labeled form. Antibodies can be detectably labeled through the use of radioisotopes, affinity labels (such as biotin, avidin, etc.), enzymatic labels (such as horseradish peroxidase, alkaline phosphatase, etc.) fluorescent labels (such as FITC or rhodamine, etc.), paramagnetic atoms, etc. Procedures for accomplishing such labeling are well-known in the art, for example, see (Sternberger, L.A. et al., J. Histochem. Cytochem. 18:315 (1970); Bayer, E.A. et al., Meth. Enzym. 62:308 (1979); Engval, E. et al., Immunol. 109:129 (1972); Goding, J.W. J. Immunol. Meth. 13:215 (1976)).

The labeled antibodies of the present invention can be used for *in vitro*, *in vivo*, and *in situ* assays to identify cells or tissues in which a fragment of the polypeptide of interest is expressed. The antibodies may also be used directly in therapies or other diagnostics. The present invention further provides the above-described antibodies immobilized on a solid support. Examples of such solid supports include plastics such as polycarbonate, complex carbohydrates such as agarose and Sepharose®, acrylic resins and such as polyacrylamide and latex beads. Techniques for coupling antibodies to such solid supports are well known in the art (Weir, D.M. et al., "Handbook of Experimental Immunology" 4th Ed., Blackwell Scientific Publications, Oxford, England, Chapter 10 (1986); Jacoby, W.D. et al., Meth. Enzym. 34 Academic Press, N.Y. (1974)). The immobilized antibodies of the present invention can be used for *in vitro*, *in vivo*, and *in situ* assays as well as for immuno-affinity purification of the proteins of the present invention.

3.11 COMPUTER READABLE SEQUENCES

In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A skilled artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention. As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention.

A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data processor structuring formats (*e.g.* text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing any of the nucleotide sequences SEQ ID NOs: 1 - 362 or a representative fragment thereof; or a nucleotide sequence at least 95% identical to any of the nucleotide sequences of SEQ ID NOs: 1 - 362 in computer readable form, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence

information provided in a computer readable medium. The examples which follow demonstrate how software which implements the BLAST (Altschul et al., J. Mol. Biol. 215:403-410 (1990)) and BLAZE (Brutlag et al., Comp. Chem. 17:203-207 (1993)) search algorithms on a Sybase system is used to identify open reading frames (ORFs)

5 within a nucleic acid sequence. Such ORFs may be protein encoding fragments and may be useful in producing commercially important proteins such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence
10 information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based systems are suitable for use in the present invention. As stated above, the computer-based systems of the present
15 invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded
20 thereon the nucleotide sequence information of the present invention.

As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of a known sequence which
25 match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, Smith-Waterman, MacPattern (EMBL), BLASTN and BLASTA (NPOLYPEPTIDEIA). A skilled artisan can readily
30 recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based

systems. As used herein, a "target sequence" can be any nucleic acid or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 300 amino acids, more preferably from about 30 to 100 nucleotide residues. However, it is well recognized that searches for commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

3.12 TRIPLE HELIX FORMATION

In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA. Polynucleotides suitable for use in these methods are preferably 20 to 40 bases in length and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 15241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Olmno, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide.

3.13 DIAGNOSTIC ASSAYS AND KITS

The present invention further provides methods to identify the presence or expression of one of the ORFs of the present invention, or homolog thereof, in a test sample, using a nucleic acid probe or antibodies of the present invention, optionally conjugated or otherwise associated with a suitable label.

In general, methods for detecting a polynucleotide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polynucleotide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polynucleotide of the invention is detected in the sample. Such methods can also comprise contacting a sample under stringent hybridization conditions with nucleic acid primers that anneal to a polynucleotide of the invention under such conditions, and amplifying annealed polynucleotides, so that if a polynucleotide is amplified, a polynucleotide of the invention is detected in the sample.

In general, methods for detecting a polypeptide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polypeptide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polypeptide of the invention is detected in the sample.

In detail, such methods comprise incubating a test sample with one or more of the antibodies or one or more of the nucleic acid probes of the present invention and assaying for binding of the nucleic acid probes or antibodies to components within the test sample.

Conditions for incubating a nucleic acid probe or antibody with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the nucleic acid probe or antibody used in the assay. One skilled in the art will recognize that any one of the commonly available hybridization, amplification or immunological assay formats can readily be adapted to employ the nucleic acid probes or antibodies of the present invention. Examples of such assays can be found in Chard, T., *An Introduction to Radioimmunoassay and Related Techniques*, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock, G.R. et al., *Techniques in Immunocytochemistry*, Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, P., *Practice and Theory of immunoassays*:

Laboratory Techniques in Biochemistry and Molecular Biology, Elsevier Science Publishers, Amsterdam, The Netherlands (1985). The test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as sputum, blood, serum, plasma, or urine. The test sample used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is compatible with the system utilized.

In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the assays of the present invention. Specifically, the invention provides a compartment kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the probes or antibodies of the present invention; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of a bound probe or antibody.

In detail, a compartment kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allows one to efficiently transfer reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated, and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the antibodies used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, etc.), and containers which contain the reagents used to detect the bound antibody or probe. Types of detection reagents include labeled nucleic acid probes, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the enzymatic, or antibody binding reagents which are capable of reacting with the labeled antibody. One skilled in the art will readily recognize that the disclosed probes and antibodies of the present invention can be readily incorporated into one of the established kit formats which are well known in the art.

3.14 MEDICAL IMAGING

The novel polypeptides and binding partners of the invention are useful in medical imaging of sites expressing the molecules of the invention (e.g., where the polypeptide of the invention is involved in the immune response, for imaging sites of inflammation or infection). See, e.g., Kunkel et al., U.S. Pat. NO. 5,413,778. Such methods involve chemical attachment of a labeling or imaging agent, administration of the labeled polypeptide to a subject in a pharmaceutically acceptable carrier, and imaging the labeled polypeptide *in vivo* at the target site.

3.15 SCREENING ASSAYS

Using the isolated proteins and polynucleotides of the invention, the present invention further provides methods of obtaining and identifying agents which bind to a polypeptide encoded by an ORF corresponding to any of the nucleotide sequences set forth in SEQ ID NOs: 1 - 362, or bind to a specific domain of the polypeptide encoded by the nucleic acid. In detail, said method comprises the steps of:

- (a) contacting an agent with an isolated protein encoded by an ORF of the present invention, or nucleic acid of the invention; and
- (b) determining whether the agent binds to said protein or said nucleic acid.

In general, therefore, such methods for identifying compounds that bind to a polynucleotide of the invention can comprise contacting a compound with a polynucleotide of the invention for a time sufficient to form a polynucleotide/compound complex, and detecting the complex, so that if a polynucleotide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Likewise, in general, therefore, such methods for identifying compounds that bind to a polypeptide of the invention can comprise contacting a compound with a polypeptide of the invention for a time sufficient to form a polypeptide/compound complex, and detecting the complex, so that if a polypeptide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Methods for identifying compounds that bind to a polypeptide of the invention can also comprise contacting a compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives

expression of a receptor gene sequence in the cell, and detecting the complex by detecting reporter gene sequence expression, so that if a polypeptide/compound complex is detected, a compound that binds a polypeptide of the invention is identified.

Compounds identified via such methods can include compounds which modulate the activity of a polypeptide of the invention (that is, increase or decrease its activity, relative to activity observed in the absence of the compound). Alternatively, compounds identified via such methods can include compounds which modulate the expression of a polynucleotide of the invention (that is, increase or decrease expression relative to expression levels observed in the absence of the compound). Compounds, such as compounds identified via the methods of the invention, can be tested using standard assays well known to those of skill in the art for their ability to modulate activity/expression.

The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling techniques.

For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by the ORF of the present invention. Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like, capable of binding to a specific peptide sequence, in order to generate rationally designed antipeptide peptides, for example see Hurby et al., Application of Synthetic Peptides: Antisense Peptides," In Synthetic Peptides, A User's Guide, W.H. Freeman, NY (1992), pp. 289-307, and Kaspaczak et al., Biochemistry 28:9230-8 (1989), or pharmaceutical agents, or the like.

In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to control gene expression through binding to one of the ORFs or EMFs of the present invention. As described above, such agents can be randomly screened or rationally designed/selected. Targeting the ORF or EMF allows a

skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF or multiple ORFs which rely on the same EMF for expression control. One class of DNA binding agents are agents which contain base residues which hybridize or form a triple helix formation by binding to DNA or RNA.

- 5 Such agents can be based on the classic phosphodiester, ribonucleic acid backbone, or can be a variety of sulfhydryl or polymeric derivatives which have base attachment capacity.

Agents suitable for use in these methods preferably contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple
10 helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization
15 blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide and other DNA binding agents.

Agents which bind to a protein encoded by one of the ORFs of the present
20 invention can be used as a diagnostic agent. Agents which bind to a protein encoded by one of the ORFs of the present invention can be formulated using known techniques to generate a pharmaceutical composition.

3.16 USE OF NUCLEIC ACIDS AS PROBES

25 Another aspect of the subject invention is to provide for polypeptide-specific nucleic acid hybridization probes capable of hybridizing with naturally occurring nucleotide sequences. The hybridization probes of the subject invention may be derived from any of the nucleotide sequences SEQ ID NOs: 1 - 362. Because the corresponding gene is only expressed in a limited number of tissues, a hybridization probe derived from
30 of any of the nucleotide sequences SEQ ID NOs: 1 - 362 can be used as an indicator of the presence of RNA of cell type of such a tissue in a sample.

Any suitable hybridization technique can be employed, such as, for example, in situ hybridization. PCR as described in US Patents Nos. 4,683,195 and 4,965,188 provides additional uses for oligonucleotides based upon the nucleotide sequences. Such probes used in PCR may be of recombinant origin, may be chemically synthesized, or a mixture of both. The probe will comprise a discrete nucleotide sequence for the detection of identical sequences or a degenerate pool of possible sequences for identification of closely related genomic sequences.

Other means for producing specific hybridization probes for nucleic acids include the cloning of nucleic acid sequences into vectors for the production of mRNA probes.

Such vectors are known in the art and are commercially available and may be used to synthesize RNA probes *in vitro* by means of the addition of the appropriate RNA polymerase as T7 or SP6 RNA polymerase and the appropriate radioactively labeled nucleotides. The nucleotide sequences may be used to construct hybridization probes for mapping their respective genomic sequences. The nucleotide sequence provided herein may be mapped to a chromosome or specific regions of a chromosome using well known genetic and/or chromosomal mapping techniques. These techniques include in situ hybridization, linkage analysis against known chromosomal markers, hybridization screening with libraries or flow-sorted chromosomal preparations specific to known chromosomes, and the like. The technique of fluorescent in situ hybridization of chromosome spreads has been described, among other places, in Verma et al (1988) Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York NY.

Fluorescent *in situ* hybridization of chromosomal preparations and other physical chromosome mapping techniques may be correlated with additional genetic map data. Examples of genetic map data can be found in the 1994 Genome Issue of Science (265:1981f). Correlation between the location of a nucleic acid on a physical chromosomal map and a specific disease (or predisposition to a specific disease) may help delimit the region of DNA associated with that genetic disease. The nucleotide sequences of the subject invention may be used to detect differences in gene sequences between normal, carrier or affected individuals.

3.17 PREPARATION OF SUPPORT BOUND OLIGONUCLEOTIDES

Oligonucleotides, i.e., small nucleic acid segments, may be readily prepared by, for example, directly synthesizing the oligonucleotide by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer.

Support bound oligonucleotides may be prepared by any of the methods known to those of skill in the art using any suitable support such as glass, polystyrene or Teflon. One strategy is to precisely spot oligonucleotides synthesized by standard synthesizers.

Immobilization can be achieved using passive adsorption (Inouye & Hondo, (1990) J. Clin. Microbiol. 28(6) 1469-72); using UV light (Nagata *et al.*, 1985; Dahlen *et al.*, 1987;

Morrissey & Collins, (1989) Mol. Cell Probes 3(2) 189-207) or by covalent binding of base modified DNA (Keller *et al.*, 1988; 1989); all references being specifically incorporated herein.

Another strategy that may be employed is the use of the strong biotin-streptavidin interaction as a linker. For example, Broude *et al.* (1994) Proc. Natl. Acad. Sci. USA 91(8) 3072-6, describe the use of biotinylated probes, although these are duplex probes, that are immobilized on streptavidin-coated magnetic beads. Streptavidin-coated beads may be purchased from Dynal, Oslo. Of course, this same linking chemistry is applicable to coating any surface with streptavidin. Biotinylated probes may be purchased from various sources, such as, e.g., Operon Technologies (Alameda, CA).

Nunc Laboratories (Naperville, IL) is also selling suitable material that could be used. Nunc Laboratories have developed a method by which DNA can be covalently bound to the microwell surface termed Covalink NH. CovaLink NH is a polystyrene surface grafted with secondary amino groups (>NH) that serve as bridge-heads for further covalent coupling. CovaLink Modules may be purchased from Nunc Laboratories. DNA molecules may be bound to CovaLink exclusively at the 5'-end by a phosphoramidate bond, allowing immobilization of more than 1 pmol of DNA (Rasmussen *et al.*, (1991) Anal. Biochem. 198(1) 138-42).

The use of CovaLink NH strips for covalent binding of DNA molecules at the 5'-end has been described (Rasmussen *et al.*, (1991). In this technology, a phosphoramidate bond is employed (Chu *et al.*, (1983) Nucleic Acids Res. 11(8) 6513-29). This is beneficial as immobilization using only a single covalent bond is preferred. The phosphoramidate bond

joins the DNA to the CovaLink NH secondary amino groups that are positioned at the end of spacer arms covalently grafted onto the polystyrene surface through a 2 nm long spacer arm. To link an oligonucleotide to CovaLink NH via an phosphoramidate bond, the oligonucleotide terminus must have a 5'-end phosphate group. It is, perhaps, even possible for biotin to be covalently bound to CovaLink and then streptavidin used to bind the probes.

More specifically, the linkage method includes dissolving DNA in water (7.5 ng/ul) and denaturing for 10 min. at 95°C and cooling on ice for 10 min. Ice-cold 0.1 M 1-methylimidazole, pH 7.0 (1-MeIm₇), is then added to a final concentration of 10 mM 1-MeIm₇. A ss DNA solution is then dispensed into CovaLink NH strips (75 ul/well) standing on ice.

Carbodiimide 0.2 M 1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide (EDC), dissolved in 10 mM 1-MeIm₇, is made fresh and 25 ul added per well. The strips are incubated for 5 hours at 50°C. After incubation the strips are washed using, e.g., Nunc-Immuno Wash; first the wells are washed 3 times, then they are soaked with washing solution for 5 min., and finally they are washed 3 times (where in the washing solution is 0.4 N NaOH, 0.25% SDS heated to 50°C).

It is contemplated that a further suitable method for use with the present invention is that described in PCT Patent Application WO 90/03382 (Southern & Maskos), incorporated herein by reference. This method of preparing an oligonucleotide bound to a support involves attaching a nucleoside 3'-reagent through the phosphate group by a covalent phosphodiester link to aliphatic hydroxyl groups carried by the support. The oligonucleotide is then synthesized on the supported nucleoside and protecting groups removed from the synthetic oligonucleotide chain under standard conditions that do not cleave the oligonucleotide from the support. Suitable reagents include nucleoside phosphoramidite and nucleoside hydrogen phosphate.

An on-chip strategy for the preparation of DNA probe for the preparation of DNA probe arrays may be employed. For example, addressable laser-activated photodeprotection may be employed in the chemical synthesis of oligonucleotides directly on a glass surface, as described by Fodor *et al.* (1991) Science 251(4995) 767-73, incorporated herein by reference. Probes may also be immobilized on nylon supports as described by Van Ness *et al.* (1991) Nucleic Acids Res. 19(12) 3345-50; or linked to Teflon using the method of

Duncan & Cavalier (1988) Anal. Biochem. 169(1) 104-8; all references being specifically incorporated herein.

To link an oligonucleotide to a nylon support, as described by Van Ness *et al.* (1991), requires activation of the nylon surface via alkylation and selective activation of the 5'-amine of oligonucleotides with cyanuric chloride.

One particular way to prepare support bound oligonucleotides is to utilize the light-generated synthesis described by Pease *et al.*, (1994) PNAS USA 91(11) 5022-6, incorporated herein by reference). These authors used current photolithographic techniques to generate arrays of immobilized oligonucleotide probes (DNA chips). These methods, in which light is used to direct the synthesis of oligonucleotide probes in high-density, miniaturized arrays, utilize photolabile 5'-protected *N*-acyl-deoxynucleoside phosphoramidites, surface linker chemistry and versatile combinatorial synthesis strategies. A matrix of 256 spatially defined oligonucleotide probes may be generated in this manner.

3.18 PREPARATION OF NUCLEIC ACID FRAGMENTS

The nucleic acids may be obtained from any appropriate source, such as cDNAs, genomic DNA, chromosomal DNA, microdissected chromosome bands, cosmid or YAC inserts, and RNA, including mRNA without any amplification steps. For example, Sambrook *et al.* (1989) describes three protocols for the isolation of high molecular weight DNA from mammalian cells (p. 9.14-9.23).

DNA fragments may be prepared as clones in M13, plasmid or lambda vectors and/or prepared directly from genomic DNA or cDNA by PCR or other amplification methods. Samples may be prepared or dispensed in multiwell plates. About 100-1000 ng of DNA samples may be prepared in 2-500 ml of final volume.

The nucleic acids would then be fragmented by any of the methods known to those of skill in the art including, for example, using restriction enzymes as described at 9.24-9.28 of Sambrook *et al.* (1989), shearing by ultrasound and NaOH treatment.

Low pressure shearing is also appropriate, as described by Schriefer *et al.* (1990) Nucleic Acids Res. 18(24) 7455-6, incorporated herein by reference). In this method, DNA samples are passed through a small French pressure cell at a variety of low to intermediate pressures. A lever device allows controlled application of low to intermediate pressures to

the cell. The results of these studies indicate that low-pressure shearing is a useful alternative to sonic and enzymatic DNA fragmentation methods.

One particularly suitable way for fragmenting DNA is contemplated to be that using the two base recognition endonuclease, *Cvi*II, described by Fitzgerald *et al.* (1992) Nucleic Acids Res. 20(14) 3753-62. These authors described an approach for the rapid fragmentation and fractionation of DNA into particular sizes that they contemplated to be suitable for shotgun cloning and sequencing.

The restriction endonuclease *Cvi*II normally cleaves the recognition sequence PuGCPy between the G and C to leave blunt ends. Atypical reaction conditions, which alter the specificity of this enzyme (*Cvi*II**), yield a quasi-random distribution of DNA fragments from the small molecule pUC19 (2688 base pairs). Fitzgerald *et al.* (1992) quantitatively evaluated the randomness of this fragmentation strategy, using a *Cvi*II** digest of pUC19 that was size fractionated by a rapid gel filtration method and directly ligated, without end repair, to a lac Z minus M13 cloning vector. Sequence analysis of 76 clones showed that *Cvi*II** restricts pyGCPy and PuGCPu, in addition to PuGCPy sites, and that new sequence data is accumulated at a rate consistent with random fragmentation.

As reported in the literature, advantages of this approach compared to sonication and agarose gel fractionation include: smaller amounts of DNA are required (0.2-0.5 ug instead of 2-5 ug); and fewer steps are involved (no preligation, end repair, chemical extraction, or agarose gel electrophoresis and elution are needed).

Irrespective of the manner in which the nucleic acid fragments are obtained or prepared, it is important to denature the DNA to give single stranded pieces available for hybridization. This is achieved by incubating the DNA solution for 2-5 minutes at 80-90°C. The solution is then cooled quickly to 2°C to prevent renaturation of the DNA fragments before they are contacted with the chip. Phosphate groups must also be removed from genomic DNA by methods known in the art.

3.19 PREPARATION OF DNA ARRAYS

Arrays may be prepared by spotting DNA samples on a support such as a nylon membrane. Spotting may be performed by using arrays of metal pins (the positions of which correspond to an array of wells in a microtiter plate) to repeated by transfer of about 20 nl of a DNA solution to a nylon membrane. By offset printing, a density of dots higher than the

density of the wells is achieved. One to 25 dots may be accommodated in 1 mm², depending on the type of label used. By avoiding spotting in some preselected number of rows and columns, separate subsets (subarrays) may be formed. Samples in one subarray may be the same genomic segment of DNA (or the same gene) from different individuals, or may be different, overlapped genomic clones. Each of the subarrays may represent replica spotting of the same samples. In one example, a selected gene segment may be amplified from 64 patients. For each patient, the amplified gene segment may be in one 96-well plate (all 96 wells containing the same sample). A plate for each of the 64 patients is prepared. By using a 96-pin device, all samples may be spotted on one 8 x 12 cm membrane. Subarrays may contain 64 samples, one from each patient. Where the 96 subarrays are identical, the dot span may be 1 mm² and there may be a 1 mm space between subarrays.

Another approach is to use membranes or plates (available from NUNC, Naperville, Illinois) which may be partitioned by physical spacers e.g. a plastic grid molded over the membrane, the grid being similar to the sort of membrane applied to the bottom of multiwell plates, or hydrophobic strips. A fixed physical spacer is not preferred for imaging by exposure to flat phosphor-storage screens or x-ray films.

The present invention is illustrated in the following examples. Upon consideration of the present disclosure, one of skill in the art will appreciate that many other embodiments and variations may be made in the scope of the present invention. Accordingly, it is intended that the broader aspects of the present invention not be limited to the disclosure of the following examples. The present invention is not to be limited in scope by the exemplified embodiments which are intended as illustrations of single aspects of the invention, and compositions and methods which are functionally equivalent are within the scope of the invention. Indeed, numerous modifications and variations in the practice of the invention are expected to occur to those skilled in the art upon consideration of the present preferred embodiments. Consequently, the only limitations which should be placed upon the scope of the invention are those which appear in the appended claims.

All references cited within the body of the instant specification are hereby incorporated by reference in their entirety.

4.0 EXAMPLES

4.1 EXAMPLE 1

Novel Nucleic Acid Sequences Obtained From Various Libraries

A plurality of novel nucleic acids were obtained from cDNA libraries prepared from various human tissues and in some cases isolated from a genomic library derived from human chromosome using standard PCR, SBH sequence signature analysis and Sanger sequencing techniques. The inserts of the library were amplified with PCR using primers specific for the vector sequences which flank the inserts. Clones from cDNA libraries were spotted on nylon membrane filters and screened with oligonucleotide probes (e.g., 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones were selected for sequencing.

In some cases, the 5' sequence of the amplified inserts was then deduced using a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems (ABI) sequencer to obtain the novel nucleic acid sequences. In some cases RACE (Random Amplification of cDNA Ends) was performed to further extend the sequence in the 5' direction.

4.2 EXAMPLE 2

Novel Nucleic Acids

The novel nucleic acids of the present invention of the invention were assembled from sequences that were obtained from a cDNA library by methods described in Example 1 above, and in some cases sequences obtained from one or more public databases. The nucleic acids were assembled using an EST sequence as a seed. Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases (i.e., Hyseq's database containing EST sequences, dbEST version 114, gb pri 114, and UniGene version 101) that belong to this assemblage. The algorithm terminated when there was no additional sequences from the above databases that would extend the assemblage. Inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score greater than 300 and percent identity greater than 95%.

Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genbank (i.e., dbEST version 120, gb pri 120, UniGene version 120, Genepet release 120). Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, ed-ext and gc-zip-2 (Hyseq, Inc.). The full-length nucleotide and amino acid sequences, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS: 1- 362.

Table 1 shows the various tissue sources of SEQ ID NO: 1-362.

The homology for SEQ ID NO: 1-362 were obtained by a BLASTP version 2.0a1 19MP-WashU search against Genpept release 120 and the amino acid version of Geneseq released on October 26, 2000, using BLAST algorithm. The results showed homologues for SEQ ID NO: 1-362 from Genpept. The homologues with identifiable functions for SEQ ID NO: 1-362 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. Table 3 shows the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the pFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the p-value and the pFam score for the identified domain within the sequence.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determine from using Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren

Brunak, and Gunnar von Heijne in the publication “ Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites” Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by reference. A maximum S score and a mean S score, as described in the Nielson et al as reference, was obtained for the

5 polypeptide sequences. Table 5 shows the position of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

TABLE 1

TISSUE ORIGIN	LIBRARY/ RNA SOURCE	HYSEQ LIBRARY NAME	SEQ ID NOS:
adult brain	GIBCO	AB3001	4 18 39-40 83 88 98 110 112-113 136 168-169 201-203
adult brain	GIBCO	ABD003	7 15-16 31-32 39-41 45 54 58 63 70 73-75 82-84 92 98 106 110 114 116-117 126 128 130 139 144 155 164 168-169 191-192 195 198 204-215 239-240 249 252 258 272-274
adult brain	Clontech	ABR001	10-11 15 19 39-40 88 106 120 144 168 215-216 258
adult brain	Clontech	ABR006	13 17 20 23 33 39-40 50 58 62 75 82 84 88 100 104 121-122 129 149 168 208 216 223 232-233 239 256 269 277 287-288 353 360
adult brain	Clontech	ABR008	4 10-11 13 17 20 23 25 28-30 32 34-35 39-41 48 50 53-54 58 61 63 68-69 74 76 78 80 84-89 91 98 104 107 112-114 118 121-122 130 134-136 143 153-155 158-160 163-166 168 172-173 184-188 199-200 203 212-213 215-216 219-220 226-227 234 239 242 244 251-252 255-257 263 268 271-272 277-280 287 291 300-301 305-306 316 322 338 346-347 360
adult brain	Clontech	ABR011	157 306
adult brain	BioChain	ABR012	36 247
adult brain	Invitrogen	ABR013	176
adult brain	Invitrogen	ABR014	50 53 100 269
adult brain	Invitrogen	ABR015	19 38 74 161-162
brain	Invitrogen	ABR016	53 74 137 139 239
adult brain	Invitrogen	ABT004	8 15 19-20 28 30 35 75 78 100 106-107 113 134 160 179 181 184 198-199 210 216 224 227 252 254-255 288 340
adipocytes	Stratagene	ADP001	9 13 19 45 74 98 121-122 131 164 187 189-190 217 239
adrenal gland	Clontech	ADR002	9 15 18-19 24-25 31-32 46 56 77-78 112 114-115 117-119 121-122 124 139 170 182 192 209 213 218 220 225 249 276 306
adult heart	GIBCO	AHR001	2 4 7 17 19-22 26-27 34 38 45-46 50 53-54 58 60-61 63 74 76-77 86-87 91 96 98 108 112 114 121-122 131 133 136-140 144 155 160 165-168 184 188 217 226 239 241-242 251 259 265 277-278 290 306
adult kidney	GIBCO	AKD001	4 6-11 13 15-17 19-20 24 30-32

TISSUE ORIGIN	LIBRARY/ RNA SOURCE	HYSEQ LIBRARY NAME	SEQ ID NOS:
			34 36-38 47 53-54 60-63 66 69 73-75 78 82-85 87 89-92 96 98 100 103 106 108 110 112-113 116 121-123 126 129 131 134 136 139-142 144 153 155 158- 159 169-170 176 181 207 237 239 266-267 271-272 306
adult kidney	Invitrogen	AKT002	7-8 10-11 13 15 19 25-27 32 37-38 53 55-56 66 75 86 90 92 108 123 144 165-166 172 182 199 218 225 233 236 238 260 266-267 332
adult lung	GIBCO	ALG001	8 22 26-28 38-40 47 54 78 91 98 104 110 112 117 139 148 168 189 196 225 239 248 351-352
lymph node	Clontech	ALN001	7 26-27 32 35 38-40 79 82 120 127 152 158-159 169 171 219 239 244
young liver	GIBCO	ALV001	7 14 16-17 19 33 37 53 72 77 107 113 116 118 134 152 168 212 249
adult liver	Invitrogen	ALV002	12 14 17 24 28 32-33 36 58 73 75-76 84 101 116 131 138 140 158-160 182 194 212 238 275 284 323 342-343
adult liver	Clontech	ALV003	271 284 358
ovary	Invitrogen	AOV001	4 6-11 13 15-16 18-21 25-27 31-32 34 36 38-40 46 48 50 53- 54 56 58 60 65 70 73-78 80 83- 84 86 91-92 95 98 100-101 103- 106 108 110-112 115 117-118 124 126-127 129-131 136 139- 142 144 148 155 157-161 163- 167 169 173-174 178 180-186 188-189 191-193 196 199-200 204-208 210-211 220-223 233 236 239 249-252 260-263 266- 270 287-288 306 315 351-352
placenta	Clontech	APL001	30 50 74 82 230
placenta	Invitrogen	APL002	45 50 59 70 75 103 163 223
adult spleen	GIBCO	ASP001	7 19 30 38 45 54 58 62 74 81 83 91 106 110 112-113 116 131 144 151 155 162 165-166 172 176 189 191 215 230 236 239 249 329
testis	GIBCO	ATS001	4 15 19-20 30 48 53 74 89 94 110 126 140 158-159 173 214- 215 220 239 245 306
bladder	Invitrogen	BLD001	30 35 59 61 74-75 123 164 221 241 318
bone marrow	Clontech	BMD001	3 6-7 9 13 17 20 26-27 30-31 34 38-40 42 46 53-54 63-79 82- 83 85 91 93-98 101 105 110 115 121-122 126 128-129 133-134

TISSUE ORIGIN	LIBRARY/ RNA SOURCE	HYSEQ LIBRARY NAME	SEQ ID NOS:
			143 145 154 161-162 176 192 205-206 234 236 239 243 264 289 306 322
bone marrow	Clontech	BMD002	3-4 7 9 13 16-17 19-20 23 30 32 34 36 38-40 47-48 54-56 58 61 68-69 74-75 79 84 108 118- 119 121-122 125 128-129 131 133 140 144 147 149 153-154 158-159 161 163 167 171 174 176 185-187 200 211 218 232 239 241 247 252 277-278 285 296 303 310 320 324 329 339 341 353 356 359
bone marrow	Clontech	BMD004	64
colon	Invitrogen	CLN001	18 32 100 106 110 143 153 163- 164 178 213 247 266-267 284
cervix	BioChain	CVX001	4 6 8-9 19 22 24-25 28 32 45- 46 53 55-56 63 74-75 77-78 83 87 91-92 95 102 105 108 110 123 127 136-137 140 169 172 182 184-186 189-191 199 211 238 249 266-267 274 283 306- 308 317 354
endothelial cells	Stratagene	EDT001	2 4 6-7 9 15 17-21 25-28 30 32 36 39-40 45 47-48 53 55-57 60 62-63 69-70 74-76 78 83 85-87 98 101-104 106 108 112-113 119 121-123 130-131 136-137 139- 142 155-156 158-159 161 174 189-192 204 208 218 220 223 230 239 251 280 306
Genomic clones from short arm of chromosome 8	Genomic Data from Genetic Research	EPM001	223
Genomic clones from short arm of chromosome 8	Genomic Data from Genetic Research	EPM003	223
Genomic clones from short arm of chromosome 8	Genomic Data from Genetic Research	EPM004	223
fetal brain	Clontech	FBR001	32 227
fetal brain	Clontech	FBR004	319
fetal brain	Clontech	FBR006	7 10-11 13 17 20 23-25 28-29 32 35 41-42 48 50 53 63 75 80 89 91 104 112 121-122 125 130 154 163 165-166 168 171 173 191 199 210 215-216 218 226 232 239 256 272 277 290 300 306 309 319-320 333 353 360
fetal brain	Invitrogen	FBT002	15 17 19 35 69 75 87 104 109 140 163 174 192-193 198-199

TISSUE ORIGIN	LIBRARY/ RNA SOURCE	HYSEQ LIBRARY NAME	SEQ ID NOS:
			207 220 228 239 252 256-258
fetal heart	Invitrogen	FHR001	3 8 19 32 41 48 77-79 91 114 119 126 163 165-166 172 174 176 200 218 232 244 263 331 351-352 360-361
fetal kidney	Clontech	FKD001	16-17 36 46 53 74 82 95 104 111 117 169 189
fetal kidney	Clontech	FKD002	26-27 165-166 218 220 232 238 263 306
fetal kidney	Invitrogen	FKD007	38 74
fetal lung	Clontech	FLG001	32 48 139 173 217
fetal lung	Invitrogen	FLG003	10-11 19 36 58 61 69 74 134 163 168 178 194 249 263 266- 267 351-352
fetal liver- spleen	Columbia University	FLS001	1-19 21-38 41-62 68 70 72 74- 78 87 90-91 93 100-104 106-121 123-125 127 130-131 133-134 141-142 144 149 155-156 161 163 165-167 169 176 194-196 200 207 210 221 224-225 227 231-233 236 238 263 303 306 313 324 336 342
fetal liver- spleen	Columbia University	FLS002	2 5 7-9 12 14 16-18 22-24 30- 33 35-40 43-46 48-50 52-53 57 70 72 76-78 84-85 87 90 92 101-102 106-108 110 112 114 116-120 124 127-128 130-131 134-135 140-142 144 155 163 172 174 187 189-190 192 195- 196 199 205-207 210 220-221 223-224 230-234 244 251 258 260-261 263 265 275 296 313- 315 331 337-338 345 362
fetal liver- spleen	Columbia University	FLS003	19 30 33 139 174 265 313 339 355
fetal liver	Invitrogen	FLV001	10-11 14 17 19 21 37 46 50 61 63 156 163 165-166 172 200 210 238 253
fetal liver	Clontech	FLV002	19 32 74 163 356
fetal liver	Clontech	FLV004	3 14 19 32-33 37 42 47-48 50 58 60 82 85 121-122 129 131 152 171 193 272 353
fetal muscle	Invitrogen	FMS001	28 32 39-40 45 48 50 57 74 107 121-122 131 137 139-140 147 173 204 230 281
fetal muscle	Invitrogen	FMS002	19 23 32 34 55-56 80-81 98 121-122 124 131-132 158-159 199 212 230 280-281 353 357 360
fetal skin	Invitrogen	FSK001	2 4 14-15 17-19 22 41 46 50 53 59 72 75-76 81-82 84 94 103 106 113 128 135 140 144 156 164 167 170 174 188 209-210 220 227 230 238-239 254 306

TISSUE ORIGIN	LIBRARY/ RNA SOURCE	HYSEQ LIBRARY NAME	SEQ ID NOS:
			321-322 333-335
fetal skin	Invitrogen	FSK002	4 34 47 54 79 84 113 126-127 129 134 156 192-193 208 223 230 241 277 285 333
fetal spleen	BioChain	FSP001	32 104
umbilical cord	BioChain	FUC001	4 19 22-23 32 38-40 46 55-56 58 61 73-75 91 98-99 103 106 110 112 116 120 123 129-130 139 160 165-166 175 182 230 234 249 251 302
fetal brain	GIBCO	HFB001	6 9 16 19-20 25 32 35-36 39-41 45 48 53-54 56 60 73 80-81 83- 92 98 107 112 114 157-159 163 165-166 172 191 197-198 211 226-227 239 350
infant brain	Columbia University	IB2002	6-8 13 15-17 19 21 32 35 41-42 48 50 60-61 77 81 84-85 88 92 104-106 112-113 116 119 134 139 144 160 165-166 168-169 173 176 191 196 199-201 215 223 225 227-228 239 261 285 290 329 339-340 348
infant brain	Columbia University	IB2003	7-9 13 32 39-41 58 92 103 105- 106 144 160 162 199 205-206 219 227-228 271 357
infant brain	Columbia University	IBM002	32 88 340
infant brain	Columbia University	IBS001	6 26-27 32 164 199 340
lung, fibroblast	Stratagene	LFB001	2 4 18-19 25 39-40 46 53 55-56 106 112 124 129 136 139 146 150 164 169 189-190 215 230 239 260 349
adult lung	Invitrogen	LGT002	2 6 8-11 15-16 19 26-28 30 32 39-40 46 48 50 53-56 60-61 66 72 74-75 85 87 92 94 96 98 103-104 108 110 112-113 117 119-120 124 130-131 139-140 149 152-153 155 158-159 167 169 174 176 178 184 189-190 195-196 217 220 229-230 234- 239 248-250 263 265-267 280 286 310 329-330 351-352
lymphocyte	ATCC	LPC001	7 13 16 19 32 39-40 54 63 74 82 96 113 120 126 130-131 133 144 150 178 184-186 223 239 241 260 262 294 305 339
leukocytes	GIBCO	LUC001	1 3-4 7-9 13 16-20 26-27 30 32 34-35 38-40 46 48 51 53-56 63 66 70 72-76 78 82 84-85 87 89 91-92 95-96 101 106 108 110- 112 114 116 120-122 126-127 129-133 136 139 144 146-152 164 175-179 187 192 232 236

TISSUE ORIGIN	LIBRARY/ RNA SOURCE	HYSEQ LIBRARY NAME	SEQ ID NOS:
			239 241 266-267 292-294 306 325-327 329 339 359
leukocytes	Clontech	LUC003	7-8 17 55-56 76 84 112 129 131 161-162 176 180 185-186 329
melanoma	Clontech	MEL004	4 13 17 28 30-31 39-40 83 85 92 113 126 129 139 160 162 182 198 232 239 303 324
mammary gland	Invitrogen	MMG001	8-11 16-21 28 30 32 35 41 45 58-59 61 72 74-75 78 84 87 92 103-104 106-107 110 113 115- 116 123 128 131 134-135 144 152 163 176 181 183 210 212 220-221 230 234 236 238-239 248 251 260 272-273 275-276 306 331 351-352 360
neuron	Stratagene	NTD001	18-19 39-40 45 74 78 85 91
neuron	Stratagene	NTR001	19 21 57 246 265
neuronal cells	Stratagene	NTU001	8-9 18-19 21 32 81 85 87 128 164 174 184
pituitary gland	Clontech	PIT004	13 47 82 87 98 112 288 354
placenta	Clontech	PLA003	13 48 50 58 77 100 106 112 126 129 152 178 232
prostate	Clontech	PRT001	16 19 22 26-27 32 34 46-47 76- 77 92 98 106 112 124 172 214 239 260 280 294
rectum	Invitrogen	REC001	8 10-11 18 30 54 74-76 106 113 123-124 143 163 172 213 220 232 237 260 322-323 340
salivary gland	Clontech	SAL001	8 19 36 74 83 104 118 124 150 176 260 295 304
skin fibroblast	ATCC	SFB002	239
small intestine	Clontech	SIN001	9 17 19 22 32 34 54 57 59-60 73 75 84-85 96 99 107 113 118 134 139 144 149 151 185-187 189 197 199 217 219 221 230- 231 248 250 253-254 260 266- 267 295 304 356
skeletal muscle	Clontech	SKM001	17 19 39-40 48 89 104 116 131 281
spinal cord	Clontech	SPC001	8 19 32 34 38-40 47 58 61 74 80 83-84 89 104 108 131 139- 140 168 187 213 226 236 239 300 350
adult spleen	Clontech	SPLc01	1 46 54 134 236
stomach	Clontech	STO001	7 32 38-40 51 66 74 76 89 117 124 128 169 229 239 253 280 294 296
thalamus	Clontech	THA002	24 30 50 87 124 127 143 163 201 207 220 223 230 266-267 269 279
thymus	Clontech	THM001	7 13 19 25 32 36 39-40 54-56 72 74 82 96 108 113 119 127

TISSUE ORIGIN	LIBRARY/ RNA SOURCE	HYSEQ LIBRARY NAME	SEQ ID NOS:
			137 139 141-142 146 169 184 192 260 276 296
thymus	Clontech	THMc02	9 17 28 30 32 39-40 48 53 61 72 74-75 77 79 82 91 107 112 119-122 125-126 131 139-142 153 171 175-176 178 184 187 205-206 222-223 227 235-236 269 278 289 297 305 310-311 325 327-329 336
thyroid gland	Clontech	THR001	7-11 15 17 19-20 25-27 32 34 36 46 48 53 59 72 82-87 89 91 96 98-99 104 106 110 118-119 121-122 127 130 136 139 144 151-152 158-159 165-167 179 187 204 208 220 239 249 281 283 295 298-299 312 316 344
trachea	Clontech	TRC001	62-63 73 75 86-87 89 101 147 192 239 266-267 282-283
uterus	Clontech	UTR001	4 8 17 19 22 26-27 32 39-40 46 63 82 98 110 130 151

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
1	L29075	Dictyostelium discoideum G-box binding factor	173	21
2	AL359215	Streptomyces coelicolor A3(2) putative phosphoglycerate mutase.	133	28
3	AF228713	Homo sapiens EDAG-1	1671	100
4	AC007130	Homo sapiens similar to 3-hydroxyisobutyrate dehydrogenase ; similar to P29266 (PID:g416873)	1557	100
5	AB040926	Homo sapiens KIAA1493 protein	1973	98
6	AF193016	Homo sapiens methyltransferase COQ3	1609	99
7	U95825	Homo sapiens androgen-induced prostate proliferative shutoff associated protein	2968	63
8	AL390081	Homo sapiens SEMA4B, Semaphorin 4B	3560	99
9	AC002130	Arabidopsis thaliana F1N21.9	258	50
10	Z38061	Saccharomyces cerevisiae mal5, stal, len: 1367, CAI: 0.3, AMYH YEAST P08640 GLUCOAMYLASE S1 (EC 3.2.1.3)	323	27
11	D88733	Equine herpesvirus 1 membrane glycoprotein	284	24
13	M80783	Homo sapiens B12 protein	1144	70
14	U72678	Mus musculus EF-9	792	92
15	AK026486	Homo sapiens unnamed protein product	427	83
16	AK025813	Homo sapiens unnamed protein product	1010	100
17	AF151036	Homo sapiens HSPC202	722	84
18	AY007148	Homo sapiens similar to Homo sapiens HSPC197 mRNA with GenBank Accession Number AF151031.1	984	100
19	X57432	Rattus rattus ribosomal protein S2	956	97
20	AF164793	Homo sapiens protein x 013	386	100
21	J02642	Homo sapiens glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12)	1639	95
22	M34573	Homo sapiens alpha-2 collagen type VI-a	515	100
23	AL109928	Homo sapiens dJ551D2.5 (novel protein)	1999	100
24	AF111858	Homo sapiens dimethylglycine dehydrogenase precursor	3918	99
25	U64854	Caenorhabditis elegans partial CDS	184	25
26	AF151072	Homo sapiens HSPC238	838	99
27	AF151072	Homo sapiens HSPC238	393	96
28	AK024825	Homo sapiens unnamed protein product	1794	99
29	AF285631	Rattus norvegicus secretory carrier membrane protein 4	894	75
30	AK024113	Homo sapiens unnamed protein	3672	99

SEQ ID NO:	ACCESSION NUMBER	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
		product		
31	AL161515	Arabidopsis thaliana putative protein	146	52
32	AJ007798	Homo sapiens stromal antigen 3, (STAG3)	6320	99
33	D31856	Bacillus subtilis HutI protein, imidazolone-5-propionate hydrolase	667	39
34	AL391145	Arabidopsis thaliana putative protein	423	24
35	AF134726	Homo sapiens G7A	1591	46
36	AJ276485	Homo sapiens integral membrane transporter protein	1502	100
37	J05158	Homo sapiens carboxypeptidase N (EC 3.4.17.3)	2274	88
38	X57351	Homo sapiens l-8D	673	97
39	AF230904	Homo sapiens c-Cbl-interacting protein	3437	100
40	AF230904	Homo sapiens c-Cbl-interacting protein	2615	99
41	AF276893	Homo sapiens p21-activated protein kinase 6	3550	100
42	AF269255	Homo sapiens lysosomal apyrase-like protein 1	3198	100
43	S85655	Homo sapiens prohibitin	742	84
44	AB040926	Homo sapiens KIAA1493 protein	1973	98
45	AF151063	Homo sapiens HSPC229	1012	100
46	X68277	Homo sapiens protein-tyrosine phosphatase	1886	100
47	Z98745	Homo sapiens dJ29K1.2	889	51
48	AF032668	Rattus norvegicus rsec15	3738	92
50	AF195534	Rattus norvegicus GERp95	4513	99
51	AF161368	Homo sapiens HSPC105	513	98
52	W73147	Amino acid sequence of the soluble complement receptor 1	651	81
53	AF271212	Homo sapiens disrupter of silencing SAS10	2431	100
54	AF116646	Homo sapiens PRO0082	598	100
55	AF145613	Drosophila melanogaster BcDNA.GH03108	817	46
56	AF145613	Drosophila melanogaster BcDNA.GH03108	884	38
57	AL023803	Homo sapiens dJ616B8.3 (novel gene)	2287	100
59	AC024877	Caenorhabditis elegans contains similarity to Pfam families PF00621 (Guanine nucleotide exchange factor for Rho/Rac/Cdc42-like GTPases, score=58.2, E=1.7e-13, N=10 and PF00169 (PH (pleckstrin homology) domain, score=17.0, E=0.00071, N=1)	296	31
60	AL390114	Leishmania major probable proteophosphoglycan	154	30
61	AL031427	Homo sapiens dJ167A19.1 (novel	732	51

SEQ ID NO:	ACCESSION NUMBER	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
		protein)		
62	AL390935	Leishmania major possible CG17807 protein	151	43
63	J04067	Canis familiaris microsomal signal peptidase	930	99
64	AF062378	Mus musculus calmodulin-binding protein SHA1	1782	60
65	AE001002	Archaeoglobus fulgidus ATP-dependent RNA helicase, putative	195	29
66	X69065	Erythroid ankyrin [Mus musculus]	181	30
68	AF017807	Homo sapiens Arp2/3 complex 16kDa subunit	371	100
69	AC007660	Arabidopsis thaliana putative translation initiation factor	173	29
70	AJ243177	Xenopus laevis Xenopus RPA interacting protein alpha	447	42
71	AF226055	Homo sapiens HTGN29	1367	100
72	AF090930	Homo sapiens PRO0478	180	89
73	AF118084	Homo sapiens PRO1914	350	98
74	AB028893	Homo sapiens ribosomal protein S11	824	100
75	AK024500	Homo sapiens FLJ00109 protein	1514	100
76	AF238866	Mus musculus LNR42	1041	99
77	AC026875	Arabidopsis thaliana T6D22.6	129	30
78	U42436	Caenorhabditis elegans Hypothetical protein C49H3.3	130	32
79	M80902	Homo sapiens AHNAK nucleoprotein	8529	99
80	W90962	Human CSGP-2 protein [homo sapiens]	2346	99
81	AF206661	Gallus gallus neuronal tetraspanin	1066	81
82	S73591	Homo sapiens brain-expressed HHCPA78 homolog VDUP1	800	42
83	AF116650	Homo sapiens PRO0786	302	100
84	L26335	Cavia porcellus zinc finger protein	1493	99
85	AF209198	Homo sapiens zinc finger protein 277	2357	100
86	AE001399	Plasmodium falciparum GAF domain protein (cyclic nt signal transduct.)	178	35
87	Y48226	Human prostate cancer-associated protein 12 [Homo sapiens]	1204	96
88	M94389	Loligo pealei neurofilament protein	165	23
89	AF121775	Homo sapiens nasopharyngeal carcinoma susceptibility protein LZ16	903	58
90	AF116675	Homo sapiens PRO1942	257	100
91	AE002760	Drosophila melanogaster CG14464 gene product	195	43
92	AK000100	Homo sapiens unnamed protein product	841	100
93	AB020236	Homo sapiens ribosomal protein L27A	754	99
94	AF119865	Homo sapiens PRO2176	470	97
96	AF138863	Homo sapiens PRO1677	868	99
97	X14361	Homo sapiens CR-1 receptor SCR9 (or	135	100

SEQ ID NO:	ACCESSION NUMBER	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
		16) C-term. (21 is 3rd base in codon) (106 is 1st base in codon)		
98	Z24725	Homo sapiens mitogen inducible gene mig-2	3576	99
99	U64598	Caenorhabditis elegans weakly similar to S. cerevisiae PTM1 precursor (SP:P32857)	398	45
100	AC004770	Homo sapiens BC269730 4	1527	84
101	AL139075	Campylobacter jejuni NOL1\NOP2\sun family protein	312	35
102	AF113694	Homo sapiens PRO1359	416	100
103	U15158	Homo sapiens ESP-2	564	41
104	AL020996	Homo sapiens dJ317E23.3 (novel protein)	1818	99
105	AF161370	Homo sapiens HSPC107	824	100
106	AK000161	Homo sapiens unnamed protein product	284	100
107	AK001784	Homo sapiens unnamed protein product	684	100
108	AE000913	Methanobacterium thermoautotrophicum conserved protein	221	25
109	AF165527	Homo sapiens DGCR8	859	100
110	AF230200	Homo sapiens OVN6-2	358	95
111	Z72516	Caenorhabditis elegans T25G3.1	180	36
112	AF201940	Homo sapiens DC6	505	100
113	AK001301	Homo sapiens unnamed protein product	2040	98
114	U23515	Caenorhabditis elegans weakly similar to gastrula zinc finger protein	205	47
115	AF228021	Bos taurus cyclophilin I	345	91
116	AF166124	Homo sapiens selenoprotein X	527	100
117	AF079445	Dictyostelium discoideum TipC	529	30
118	AB032179	Homo sapiens similar to mouse Ehm2	2255	100
119	U89867	Homo sapiens nuclear matrix protein 55	2449	98
120	U29056	Mus musculus Src-like adapter protein	352	47
121	U22015	Mus musculus retinoid X receptor interacting protein	2190	73
122	AF113538	Homo sapiens retinoid x receptor interacting protein	1800	100
123	AK000158	Homo sapiens unnamed protein product	740	100
124	AF260924	Mus musculus UFD2/D4COLE1E fusion protein	1222	82
125	U12465	Homo sapiens ribosomal protein L35	591	97
126	AJ277591	Homo sapiens p15-2a protein	749	100
127	AF205599	Mus musculus transposase-like protein	2406	74
128	U58975	Homo sapiens proto-oncogene	659	90

SEQ ID NO:	ACCESSION NUMBER	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
129	X98374	Rattus norvegicus KIS	2193	99
130	AF151049	Homo sapiens HSPC215	627	100
131	M59807	Homo sapiens putative	907	99
132	U12979	Homo sapiens PC4	563	99
133	AF076642	Homo sapiens regulator of G-protein signaling 13	1218	100
134	AF116718	Homo sapiens PRO2900	396	100
135	AC018758	Homo sapiens GPI-anchored metastasis-associated protein homolog	213	31
136	AC025416	Arabidopsis thaliana F5011.12	135	36
137	M83186	Homo sapiens cytochrome c oxidase subunit VIIa	247	100
138	AF232937	Mus musculus thymic stroma derived lymphopoietin	247	41
139	M15841	Homo sapiens U2 small nuclear ribonucleoprotein B''	638	100
140	AK026916	Homo sapiens unnamed protein product	2612	99
141	Y05317	Human secreted protein bn97_1 [Homo sapiens]	1508	100
142	Y05317	Human secreted protein bn97_1 [Homo sapiens]	851	99
143	AF041083	Rattus norvegicus RoBo-1	139	25
144	AC024260	Arabidopsis thaliana cell division control protein, putative; 15914-18846	194	25
146	AL022398	Homo sapiens dJ434014.3.2 (putative protein) (isoform 2)	575	100
147	AF212842	Homo sapiens immunoglobulin-like transcript 11 protein	1280	99
148	AB042827	Rattus norvegicus Nadrin	477	66
149	AK001841	Homo sapiens unnamed protein product	1916	100
150	AJ278120	Homo sapiens putative ankyrin-repeat containing protein	540	98
151	AL135959	Homo sapiens dJ233G16.1 (novel protein)	770	100
152	Y58196	[Homo sapiens] Human STRAP-3 protein, encoded by testis EST AI139607	671	100
153	U41060	Homo sapiens LIV-1 protein	373	50
154	AJ007590	Homo sapiens XRP2 protein	1766	100
155	AB046868	Xenopus laevis beta-catenin-interacting protein	125	46
156	AB027258	Homo sapiens basal transcriptional activator hABT1	1408	100
157	AF039656	Homo sapiens neuronal tissue-enriched acidic protein	1109	96
158	AK001425	Homo sapiens unnamed protein product	1695	99
159	AK001425	Homo sapiens unnamed protein	858	98

SEQ ID NO:	ACCESSION NUMBER	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
		product		
160	AK002030	Homo sapiens unnamed protein product	1029	100
161	X79417	Sus scrofa 40S ribosomal protein S12	510	83
162	X12597	Homo sapiens HMG-1 protein (AA 1-215)	1140	99
163	AK001159	Homo sapiens unnamed protein product	764	100
164	AK000020	Homo sapiens unnamed protein product	1613	100
165	AK001322	Homo sapiens unnamed protein product	1207	100
166	AK001322	Homo sapiens unnamed protein product	892	98
167	AE003822	Drosophila melanogaster CG8493 gene product	357	36
168	AF023451	Bos taurus guanine nucleotide-exchange protein	187	21
169	AK000154	Homo sapiens unnamed protein product	673	100
170	AJ132702	Mus musculus ATFa-associated factor	435	64
172	AL022311	Homo sapiens dJ1014D13.3 (novel protein)	405	38
174	AB017634	Mus musculus ENP	770	65
175	U40407	synthetic construct T cell receptor alpha chain	1119	80
176	AF043179	Homo sapiens T cell receptor beta chain	681	73
177	AF116678	Homo sapiens PRO1995	587	100
178	AF217522	Homo sapiens uncharacterized bone marrow protein BM046	262	42
179	AB046074	Macaca fascicularis unnamed protein product	515	83
180	X79417	Sus scrofa 40S ribosomal protein S12	429	84
181	AF002668	Homo sapiens MLD	1235	65
182	AB036422	Bos taurus molybdopterin cofactor sulfurase	3509	79
184	AF036696	Caenorhabditis elegans contains similarity to Brassica oleracea non-green plastid phosphate/triose-phosphate translocator precursor (GB:U13632)	662	42
185	AJ277276	Homo sapiens rapa-2	5155	99
186	AJ277275	Homo sapiens rapa-1	5086	100
187	U22296	Rattus norvegicus casein kinase 1 gamma 1 isoform	1444	93
188	AE003750	Drosophila melanogaster CG9996 gene product	468	44
189	Z97056	Homo sapiens dJ434P1.2 (KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum	1103	100

SEQ ID NO:	ACCESSION NUMBER	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
		protein retention receptor 3)		
190	AF081126	Drosophila melanogaster ER lumen protein retaining receptor	409	75
192	AF226047	Homo sapiens GL002	863	100
193	AF269167	Homo sapiens arsenite related gene 1	906	60
195	U41805	Mus musculus putative T1/ST2 receptor binding protein precursor	162	26
197	AL357374	Homo sapiens bA353C18.2 (novel protein)	404	97
199	M34551	Homo sapiens 52-kD Ro/SSA ribonucleoprotein	964	42
202	AF230201	Homo sapiens OVC10-2	396	100
203	AK001984	Homo sapiens unnamed protein product	658	100
204	AK000530	Homo sapiens unnamed protein product	691	100
205	U37134	Drosophila melanogaster inturnd protein	248	23
206	U37134	Drosophila melanogaster inturnd protein	244	23
208	AB033130	Mus musculus testis-specific gene	871	85
209	AK000464	Homo sapiens unnamed protein product	221	100
210	AJ277557	Homo sapiens mitochondrial 5'(3')-deoxyribonucleotidase (dNT-2)	617	100
211	AF127564	Arabidopsis thaliana ubiquitin-protein ligase 1	854	42
213	Y17108	Homo sapiens rhomboid-related protein	485	39
214	AL132776	Homo sapiens dJ393D12.2 (novel LIM domain protein)	1660	99
215	U73819	Mus musculus polypeptide GalNAc transferase-T4	1039	42
216	AL035406	Homo sapiens dJ233K16.1 (KIAA0444, a putative chromodomain helicase DNA binding protein 3 (CHD3))	3844	100
217	M15800	Homo sapiens MAL protein	308	42
218	L29554	Rattus norvegicus alpha 2,6-sialyltransferase	942	80
219	AL137315	Homo sapiens hypothetical protein	983	100
220	AK026027	Homo sapiens unnamed protein product	647	100
221	AL137584	Homo sapiens hypothetical protein	246	97
223	AC005498	Homo sapiens R31665 1	1752	78
225	AC010155	Arabidopsis thaliana F3M18.5	171	34
226	AL080276	Homo sapiens dJ101K10.2 (regulator of G-protein signaling 17 (RGS17) (RGSZ2))	1126	100
227	AF042345	Homo sapiens truncated EVI5	1815	64
228	J04214	Bos taurus retinaldehyde-binding protein precursor	504	39

SEQ ID NO:	ACCESSION NUMBER	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
230	AF181263	Homo sapiens EH domain containing 2	2816	99
231	AP001660	Homo sapiens putative gene, multidrug resistance associated protein like	1424	100
232	AB000910	Sus scrofa ribosomal protein	542	100
233	AL133404	Homo sapiens dJ238023.9 (novel protein similar to rat SAC (soluble adenylyl cyclase))	298	100
234	X51397	Mus musculus MyD88 protein (AA 1-243)	136	25
235	X01403	Homo sapiens T-cell receptor alpha-chain	840	90
236	X14254	Rattus rattus invariant chain (AA 1-280)	745	77
238	U23084	Saccharomyces cerevisiae Ynl0470p	344	35
239	X03342	Homo sapiens rpL32 (aa 1-135)	152	96
240	AF116669	Homo sapiens PRO1828	237	100
241	U23181	Caenorhabditis elegans final exon in repeat region; similar to long tandem repeat region of sialidase (SP:TCNA_TRYCR, P23253) and neurofilament H protein	135	25
242	AF263913	Mus musculus fidgetin	3864	97
243	AF090892	Homo sapiens PRO0106	290	100
244	U21310	Caenorhabditis elegans F40H6.3 gene product	153	27
246	AK001673	Homo sapiens unnamed protein product	3661	100
247	AL022603	Arabidopsis thaliana putative protein	166	43
248	AL023803	Homo sapiens dJ616B8.3 (novel gene)	339	42
249	X52140	Rattus norvegicus precursor polypeptide (AA -28 to 1152)	5429	87
250	AB020755	Arabidopsis thaliana gene id:MZN1.18~unknown protein	139	46
251	AE003619	Drosophila melanogaster CG7224 gene product	186	43
252	AC004997	Homo sapiens match to ESTs Z43979 (NID:g573097), R19699 (NID:g774333), and C01164 (NID:g1433394); alternatively spliced form of H_DJ130H16.1a (C-terminal truncation confirmed by C01164)	388	67
254	AE003588	Drosophila melanogaster CG13947 gene product	115	42
256	Y50934	Human fetal brain cDNA clone vc30_1 derived protein #1 [Homo sapiens]	498	100
257	AF242768	Homo sapiens mesenchymal stem cell protein DSC43	1554	100
259	M95779	Bos taurus G protein gamma-5 subunit	333	98

SEQ ID NO:	ACCESSION NUMBER	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
260	AL035521	Arabidopsis thaliana putative protein	145	28
261	AF247501	Drosophila melanogaster PINEAPPLE EYE	333	36
263	AL034548	Homo sapiens dJ1103G7.2 (novel protein)	262	100
264	AF119851	Homo sapiens PRO1722	143	63
265	L41834	Ensis minor nuclear protein	173	26
266	X97966	Homo sapiens calcyphosine	963	100
267	X97966	Homo sapiens calcyphosine	660	95
269	AF022383	Homo sapiens complexin I	668	99
271	Y10054	Rattus norvegicus 3-hydroxy-3-methylglutaryl CoA lyase	224	67
274	AF153201	Homo sapiens zinc finger protein dp	179	36
275	X85738	Bos taurus novel brain-specific protein	326	55
277	AF250342	Arabidopsis thaliana SMC-related protein MSS2	266	39
278	AL080242	Homo sapiens bA554C12.1 (RBX1 or ROC1 (ring-box or ring finger protein 1))	131	100
279	Z83760	Ciona intestinalis COS41.4	1162	62
280	U41534	Caenorhabditis elegans similar to yeast MAK16 protein (SP:MK16 YEAST,P10962)	721	54
281	AF272975	Gallus gallus smoothelin-C	543	37
282	AL035414	Homo sapiens dJ667H12.2.2 (novel protein (isoform 2))	588	100
283	AF116661	Homo sapiens PRO1438	145	62
285	AK001757	Homo sapiens unnamed protein product	1300	100
287	U20897	Homo sapiens melanoma ubiquitous mutated protein	2133	100
289	U09847	Homo sapiens zinc finger protein	880	100
290	AJ000079	Trypanosoma cruzi glycosylphosphatidylinositol-specific phospholipase C	225	26
291	AF156549	Mus musculus putative E1-E2 ATPase	2108	49
293	AF161345	Homo sapiens HSPC082	439	100
294	AF116694	Homo sapiens PRO2219	351	88
295	M74027	Homo sapiens mucin	461	39
298	AL133640	Homo sapiens hypothetical protein	2149	100
299	M17886	Homo sapiens acidic ribosomal phosphoprotein (P1)	161	76
300	Y99368	Human PRO1326 (UNQ686) amino acid sequence SEQ ID NO:100 [Homo sapiens]	300	32
303	AE003708	Drosophila melanogaster CG6171 gene product	144	27
304	M32639	Homo sapiens statherin precursor	276	87
305	Z83844	Homo sapiens dJ37E16.2 (SH3-domain binding protein 1)	897	96

SEQ ID NO:	ACCESSION NUMBER	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
306	AE003791	Drosophila melanogaster CG18065 gene product	120	32
307	AF135026	Homo sapiens kallikrein-like protein 3 splice variant 1	1392	100
310	AF198257	Felis catus immunoglobulin kappa light chain	678	76
311	X57725	Homo sapiens TCR Vbeta 22a	626	100
312	AC018513	Homo sapiens unknown	818	100
313	X03249	Bos taurus epsilon-4 beta-globin	321	79
314	AB046099	Macaca fascicularis unnamed protein product	395	88
315	AC006033	Homo sapiens T cell receptor gamma chain; match to S08328 (PID:g106470)	1017	95
316	AB046103	Macaca fascicularis unnamed protein product	801	94
317	U88895	Homo sapiens ORF2	399	81
318	U09848	Homo sapiens zinc finger protein	242	49
319	AB003184	Homo sapiens ISLR	880	59
320	AB036921	Chrysophrys major maturation-inducing protein	797	69
322	AF284422	Homo sapiens cation-chloride cotransporter-interacting protein	4694	100
325	AE000659	Homo sapiens TCRAV8S2	577	100
327	R59748	T cell receptor Valpha2.3 chain [homo sapiens]	636	100
328	AJ004871	Homo sapiens TCR alpha chain	1328	94
329	AF043179	Homo sapiens T cell receptor beta chain	1286	92
330	AF090930	Homo sapiens PRO0478	140	50
332	AF077043	Homo sapiens 60S ribosomal protein L36	275	87
333	AL121988	Homo sapiens dJ34M23.3 (gap junction protein, beta 4 (connexin 30.3))	1457	100
334	D86424	Mus musculus high-sulfur keratin protein	521	87
335	AF090434	Fundulus heteroclitus cytochrome P450 2N1	760	40
336	AF116688	Homo sapiens PRO2133	370	98
337	X85372	Homo sapiens Sm protein F	222	84
338	D87009	Homo sapiens putative	1822	99
339	AE000860	Methanobacterium thermoautotrophicum conserved protein	631	35
340	AL049759	Homo sapiens dJ930L11.1 (similar to KIAA0397)	1305	98
341	AE000004	Mycoplasma pneumonia MG207 homolog, from M. genitalium	141	27
342	AF151076	Homo sapiens HSPC242	135	100
343	AB037902	Homo sapiens truncated aldo-keto reductase	670	100

SEQ ID NO:	ACCESSION NUMBER	DESCRIPTION	SMITH- WATERMAN SCORE	% IDENTITY
345	M33014	Drosophila melanogaster ubiquitin	153	62
346	AF053356	Homo sapiens leucin rich neuronal protein	580	46
348	AL137512	Homo sapiens hypothetical protein	751	100
349	S68015	Homo sapiens c6.1A	1664	100
350	AF151037	Homo sapiens HSPC203	318	100
351	AB036432	Homo sapiens advanced glycation endproducts receptor	2133	100
352	AB036432	Homo sapiens advanced glycation endproducts receptor	2094	96
353	AC006942	Homo sapiens R31181_2, partial protein	547	100
354	AF125535	Homo sapiens pp21 homolog	502	95
355	AF227130	Homo sapiens candidate taste receptor T2R3	1629	100
357	AB046626	Macaca fascicularis hypothetical protein	291	93
358	Z69597	Canis familiaris Rod transducin alpha subunit	1145	100
359	AE000659	Homo sapiens TCRAV16S1	565	100
360	Y99368	Human PRO1326 (UNQ686) Amino acid sequence SEQ ID NO:100. [Homo sapiens]	2034	100
362	L06499	Homo sapiens ribosomal protein L37a	187	55

TABLE 3

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
1	PR00651	5-HYDROXYTRYPTAMINE 2B RECEPTOR SIGNATURE	PR00651E 10.53 4.025e-06 60-80
2	BL00126	3'5'-cyclic nucleotide phosphodiesterases proteins.	BL00126B 15.20 7.750e-06 208-220
3	DM00892	3 RETROVIRAL PROTEINASE.	DM00892C 23.55 9.438e-07 285-319
4	BL00895	3-hydroxyisobutyrate dehydrogenase proteins.	BL00895B 21.14 7.061e-22 151-190 BL00895C 20.10 8.071e-22 200-236 BL00895A 12.61 1.973e-18 42-63
5	DM00099	4 kw A55R REDUCTASE TERMINAL DIHYDROPTERIDINE.	DM00099A 5.17 5.263e-06 409-415
7	PF00598	Influenza Matrix protein (M1).	PF00598C 19.35 3.333e-07 531-563
9	DM00522	499 kw TRYPSIN KINASE KUNITZ PANCREATIC.	DM00522A 8.30 3.250e-06 287-297
10	PR00514	5-HYDROXYTRYPTAMINE 1D RECEPTOR SIGNATURE	PR00514C 11.01 9.061e-07 81-100
11	PR00514	5-HYDROXYTRYPTAMINE 1D RECEPTOR SIGNATURE	PR00514C 11.01 9.061e-07 81-100
12	PR00775	90 KD HEAT SHOCK PROTEIN SIGNATURE	PR00775G 10.64 3.487e-07 8-27
13	PR00902	VP6 BLUE-TONGUE VIRUS INNER CAPSID PROTEIN SIGNATURE	PR00902K 11.09 1.000e-05 176-200
14	PR00875	MOLLUSC METALLOTHIONEIN SIGNATURE	PR00875A 5.83 1.127e-07 159-171 PR00875D 5.00 1.000e-05 158-169
15	DM01803	1 HERPESVIRUS GLYCOPROTEIN H.	DM01803C 7.00 9.200e-07 181-191 DM01803A 10.51 1.000e-06 178-199 DM01803C 7.00 7.337e-06 214-224
16	PF00803	3A movement protein.	PF00803D 14.15 2.622e-06 41-71
17	PR00170	SODIUM CHANNEL SIGNATURE	PR00170G 7.74 1.000e-05 24-53
18	PR00701	60KD INNER MEMBRANE PROTEIN SIGNATURE	PR00701E 13.83 5.684e-06 117-133
20	DM01415	6 SALIVARY GLUE PROTEIN.	DM01415A 6.65 6.063e-06 55-68
21	DM01418	352 FIBRILLAR COLLAGEN CARBOXYL-TERMINAL.	DM01418A 20.83 7.731e-06 64-112
22	BL00616	Histidine acid phosphatases phosphohistidine proteins.	BL00616D 15.83 7.268e-06 117-133

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
23	DM00611	9 kw LECTIN HTPG SERINE GNTR.	DM00611A 7.73 5.826e-06 173-181
24	BL00832	2'-5'-oligoadenylate synthetases proteins.	BL00832D 21.81 5.017e-06 425-449
25	PR00354	7FE FERREDOXIN SIGNATURE	PR00354C 5.72 8.590e-09 543-561
26	PR00217	43 KD POSTSYNAPTIC PROTEIN SIGNATURE	PR00217C 10.91 3.851e-07 89-105
27	PR00513	5-HYDROXYTRYPTAMINE 1B RECEPTOR SIGNATURE	PR00513A 7.75 1.439e-06 168-180
28	DM00552	GROWTH FACTOR AND CYTOKINES RECEPTORS FAMILY.	DM00552A 11.97 1.000e-05 130-152
29	PR00701	60KD INNER MEMBRANE PROTEIN SIGNATURE	PR00701I 8.59 3.088e-06 102-126
30	DM00060	338 kw NEUREXIN ALPHA III CYSTEINE.	DM00060 6.92 3.284e-07 680-690
34	PR00517	5-HYDROXYTRYPTAMINE 2C RECEPTOR SIGNATURE	PR00517D 7.66 6.971e-07 484-496
35	PR00701	60KD INNER MEMBRANE PROTEIN SIGNATURE	PR00701A 14.28 4.183e-06 722-744
37	PR00513	5-HYDROXYTRYPTAMINE 1B RECEPTOR SIGNATURE	PR00513C 10.79 8.927e-07 287-304
38	PR00166	AROMATIC AMINO ACID PERMEASE SIGNATURE	PR00166I 11.06 1.000e-05 98-118
39	PR00003	4-DISULPHIDE CORE SIGNATURE	PR00003A 14.69 3.803e-06 311-321
40	PR00003	4-DISULPHIDE CORE SIGNATURE	PR00003A 14.69 3.803e-06 311-321
41	PR00517	5-HYDROXYTRYPTAMINE 2C RECEPTOR SIGNATURE	PR00517D 7.66 8.788e-07 2-14
42	PR00701	60KD INNER MEMBRANE PROTEIN SIGNATURE	PR00701F 14.45 7.750e-06 25-46
43	DM00895	7 kw REVERSE TRANSCRIPTASE RNA POLYMERASE.	DM00895B 8.85 4.185e-06 157-167
44	DM00099	4 kw A55R REDUCTASE TERMINAL DIHYDROPTERIDINE.	DM00099A 5.17 5.263e-06 409-415
45	PR00519	5-HYDROXYTRYPTAMINE 5B RECEPTOR SIGNATURE	PR00519A 8.06 8.984e-06 137-154
46	PR00519	5-HYDROXYTRYPTAMINE 5B RECEPTOR SIGNATURE	PR00519B 9.99 1.828e-07 151-168
47	DM00892	3 RETROVIRAL PROTEINASE.	DM00892B 9.78 2.047e-06 21-27
48	BL00832	2'-5'-oligoadenylate synthetases	BL00832B 15.45 6.836e-07 375-416

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		proteins.	
49	DM00588	8 kw CHO2 ALPHA ANTIGEN PARAMYOSIN.	DM00588A 10.87 7.128e-06 20-31
50	DM00604	2 SHIGA/RICIN RIBOSOMAL INACTIVATING TOXINS.	DM00604D 13.26 8.250e-06 263-273
51	BL01193	Ribosomal protein S8e proteins.	BL01193A 13.21 1.000e-05 19-50
52	PR00172	GLUCOSE TRANSPORTER SIGNATURE	PR00172F 8.47 9.901e-06 69-90
53	PR00297	10 KD CHAPERONIN SIGNATURE	PR00297A 13.91 4.740e-06 379-395
54	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320A 16.74 9.710e-06 81-96
55	PR00517	5-HYDROXYTRYPTAMINE 2C RECEPTOR SIGNATURE	PR00517C 5.36 4.126e-07 352-365
56	PR00517	5-HYDROXYTRYPTAMINE 2C RECEPTOR SIGNATURE	PR00517C 5.36 4.126e-07 352-365
57	DM00547	1 kw CHROMO BROMODOMAIN SHADOW GLOBAL.	DM00547E 13.94 4.656e-06 229-252
58	PF00506	Influenza virus nucleoprotein.	PF00506I 10.26 3.723e-06 32-68
60	DM00522	499 kw TRYPSIN KINASE KUNITZ PANCREATIC.	DM00522B 9.43 7.338e-07 171-185
61	DM01123	5 kw RESISTANCE TETRACYCLINE METHYLENOMYCIN EXPORT.	DM01123B 20.06 3.187e-06 205-244
62	PR00439	11-S SEED STORAGE PROTEIN FAMILY SIGNATURE	PR00439G 17.85 9.239e-07 82-100
63	PR00652	5-HYDROXYTRYPTAMINE 7 RECEPTOR SIGNATURE	PR00652F 11.66 4.767e-06 100-122
64	DM01785	72 PYRUVATE (FLAVODOXIN) DEHYDROGENASE.	DM01785A 14.90 2.196e-06 218-261
65	PR00652	5-HYDROXYTRYPTAMINE 7 RECEPTOR SIGNATURE	PR00652A 8.92 5.104e-06 315-336
67	BL00405	43 Kd postsynaptic protein.	BL00405F 8.07 9.920e-06 13-44
68	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380D 9.93 9.043e-06 44-66
69	PR00683	SPECTRIN PLECKSTRIN HOMOLOGY DOMAIN SIGNATURE	PR00683D 15.87 9.571e-06 46-65
70	PR00753	1-AMINOCYCLOPROPANE- 1-CARBOXYLATE SYNTHASE SIGNATURE	PR00753C 13.93 7.330e-06 192-213
71	PF00602	Influenza RNA- dependant RNA	PF00602J 9.52 9.727e-06 47-102

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		polymerase subunit PB1.	
72	DM01855	PROTEIN-GLUTAMATE O-METHYLTRANSFERASE.	DM01855A 11.54 7.594e-06 27-44
74	BL01277	Ribonuclease PH proteins.	BL01277A 17.39 1.000e-05 50-88
75	PR00517	5-HYDROXYTRYPTAMINE 2C RECEPTOR SIGNATURE	PR00517G 16.45 6.919e-06 755-771
77	PF01073	3-beta hydroxysteriod dehydrogenase/isomerase family.	PF01073B 12.26 9.767e-07 102-147
78	PR00351	MAS20 PROTEIN IMPORT RECEPTOR SIGNATURE	PR00351C 7.03 6.182e-06 99-112 PR00351C 7.03 1.000e-05 5-18
79	DM00611	9 kw LECTIN HTPG SERINE GNTR.	DM00611C 11.08 4.549e-06 1489-1501
80	DM01111	4 kw PHOSPHATASE TRANSFORMING 61K PDF1.	DM01111C 9.35 2.800e-06 44-73
82	PD02407	3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCER.	PD02407B 16.51 1.000e-06 94-111
83	PR00116	ARGINASE SIGNATURE	PR00116D 14.91 9.850e-06 14-44
84	PR00517	5-HYDROXYTRYPTAMINE 2C RECEPTOR SIGNATURE	PR00517F 11.48 7.250e-06 45-62
87	DM00522	499 kw TRYPSIN KINASE KUNITZ PANCREATIC.	DM00522B 9.43 3.535e-07 223-237
88	DM00303	6 LEA 11-MER REPEAT REPEAT.	DM00303A 13.20 8.034e-08 270-320
91	DM01242	3 THREONINE--TRNA LIGASE.	DM01242B 23.57 4.672e-06 71-120
92	PR00388	3',5'-CYCLIC NUCLEOTIDE CLASS II PHOSPHODIESTERASE SIGNATURE	PR00388E 6.66 3.797e-06 124-136
93	PD02407	3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCER.	PD02407B 16.51 9.676e-06 15-32
94	PF00506	Influenza virus nucleoprotein.	PF00506I 10.26 4.555e-06 16-52
95	PR00551	2-S GLOBULIN FAMILY SIGNATURE	PR00551H 11.29 8.740e-06 21-39
96	PR00756	MEMBRANE ALANYL DIPEPTIDASE (M1) FAMILY SIGNATURE	PR00756E 11.91 9.338e-06 68-81
97	PR00547	X OPIOID RECEPTOR SIGNATURE	PR00547B 6.96 3.268e-06 17-36
98	PR00651	5-HYDROXYTRYPTAMINE 2B RECEPTOR	PR00651A 16.53 4.000e-06 653-674

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		SIGNATURE	
99	PR00208	GLIADIN AND LMW GLUTENIN SUPERFAMILY SIGNATURE	PR00208C 11.51 9.775e-06 54-71
101	PR00451	CHITIN-BINDING DOMAIN SIGNATURE	PR00451A 6.49 1.000e-05 152-161
102	BL00832	2'-5'-oligoadenylate synthetases proteins.	BL00832B 15.45 7.569e-06 1-42
103	BL00405	43 Kd postsynaptic protein.	BL00405J 13.28 6.952e-06 142-176
104	DM01242	3 THREONINE--TRNA LIGASE.	DM01242F 10.61 5.500e-07 187-201
105	DM01834	8 HYDROGENASE (FE) SMALL CHAIN.	DM01834A 4.96 7.097e-06 53-60
107	PR00101	ASPARTATE CARBAMOYLTRANSFERASE SIGNATURE	PR00101E 5.52 1.000e-05 111-117
109	PR00902	VP6 BLUE-TONGUE VIRUS INNER CAPSID PROTEIN SIGNATURE	PR00902K 11.09 9.922e-06 91-115
110	PR00259	TRANSMEMBRANE FOUR FAMILY SIGNATURE	PR00259A 9.27 9.716e-06 9-33
111	BL00785	5'-nucleotidase proteins.	BL00785B 10.65 6.507e-06 53-67
112	PR00652	5-HYDROXYTRYPTAMINE 7 RECEPTOR SIGNATURE	PR00652G 10.94 5.429e-06 14-32
113	PR00517	5-HYDROXYTRYPTAMINE 2C RECEPTOR SIGNATURE	PR00517D 7.66 3.661e-06 372-384
114	PF00637	7-fold repeat proteins in Clathrin, also in VPS proteins.	PF00637D 7.09 9.449e-07 32-44
115	DM01235	5 kw T4 55.10 METHYLCYTOSINE TRANSCRIPTASE.	DM01235 20.29 9.832e-06 77-108
116	PR00873	ECHINOIDEA (SEA URCHIN) METALLOTHIONEIN SIGNATURE	PR00873C 6.16 9.906e-06 70-81
117	PR00387	3'5'-CYCLIC NUCLEOTIDE PHOSPHODIESTERASE SIGNATURE	PR00387D 10.81 4.889e-06 155-172
118	PF00598	Influenza Matrix protein (M1).	PF00598A 14.24 7.158e-06 211-254
119	BL00895	3-hydroxyisobutyrate dehydrogenase proteins.	BL00895B 21.14 8.036e-06 428-467
120	PR00419	ADRENODOXIN REDUCTASE FAMILY SIGNATURE	PR00419D 10.62 9.430e-06 18-33
121	DM00396	5 kw INTRON COI ND4L	DM00396B 7.85 3.739e-07 381-389

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		ND5.	
122	BL00198	4Fe-4S ferredoxins, iron-sulfur binding region proteins.	BL00198 10.43 5.500e-06 135-147
123	DM01554	1 THYROLIBERIN PRECURSOR.	DM01554E 10.78 4.208e-06 93-110
124	BL00405	43 Kd postsynaptic protein.	BL00405G 7.78 6.294e-06 130-167
125	PR00298	60 KD CHAPERONIN SIGNATURE	PR00298D 10.23 3.847e-06 14-40
126	PR00317	EPENDYMIN SIGNATURE	PR00317A 13.39 9.897e-06 79-99
127	PR00513	5-HYDROXYTRYPTAMINE 1B RECEPTOR SIGNATURE	PR00513B 17.51 3.971e-06 277-290
130	PR00516	5-HYDROXYTRYPTAMINE 2A RECEPTOR SIGNATURE	PR00516G 15.11 8.811e-06 18-35
131	PR00828	FORMIN SIGNATURE	PR00828F 8.56 1.000e-05 61-81
132	DM01269	303 kw ACTIVATING RAN GTPASE ISOZYME.	DM01269A 23.35 7.279e-06 28-56
133	PR00586	PROSTANOID EP4 RECEPTOR SIGNATURE	PR00586B 14.97 7.322e-06 10-28 PR00586H 8.65 9.791e-06 16-40
134	PF00954	S-locus glycoprotein family.	PF00954D 18.68 9.843e-06 9-44
135	PR00018	KRINGLE DOMAIN SIGNATURE	PR00018A 14.52 1.000e-05 120-136
136	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.	BL00115E 14.13 9.921e-06 40-69
137	PR00521	ANDROGEN RECEPTOR SIGNATURE	PR00521A 17.02 9.729e-06 5-25
138	PR00701	60KD INNER MEMBRANE PROTEIN SIGNATURE	PR00701I 8.59 5.267e-07 16-40
139	DM01269	303 kw ACTIVATING RAN GTPASE ISOZYME.	DM01269A 23.35 7.085e-08 93-121
140	PR00915	LUTEOVIRUS GROUP 1 COAT PROTEIN SIGNATURE	PR00915D 16.14 1.000e-05 374-392
143	DM00522	499 kw TRYPSIN KINASE KUNITZ PANCREATIC.	DM00522A 8.30 4.441e-06 94-104
144	PF00598	Influenza Matrix protein (M1).	PF00598B 13.10 1.623e-06 89-133
145	PR00217	43 KD POSTSYNAPTIC PROTEIN SIGNATURE	PR00217C 10.91 6.250e-06 24-40
147	PR00701	60KD INNER MEMBRANE PROTEIN SIGNATURE	PR00701A 14.28 6.049e-06 266-288
148	PR00513	5-HYDROXYTRYPTAMINE 1B RECEPTOR SIGNATURE	PR00513D 11.06 9.920e-06 103-121
149	PF00603	Influenza RNA- dependant RNA polymerase subunit	PF00603D 8.49 9.319e-07 30-85

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		PA.	
150	DM01688	2 POLY-IG RECEPTOR.	DM01688N 11.93 9.920e-08 72-100
151	PF00637	7-fold repeat proteins in Clathrin, also in VPS proteins.	PF00637B 10.68 6.906e-06 186-195
152	BL00461	6-phosphogluconate dehydrogenase proteins.	BL00461A 15.90 1.764e-08 21-57
153	DM01554	1 THYROLIBERIN PRECURSOR.	DM01554A 6.07 2.565e-06 589-599
154	BL00405	43 Kd postsynaptic protein.	BL00405E 8.84 8.125e-06 109-135
155	PF00637	7-fold repeat proteins in Clathrin, also in VPS proteins.	PF00637A 15.49 5.179e-06 42-65
156	PR00517	5-HYDROXYTRYPTAMINE 2C RECEPTOR SIGNATURE	PR00517D 7.66 7.339e-06 85-97
157	DM01688	2 POLY-IG RECEPTOR.	DM01688P 13.54 1.925e-07 44-89 DM01688L 4.36 2.367e-07 123-133
159	PR00933	B-LYTIC METALLOENDOPEPTIDASE (M23) SIGNATURE	PR00933D 13.92 1.000e-05 85-106
161	PR00352	3FE-4S FERREDOXIN SIGNATURE	PR00352A 11.15 6.162e-06 94-106
163	BL00785	5'-nucleotidase proteins.	BL00785E 15.85 4.000e-06 95-111
164	PR00916	2C ENDOPEPTIDASE (C24) CYSTEINE PROTEASE FAMILY SIGNATURE	PR00916C 8.02 2.655e-06 121-133
165	BL00785	5'-nucleotidase proteins.	BL00785D 9.89 3.045e-06 154-164
166	BL00785	5'-nucleotidase proteins.	BL00785D 9.89 3.045e-06 123-133
167	DM01023	2 GLYCOSYL HYDROLASES FAMILY 5.	DM01023C 13.51 6.486e-06 149-175
168	PF00803	3A movement protein.	PF00803A 15.38 8.088e-06 255-290
169	PR00282	SNAKE CYTOTOXIN SIGNATURE	PR00282D 11.82 9.882e-06 74-85
170	PR00519	5-HYDROXYTRYPTAMINE 5B RECEPTOR SIGNATURE	PR00519B 9.99 5.787e-06 83-100
172	DM01803	1 HERPESVIRUS GLYCOPROTEIN H.	DM01803A 10.51 6.804e-06 136-157
173	PR00701	60KD INNER MEMBRANE PROTEIN SIGNATURE	PR00701E 13.83 9.724e-06 14-30
174	BL00118	Phospholipase A2 histidine proteins.	BL00118A 16.00 9.842e-06 132-145
175	DM01688	2 POLY-IG RECEPTOR.	DM01688G 16.45 1.825e-06 89-121
176	DM01930	2 kw FINGER SMCX SMCY YDR096W.	DM01930A 7.97 2.403e-07 146-159

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
177	PR00510	NEBULIN SIGNATURE	PR00510F 9.88 8.552e-06 34-51
179	PF00432	Prenyltransferase and squalene oxidase repeat proteins.	PF00432A 11.90 1.000e-05 27-39
180	PR00537	MU OPIOID RECEPTOR SIGNATURE	PR00537A 8.17 1.000e-05 27-41
183	PR00536	MELANOCYTE STIMULATING HORMONE RECEPTOR SIGNATURE	PR00536C 8.58 8.833e-06 64-82
184	DM00973	3 kw RESISTANCE BENOMYL YLL028W CYCLOHEXIMIDE.	DM00973B 17.81 8.261e-06 158-184
185	PR00517	5-HYDROXYTRYPTAMINE 2C RECEPTOR SIGNATURE	PR00517C 5.36 4.265e-06 718-731
186	PR00517	5-HYDROXYTRYPTAMINE 2C RECEPTOR SIGNATURE	PR00517C 5.36 4.265e-06 718-731
187	PR00651	5-HYDROXYTRYPTAMINE 2B RECEPTOR SIGNATURE	PR00651A 16.53 6.447e-06 144-165
188	BL01017	Ergosterol biosynthesis ERG4/ERG24 family proteins.	BL01017D 20.82 9.737e-06 21-67
191	DM00315	072 RIBONUCLEASE INHIBITOR.	DM00315B 6.84 7.459e-06 95-107
192	PR00930	HIGH MOBILITY GROUP PROTEIN (HMGY) SIGNATURE	PR00930E 5.98 9.740e-06 285-298
193	BL00794	7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase proteins.	BL00794B 22.12 8.967e-06 150-191
194	PR00517	5-HYDROXYTRYPTAMINE 2C RECEPTOR SIGNATURE	PR00517C 5.36 5.853e-06 115-128
196	DM01803	1 HERPESVIRUS GLYCOPROTEIN H.	DM01803A 10.51 7.031e-07 11-32
197	PR00171	SUGAR TRANSPORTER SIGNATURE	PR00171B 14.73 1.000e-05 15-35
198	PD02407	3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCER.	PD02407J 10.55 6.610e-06 69-81
199	PF00604	Influenza RNA-dependant RNA polymerase subunit PB2.	PF00604F 10.21 2.417e-06 276-331
201	PR00409	PHTHALATE DIOXYGENASE REDUCTASE FAMILY SIGNATURE	PR00409D 13.02 9.900e-06 43-58
202	BL00660	Band 4.1 family	BL00660A 31.50 9.595e-06 1-54

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		domain proteins.	
203	PR00745	GLYCOSYL HYDROLASE FAMILY 39 SIGNATURE	PR00745D 15.85 9.700e-06 68-83
204	PD01364	MUCIN GLYCOPROTEIN PRECURSOR MEM.	PD01364A 6.18 9.667e-06 9-16
205	BL00794	7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase proteins.	BL00794C 19.62 7.690e-07 309-347
206	BL00794	7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase proteins.	BL00794C 19.62 7.690e-07 309-347
207	DM00895	7 kw REVERSE TRANSCRIPTASE RNA POLYMERASE.	DM00895E 15.72 3.170e-06 241-266
208	PR00517	5-HYDROXYTRYPTAMINE 2C RECEPTOR SIGNATURE	PR00517D 7.66 4.835e-06 59-71
209	PD02365	CHAIN FACTOR INTERLEUKIN-12 BETA PRECURSOR IL-1.	PD02365C 7.89 9.719e-06 20-50
210	PR00551	2-S GLOBULIN FAMILY SIGNATURE	PR00551E 10.27 9.432e-06 19-34
211	DM01418	352 FIBRILLAR COLLAGEN CARBOXYL-TERMINAL.	DM01418B 22.51 3.289e-06 527-569
213	DM01785	72 PYRUVATE (FLAVODOXIN) DEHYDROGENASE.	DM01785E 12.98 6.400e-06 165-216
214	DM01834	8 HYDROGENASE (FE) SMALL CHAIN.	DM01834B 15.29 3.382e-06 64-90
215	PR00217	43 KD POSTSYNAPTIC PROTEIN SIGNATURE	PR00217C 10.91 4.583e-06 407-423
216	DM00547	1 kw CHROMO BROMODOMAIN SHADOW GLOBAL.	DM00547F 23.43 6.538e-36 628-675 DM00547E 13.94 2.400e-18 387-410 DM00547C 17.30 9.486e-16 266-288 DM00547B 11.28 9.217e-15 237-251 DM00547D 11.60 4.951e-12 357-371 DM00547A 12.38 6.455e-11 216-228
217	BL00407	Connexins proteins.	BL00407D 17.61 1.000e-05 57-87
218	BL00198	4Fe-4S ferredoxins, iron-sulfur binding region proteins.	BL00198 10.43 9.481e-06 74-86
219	DM01417	6 kw INDUCING XPMC2 MUSHROOM SPAC22G7.04.	DM01417B 15.47 3.550e-06 90-102
220	PR00519	5-HYDROXYTRYPTAMINE 5B RECEPTOR SIGNATURE	PR00519E 3.58 2.404e-07 184-199
221	PD01313	INTRON PROBABLE MATURASE CHLOROPLAST MR.	PD01313B 23.27 1.000e-05 10-45
222	PR00047	C4-TYPE STEROID	PR00047A 15.70 9.878e-06 99-116

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		RECEPTOR ZINC FINGER SIGNATURE	
223	DM01554	1 THYROLIBERIN PRECURSOR.	DM01554C 11.76 3.571e-06 255-271
224	DM01123	5 kw RESISTANCE TETRACYCLINE METHYLENOMYCIN EXPORT.	DM01123B 20.06 5.206e-06 28-67
226	BL00198	4Fe-4S ferredoxins, iron-sulfur binding region proteins.	BL00198 10.43 8.630e-07 28-40
227	BL00895	3-hydroxyisobutyrate dehydrogenase proteins.	BL00895B 21.14 5.173e-06 185-224
229	PR00907	THROMBOMODULIN SIGNATURE	PR00907G 11.63 9.794e-06 13-40
230	PR00651	5-HYDROXYTRYPTAMINE 2B RECEPTOR SIGNATURE	PR00651B 9.95 6.416e-06 62-77
231	DM00611	9 kw LECTIN HTPG SERINE GNTR.	DM00611C 11.08 9.113e-06 214-226
232	PR00582	PROSTANOID EP3 RECEPTOR SIGNATURE	PR00582B 9.74 1.000e-05 76-95
233	PR00407	EUKARYOTIC MOLYBDOPTERIN DOMAIN SIGNATURE	PR00407E 13.51 9.438e-06 176-192
234	DM00892	3 RETROVIRAL PROTEINASE.	DM00892C 23.55 9.913e-06 6-40
235	DM01688	2 POLY-IG RECEPTOR.	DM01688G 16.45 4.450e-06 94-126 DM01688J 14.69 6.000e-06 34-71
236	PD00930	PROTEIN GTPASE DOMAIN ACTIVATION.	PD00930A 25.62 1.000e-05 80-106
237	PR00076	6-PHOSPHOGLUCONATE DEHYDROGENASE SIGNATURE	PR00076B 11.24 6.418e-07 14-44
239	PR00243	MUSCARINIC ACETYLCHOLINE RECEPTOR SIGNATURE	PR00243F 16.45 9.182e-06 7-18
240	BL00854	Proteasome B-type subunits proteins.	BL00854B 10.97 1.000e-05 1-9
241	PR00513	5-HYDROXYTRYPTAMINE 1B RECEPTOR SIGNATURE	PR00513B 17.51 5.263e-07 876-889
242	DM01111	4 kw PHOSPHATASE TRANSFORMING 61K PDF1.	DM01111I 15.32 2.473e-07 522-552
243	BL00415	Synapsins proteins.	BL00415B 9.91 9.778e-06 53-89
244	BL00514	Fibrinogen beta and gamma chains C- terminal domain proteins.	BL00514E 14.28 1.000e-05 221-238
245	PR00187	ARTHROPOD HAEMOCYANIN SIGNATURE	PR00187B 15.70 1.000e-05 37-55

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
246	PF00637	7-fold repeat proteins in Clathrin, also in VPS proteins.	PF00637C 27.33 1.184e-06 368-415
247	BL00785	5'-nucleotidase proteins.	BL00785A 9.73 7.557e-06 57-68
248	PR00651	5-HYDROXYTRYPTAMINE 2B RECEPTOR SIGNATURE	PR00651D 12.56 2.615e-06 228-249
249	PR00516	5-HYDROXYTRYPTAMINE 2A RECEPTOR SIGNATURE	PR00516B 10.78 1.811e-06 310-325
250	BL00461	6-phosphogluconate dehydrogenase proteins.	BL00461C 18.34 9.495e-06 30-58
251	BL00888	Cyclic nucleotide- binding domain proteins.	BL00888A 18.03 9.667e-06 20-37
252	DM01242	3 THREONINE--TRNA LIGASE.	DM01242E 23.00 6.215e-07 119-161
253	DM00250	kw ANNEXIN ANTIGEN PROLINE TUMOR.	DM00250A 10.52 6.488e-06 16-32
254	BL00291	Prion protein.	BL00291A 4.49 2.469e-07 51-86 BL00291A 4.49 6.878e-07 40-75 BL00291A 4.49 5.330e-06 22-57 BL00291A 4.49 1.000e-05 30-65
255	PF00506	Influenza virus nucleoprotein.	PF00506F 9.40 5.459e-08 17-55
256	BL00126	3'5'-cyclic nucleotide phosphodiesterases proteins.	BL00126A 27.56 6.026e-06 25-62
257	PR00003	4-DISULPHIDE CORE SIGNATURE	PR00003D 8.10 5.131e-06 291-300
258	DM01803	1 HERPESVIRUS GLYCOPROTEIN H.	DM01803C 7.00 7.061e-06 10-20
259	DM01803	1 HERPESVIRUS GLYCOPROTEIN H.	DM01803C 7.00 8.071e-06 3-13
260	PR00775	90 KD HEAT SHOCK PROTEIN SIGNATURE	PR00775D 8.91 3.831e-06 147-165
261	PR00217	43 KD POSTSYNAPTIC PROTEIN SIGNATURE	PR00217C 10.91 1.167e-06 75-91
262	PR00388	3',5'-CYCLIC NUCLEOTIDE CLASS II PHOSPHODIESTERASE SIGNATURE	PR00388D 14.87 8.079e-06 69-83
263	PR00023	ZONA PELLUCIDA SPERM-BINDING PROTEIN SIGNATURE	PR00023A 17.17 9.036e-06 24-39
264	BL00024	Hemopexin domain proteins.	BL00024F 11.30 9.894e-06 3-24
265	DM00303	6 LEA 11-MER REPEAT REPEAT.	DM00303A 13.20 6.294e-06 177-227
266	PR00652	5-HYDROXYTRYPTAMINE	PR00652A 8.92 9.224e-07 69-90

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		7 RECEPTOR SIGNATURE	
267	PR00652	5-HYDROXYTRYPTAMINE 7 RECEPTOR SIGNATURE	PR00652A 8.92 9.224e-07 69-90
268	DM01803	1 HERPESVIRUS GLYCOPROTEIN H.	DM01803A 10.51 1.673e-06 14-35
270	PR00875	MOLLUSC METALLOTHIONEIN SIGNATURE	PR00875C 8.64 9.550e-06 65-77
271	DM01803	1 HERPESVIRUS GLYCOPROTEIN H.	DM01803A 10.51 7.308e-06 21-42
272	PF00598	Influenza Matrix protein (M1).	PF00598A 14.24 4.383e-06 46-89
273	PR00113	ALKALINE PHOSPHATASE SIGNATURE	PR00113D 6.87 9.260e-06 8-19
274	PD01841	PHOSPHORYLASE KINASE ALPHA MUSCL.	PD01841E 18.60 9.446e-06 80-118
275	PF00600	Influenza non- structural protein (NS1).	PF00600A 20.40 1.563e-06 40-67
276	PR00877	PLANT PEC FAMILY METALLOTHIONEIN SIGNATURE	PR00877B 4.74 9.878e-06 31-38
277	PR00076	6-PHOSPHOGLUCONATE DEHYDROGENASE SIGNATURE	PR00076E 12.73 6.417e-06 71-99
279	BL00101	Hexapeptide-repeat containing- transferases proteins.	BL00101A 10.95 1.000e-05 71-78
280	DM01111	4 kw PHOSPHATASE TRANSFORMING 61K PDF1.	DM01111M 10.67 2.629e-06 163-187
282	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 9.934e-06 35-50
283	PR00519	5-HYDROXYTRYPTAMINE 5B RECEPTOR SIGNATURE	PR00519C 9.73 1.227e-06 22-37
284	PR00304	TAILLESS COMPLEX POLYPEPTIDE 1 (CHAPERONE) SIGNATURE	PR00304E 7.79 1.000e-05 54-67
285	BL00197	2Fe-2S ferredoxins, iron-sulfur binding region proteins.	BL00197A 18.23 9.866e-07 49-79
286	PR00753	1-AMINOCYCLOPROPANE- 1-CARBOXYLATE SYNTHASE SIGNATURE	PR00753D 6.85 8.636e-06 61-83
287	PR00003	4-DISULPHIDE CORE SIGNATURE	PR00003B 7.64 1.300e-06 166-174
288	BL00940	Gamma-thionins family proteins.	BL00940A 20.51 9.671e-06 16-40
289	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 9.609e-11 122-135 PD00066 13.92 1.900e-09 94-107 PD00066 13.92 2.703e-07 66-79

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			PD00066 13.92 1.000e-05 38-51
291	PR00516	5-HYDROXYTRYPTAMINE 2A RECEPTOR SIGNATURE	PR00516F 10.18 9.609e-07 761-779
293	PR00651	5-HYDROXYTRYPTAMINE 2B RECEPTOR SIGNATURE	PR00651E 10.53 8.487e-06 51-71
296	PR00635	AT1 ANGIOTENSIN II RECEPTOR SIGNATURE	PR00635C 7.44 8.602e-06 28-45
297	PF00915	Calicivirus coat protein.	PF00915E 5.71 1.000e-05 102-112
298	PR00519	5-HYDROXYTRYPTAMINE 5B RECEPTOR SIGNATURE	PR00519B 9.99 3.968e-06 495-512
299	PR00784	MITOCHONDRIAL BROWN FAT UNCOUPLING PROTEIN SIGNATURE	PR00784D 15.86 9.730e-06 22-40
300	DM00973	3 kw RESISTANCE BENOMYL YLL028W CYCLOHEXIMIDE.	DM00973A 21.17 1.273e-06 7-44
301	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 8.752e-06 42-57
302	BL00283	Soybean trypsin inhibitor (Kunitz) protease inhibitors family.	BL00283B 16.55 1.000e-05 15-30
303	DM01753	6 kw OSTEOLAST MAJOR IMMUNOGENIC MPB70.	DM01753A 21.93 9.830e-06 59-94
304	PR00516	5-HYDROXYTRYPTAMINE 2A RECEPTOR SIGNATURE	PR00516E 14.87 6.516e-06 20-38
305	DM01554	1 THYROLIBERIN PRECURSOR.	DM01554E 10.78 5.452e-07 20-37
306	PR00331	HAEMAGGLUTININ HA2 CHAIN SIGNATURE	PR00331E 18.67 1.000e-05 75-93
307	PR00651	5-HYDROXYTRYPTAMINE 2B RECEPTOR SIGNATURE	PR00651H 5.59 8.858e-06 152-175
308	BL00208	Plant hemoglobins proteins.	BL00208A 18.41 1.000e-05 5-47
309	PR00240	ALPHA-1A ADRENERGIC RECEPTOR SIGNATURE	PR00240E 9.25 9.391e-06 36-56
310	PR00701	60KD INNER MEMBRANE PROTEIN SIGNATURE	PR00701C 10.53 8.255e-06 55-76
311	PR00423	CELL DIVISION PROTEIN FTSZ SIGNATURE	PR00423B 7.15 1.000e-05 5-26
312	PF00602	Influenza RNA-dependant RNA polymerase subunit PB1.	PF00602C 12.16 2.068e-07 26-66
313	PR00246	SOMATOSTATIN RECEPTOR SIGNATURE	PR00246D 7.36 1.000e-05 4-14

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
314	BL00216	Sugar transport proteins.	BL00216A 13.29 9.526e-06 26-38
316	PF00721	Tobacco mosaic virus coat.	PF00721A 14.59 9.845e-06 131-167
317	PD00489	PROTEIN TRANSMEMBRANE TRANSPORT C.	PD00489A 15.57 1.000e-05 55-71
318	PR00163	RUBREDOXIN SIGNATURE	PR00163A 10.47 9.888e-06 59-76
319	PR00513	5-HYDROXYTRYPTAMINE 1B RECEPTOR SIGNATURE	PR00513A 7.75 9.149e-07 205-217
320	DM01418	352 FIBRILLAR COLLAGEN CARBOXYL-TERMINAL.	DM01418C 20.48 5.142e-06 377-419
321	BL00067	3-hydroxyacyl-CoA dehydrogenase proteins.	BL00067D 21.49 7.441e-06 9-42
322	DM01857	5 kw NUCLEOSIDE TRANSPORT DEPENDENT NA.	DM01857B 14.94 7.821e-08 52-80
323	DM01803	1 HERPESVIRUS GLYCOPROTEIN H.	DM01803C 7.00 5.133e-06 43-53
324	PD01672	+ TRANSPORT EXCHANGER NA H TRANS.	PD01672B 15.16 1.000e-05 6-55
325	DM01688	2 POLY-IG RECEPTOR.	DM01688J 14.69 5.538e-06 31-68
327	DM00372	CARCINOEMBRYONIC ANTIGEN PRECURSOR AMINO-TERMINAL DOMAIN.	DM00372A 19.18 1.000e-05 9-54
328	DM01688	2 POLY-IG RECEPTOR.	DM01688J 14.69 4.308e-06 31-68
329	DM01930	2 kw FINGER SMCX SMCY YDR096W.	DM01930A 7.97 2.403e-07 144-157
330	PF00685	Sulfotransferase proteins.	PF00685A 19.12 9.370e-06 49-82
331	PR00347	PATHOGENESIS-RELATED PROTEIN SIGNATURE	PR00347A 13.98 9.649e-06 55-68
332	PR00538	MUSCARINIC M1 RECEPTOR SIGNATURE	PR00538F 10.59 8.667e-06 30-48
334	PR00159	2FE-2S FERREDOXIN SIGNATURE	PR00159A 9.58 1.153e-06 23-32
336	PR00554	ADENOSINE A2B RECEPTOR SIGNATURE	PR00554B 12.52 9.778e-06 41-50
337	DM01111	4 kw PHOSPHATASE TRANSFORMING 61K PDF1.	DM01111G 10.39 7.250e-06 3-44
338	PR00516	5-HYDROXYTRYPTAMINE 2A RECEPTOR SIGNATURE	PR00516B 10.78 7.649e-06 214-229
340	PR00388	3',5'-CYCLIC NUCLEOTIDE CLASS II PHOSPHODIESTERASE SIGNATURE	PR00388A 10.45 5.050e-06 141-160
342	DM01664	kw.	DM01664D 16.63 1.000e-05 22-47

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
343	PD01841	PHOSPHORYLASE KINASE ALPHA MUSCL.	PD01841K 14.81 1.000e-05 65-95
344	PR00416	EUKARYOTIC DNA TOPOISOMERASE I SIGNATURE	PR00416D 12.12 9.772e-06 23-40
345	BL00726	AP endonucleases family 1 proteins.	BL00726C 19.90 1.000e-05 7-33
346	BL00305	11-S plant seed storage proteins.	BL00305D 21.08 4.566e-06 465-507
347	PR00332	HISTIDINE TRIAD FAMILY SIGNATURE	PR00332A 10.15 9.890e-06 16-33
348	PR00518	5-HYDROXYTRYPTAMINE 5A RECEPTOR SIGNATURE	PR00518A 8.62 7.807e-06 19-36
349	BL00305	11-S plant seed storage proteins.	BL00305D 21.08 4.736e-06 276-318
350	PR00503	BROMODOMAIN SIGNATURE	PR00503C 19.84 9.731e-06 28-47
351	DM01688	2 POLY-IG RECEPTOR.	DM01688K 17.19 9.066e-07 81-120
352	DM01688	2 POLY-IG RECEPTOR.	DM01688K 17.19 9.066e-07 81-120
353	DM01415	6 SALIVARY GLUE PROTEIN.	DM01415B 13.78 5.273e-06 99-147
354	PR00216	OSTEOPONTIN SIGNATURE	PR00216F 11.79 9.913e-06 50-69
356	DM00895	7 kw REVERSE TRANSCRIPTASE RNA POLYMERASE.	DM00895G 3.62 9.913e-06 62-72
357	BL00126	3'5'-cyclic nucleotide phosphodiesterases proteins.	BL00126B 15.20 6.329e-06 35-47
358	PR00512	5-HYDROXYTRYPTAMINE 1A RECEPTOR SIGNATURE	PR00512G 6.54 3.139e-06 3-19
359	PD02455	ELEMENT TRANSPOSABLE INSERTION PROTEIN TRANSPOSITION DNA.	PD02455D 18.65 1.000e-05 58-77
360	DM01415	6 SALIVARY GLUE PROTEIN.	DM01415A 6.65 3.250e-07 16-29
361	BL00794	7,8-dihydro-6- hydroxymethylpterin- pyrophosphokinase proteins.	BL00794C 19.62 9.702e-06 27-65
362	PR00866	RNA-DEPENDENT DNA- POLYMERASE (MSDNA) SIGNATURE	PR00866B 9.86 9.786e-06 60-73

* Results include in order: accession number subtype; raw score; p-value; position of signature in amino acid sequence.

TABLE 4

SEQ ID NO:	pFAM NAME	DESCRIPTION	p-value	pFAM SCORE
2	PGAM	Phosphoglycerate mutase family	2.5e-05	23.4
6	Ubie_methyltran	ubiE/COQ5 methyltransferase family	0.035	-133.9
8	Plexin repeat	Plexin repeat	0.03	18.4
13	K_tetra	K ⁺ channel tetramerisation domain	2.3e-31	117.6
14	EGF	EGF-like domain	7.8e-14	59.4
16	Armadillo_seg	Armadillo/beta-catenin-like repeats	1.3e-05	32.1
19	Ribosomal S5	Ribosomal protein S5	1.7e-46	167.9
21	gpdh	glyceraldehyde 3-phosphate dehydrogenases	1.3e-230	773.2
24	GCV_T	Glycine cleavage T-protein (aminomethyl tran	9.3e-156	530.9
25	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.015	12.5
26	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	1.6e-10	38.4
33	urease	Urease	0.014	11.0
35	tRNA-synt_1e	tRNA synthetases class I (C)	0.0091	12.1
37	LRRNT	Leucine rich repeat N-terminal domain	0.00049	26.8
39	SH3	SH3 domain	3.4e-60	213.4
40	SH3	SH3 domain	3.4e-60	213.4
41	PBD	P21-Rho-binding domain	1e-08	42.4
42	GDA1_CD39	GDA1/CD39 (nucleoside phosphatase) family	9e-94	324.9
43	Band 7	SPFH domain / Band 7 family	1.7e-21	84.9
46	Rhodanese	Rhodanese-like domain	2.9e-24	94.0
47	zf-C2H2	Zinc finger, C2H2 type	6.2e-32	119.5
50	ZAP	ZAP domain	1.6e-50	181.3
52	sushi	Sushi domain (SCR repeat)	9.5e-27	102.3
55	zf-C2H2	Zinc finger, C2H2 type	0.047	20.3
56	zf-C2H2	Zinc finger, C2H2 type	0.00021	28.1
59	PH	PH domain	2.6e-06	27.6
60	PHD	PHD-finger	2e-09	44.8
64	IQ	IQ calmodulin-binding motif	6.4e-42	152.7
66	ank	Ank repeat	2.7e-23	90.8
69	eIF-1a	Eukaryotic initiation factor 1A	0.0047	-2.4
74	Ribosomal S17	Ribosomal protein S17	6e-43	148.6
75	LIM	LIM domain containing proteins	0.00067	19.0
80	Phosphodiester	Type I phosphodiesterase / nucleotide py	2.7e-49	177.2
81	transmembrane4	Transmembrane 4 family	6.6e-61	197.7
84	zf-C2H2	Zinc finger, C2H2 type	1.6e-64	227.8
85	zf-C2H2	Zinc finger, C2H2 type	1.4e-07	38.6
89	ank	Ank repeat	4e-31	116.8
93	L15	Ribosomal protein L15	3.5e-21	61.9

SEQ ID NO:	pFAM NAME	DESCRIPTION	p-value	pFAM SCORE
98	Band 41	FERM domain (Band 4.1 family)	0.00015	16.7
101	Nol1 Nop2 Sun	NOL1/NOP2/sun family	4.5e-19	68.6
103	LIM	LIM domain containing proteins	1.3e-30	113.2
113	WD40	WD domain, G-beta repeat	0.00018	28.3
115	pro_isomerase	Cyclophilin type peptidyl-prolyl cis-tr	5.3e-34	120.4
116	DUF25	Domain of unknown function DUF25	1.1e-11	46.9
118	Band 41	FERM domain (Band 4.1 family)	3.2e-77	242.4
119	rrm	RNA recognition motif. (a.k.a. RRM, RBD, or	1.1e-33	125.4
120	SH3	SH3 domain	3e-05	30.9
125	Ribosomal L29	Ribosomal L29 protein	1.6e-15	65.0
126	NTF2	Nuclear transport factor 2 (NTF2) domain	7.6e-06	32.2
129	rrm	RNA recognition motif. (a.k.a. RRM, RBD, or	0.0016	25.2
130	Fork head	Fork head domain	1e-28	108.8
132	PC4	Transcriptional Coactivator p15 (PC4)	2.1e-38	141.0
133	RGS	Regulator of G protein signaling domain	2.6e-45	164.0
137	COX7a	Cytochrome c oxidase subunit VIIa	2.3e-40	147.5
139	rrm	RNA recognition motif. (a.k.a. RRM, RBD, or	3.2e-15	64.0
141	lectin_c	Lectin C-type domain	5.1e-05	30.0
142	lectin_c	Lectin C-type domain	5.1e-05	30.0
147	ig	Immunoglobulin domain	9.1e-07	26.9
150	ank	Ank repeat	8.6e-09	42.6
161	Ribosomal L7Ae	Ribosomal protein L7Ae	0.03	0.8
162	HMG box	HMG (high mobility group) box	8e-53	188.9
163	PH	PH domain	3e-13	52.4
168	Peptidase C6	Helper component proteinase	0.0056	7.9
175	ig	Immunoglobulin domain	2.3e-09	35.2
176	ig	Immunoglobulin domain	9.2e-09	33.3
178	WW	WW domain	0.054	17.2
180	Ribosomal S12e	Ribosomal protein S12e	1.9e-38	141.1
185	myb_DNA-binding	Myb-like DNA-binding domain	0.00011	29.1
186	myb_DNA-binding	Myb-like DNA-binding domain	0.00011	29.1
187	pkinase	Eukaryotic protein kinase domain	3.4e-26	98.4
189	ER_lumen_recept	ER lumen protein retaining receptor	3.9e-144	492.2
190	ER_lumen_recept	ER lumen protein retaining receptor	2.1e-88	307.1
195	EMP24 GP25L	emp24/gp25L/p24 family	6.9e-06	28.1
199	zf-B box	B-box zinc finger.	5.2e-07	36.7
211	HECT	HECT-domain (ubiquitin-transferase).	1.1e-115	397.8
213	Rhomboid	Rhomboid family	4.2e-42	153.3
214	LIM	LIM domain containing	8.8e-35	127.8

SEQ ID NO:	pFAM NAME	DESCRIPTION	p-value	pFAM SCORE
		proteins		
215	Ricin_B_lectin	Similarity to lectin domain of ricin	0.0015	19.2
216	chromo	'chromo' (CHRromatin Organization Modifier	2.1e-09	37.1
218	Sialyltransf	Sialyltransferase family	7.3e-20	79.4
219	PG_binding_2	Putative peptidoglycan binding domain	5e-06	33.5
223	zf-C2H2	Zinc finger, C2H2 type	1.5e-104	360.7
226	RGS	Regulator of G protein signaling domain	5.1e-52	186.2
227	TBC	TBC domain	7.2e-35	129.3
228	CRAL TRIO	CRAL/TRIO domain.	4.5e-47	158.6
232	Ribosomal L44	Ribosomal protein L44	1e-48	175.3
235	ig	Immunoglobulin domain	3.5e-08	31.4
236	thyroglobulin 1	Thyroglobulin type-1 repeat	3.9e-24	93.6
238	TBC	TBC domain	1.2e-54	195.0
241	zf-C2H2	Zinc finger, C2H2 type	3.8e-08	40.5
242	AAA	ATPases associated with various cellular act	2.1e-43	157.6
249	integrin_A	Integrin alpha cytoplasmic region	0.091	18.0
256	PAP2	PAP2 superfamily	0.00084	22.8
257	zf-C2H2	Zinc finger, C2H2 type	1.2e-60	214.9
259	G-gamma	GGL domain	5.5e-30	108.3
266	efhand	EF hand	3.4e-07	37.4
267	efhand	EF hand	3.4e-07	37.4
274	zf-C2H2	Zinc finger, C2H2 type	0.00014	28.6
277	RecF	RecF protein	0.036	11.1
281	CH	Calponin homology (CH) domain	7.9e-22	86.0
285	cyclin	Cyclin	3.9e-07	28.5
289	zf-C2H2	Zinc finger, C2H2 type	1.9e-21	84.7
290	PI-PLC-X	Phosphatidylinositol-specific phospholipase	0.073	10.8
299	60s ribosomal	60s Acidic ribosomal protein	4.1e-07	25.8
307	trypsin	Trypsin	6.9e-81	257.3
310	ig	Immunoglobulin domain	1.3e-10	39.3
311	ig	Immunoglobulin domain	6.1e-07	27.4
313	globin	Globin	3.8e-21	78.2
315	ig	Immunoglobulin domain	1.6e-05	22.8
318	zf-C2H2	Zinc finger, C2H2 type	9e-19	75.8
319	ig	Immunoglobulin domain	0.01	13.8
320	BTB	BTB/POZ domain	5e-17	70.0
322	aa permeases	Amino acid permease	0.0058	-262.2
325	ig	Immunoglobulin domain	1.6e-10	38.9
327	ig	Immunoglobulin domain	1.9e-09	35.5
328	ig	Immunoglobulin domain	2.9e-09	34.9
329	ig	Immunoglobulin domain	7.4e-14	49.7
332	Ribosomal L36e	Ribosomal protein L36e	6.3e-17	69.7
333	connexin	Connexin	7.6e-148	504.6
335	p450	Cytochrome P450	2.1e-100	347.0
337	Sm	Sm protein	0.00012	28.8
338	zf-C2H2	Zinc finger, C2H2 type	0.0025	24.5

SEQ ID NO:	pFAM NAME	DESCRIPTION	p-value	pFAM SCORE
343	aldo ket red	Aldo/keto reductase family	2.4e-53	190.7
345	ubiquitin	Ubiquitin family	3.1e-13	45.5
346	CH	Calponin homology (CH) domain	0.0017	23.8
351	ig	Immunoglobulin domain	4.8e-18	63.2
352	ig	Immunoglobulin domain	4.8e-18	63.2
358	G-alpha	G-protein alpha subunit	4.5e-148	505.3
359	ig	Immunoglobulin domain	8.9e-09	33.3
362	Ribosomal_L37ae	Ribosomal L37ae protein family	0.00083	-3.0

TABLE 5

SEQ ID NO:	POSITION OF SIGNAL IN AMINO ACID SEQUENCE	maxS (MAXIMUM SCORE)	meanS (MEAN SCORE)
2	1-29	0.942	0.664
12	1-15	0.909	0.589
14	1-17	0.974	0.943
20	1-22	0.932	0.802
25	1-16	0.988	0.881
28	1-13	0.896	0.771
37	1-21	0.992	0.929
42	1-46	0.978	0.754
52	1-34	0.954	0.756
63	1-31	0.960	0.773
71	1-45	0.981	0.652
80	1-22	0.982	0.882
81	1-42	0.993	0.715
83	1-30	0.966	0.767
95	1-18	0.997	0.971
102	1-13	0.981	0.764
107	1-45	0.890	0.631
110	1-27	0.992	0.969
138	1-33	0.961	0.864
144	1-45	0.987	0.658
145	1-20	0.992	0.967
175	1-20	0.957	0.874
176	1-21	0.989	0.945
179	1-42	0.980	0.577
184	1-20	0.972	0.771
189	1-28	0.941	0.755
190	1-28	0.941	0.755
191	1-12	0.907	0.779
195	1-21	0.958	0.779
200	1-15	0.970	0.875
211	1-20	0.895	0.595
215	1-31	0.987	0.895
218	1-30	0.971	0.889
225	1-17	0.884	0.588
235	1-23	0.965	0.817
237	1-29	0.933	0.725
249	1-28	0.972	0.870
251	1-17	0.966	0.905
260	1-26	0.921	0.587
270	1-20	0.938	0.631
283	1-18	0.901	0.763
288	1-20	0.940	0.693
293	1-26	0.937	0.784
295	1-22	0.972	0.745
296	1-15	0.930	0.748
297	1-35	0.906	0.600
300	1-29	0.981	0.864
307	1-19	0.976	0.916
308	1-27	0.973	0.931

SEQ ID NO:	POSITION OF SIGNAL IN AMINO ACID SEQUENCE	maxS (MAXIMUM SCORE)	meanS (MEAN SCORE)
309	1-29	0.950	0.629
310	1-19	0.969	0.913
311	1-21	0.956	0.823
315	1-17	0.976	0.938
317	1-19	0.943	0.837
319	1-18	0.991	0.978
324	1-26	0.968	0.806
325	1-20	0.972	0.828
326	1-27	0.893	0.567
327	1-21	0.994	0.959
328	1-20	0.945	0.891
329	1-21	0.984	0.858
330	1-27	0.891	0.593
333	1-40	0.955	0.703
347	1-22	0.968	0.806
351	1-23	0.982	0.945
352	1-23	0.982	0.945
355	1-32	0.955	0.617
356	1-23	0.936	0.677
359	1-20	0.937	0.859
360	1-29	0.956	0.765
361	1-23	0.968	0.819

CLAIMS

WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1 – 362, a mature protein coding portion of SEQ ID NO: 1 – 362, an active domain of SEQ ID NO: 1 – 362, and complementary sequences thereof.
2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.
3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.
5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
6. A vector comprising the polynucleotide of claim 1.
7. An expression vector comprising the polynucleotide of claim 1.
8. A host cell genetically engineered to comprise the polynucleotide of claim 1.
9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:
 - (a) a polypeptide encoded by any one of the polynucleotides of claim 1; and

(b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO: 1 – 362.

11. A composition comprising the polypeptide of claim 10 and a carrier.

5

12. An antibody directed against the polypeptide of claim 10.

13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

10 a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and

b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.

14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

15 a) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;

20 b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and

c) detecting said product and thereby the polynucleotide of claim 1 in the sample.

25 15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.

16. A method for detecting the polypeptide of claim 10 in a sample, comprising:

30 a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and

b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.

17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

- a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and
- 5 b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

10 18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

- a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and
- 15 b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

19. A method of producing the polypeptide of claim 10, comprising,

- a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO: 1-362, a mature protein coding portion of SEQ ID NO: 1-362, an active domain of SEQ ID NO: 1-362, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO: 1-362, under conditions sufficient to express the polypeptide in said cell; and
- 20 b) isolating the polypeptide from the cell culture or cells of step (a).

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of any one of the polypeptides from the Sequence Listing, the mature protein portion thereof, or the active domain thereof.

30

21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.

22. A collection of polynucleotides, wherein the collection comprising the sequence information of at least one of SEQ ID NO: 1 – 362.

23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.

24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.

25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.

26. The collection of claim 22, wherein the collection is provided in a computer-readable format.

27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

28. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

[illegible]

DECLARATION FOR PATENT APPLICATION AND POWER OF ATTORNEY

As [a] below named inventor(s), I/we hereby declare that:

**Y. Tom Tang, Ping Zhou, Ryle Goodrich, Chenghua Liu, Vinod Asundi, Feiyan Ren,
Jie Zhang, Qing A. Zhao, Aidong J. Xue, Yonghong Yang, Tom Wehrman,
Radoje T. Drmanac**

My/our residence, post office address and citizenship is/are as stated below next to my/our name(s).

I/we believe I/we am/are an/the original, first and sole/joint inventor of the subject matter which is claimed and for which a patent is sought on the invention entitled: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES, the specification of which

 X is attached hereto.

 was filed on [date] as Application Serial Number []
and was amended on [date].

I/We hereby state that I/we have reviewed and understand the contents of the above-identified specification, including the claims as amended by any amendment referred to above.

I/We acknowledge the duty to disclose information which is material to the examination of this application in accordance with Title 37, Code of Federal Regulations, Section 1.56(a).

I/We hereby claim foreign priority benefits under Title 35, United States Code, § 119 of any foreign application(s) for patent or inventor's certificate, listed below and so identified, and I/we have also identified below any foreign application for patent or inventor's certificate on this invention filed by me or my legal representatives or assigns and having a filing date before that of the application on which priority is claimed:

NUMBER	COUNTRY	DAY/MONTH/ YEAR FILED	PRIORITY CLAIMED - YES OR NO

I/We hereby claim the benefit under Title 35, United States Code, § 120 of any United States application(s) listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States application in the manner provided by the first paragraph of Title 35, United States Code, § 112, I/we acknowledge the duty to disclose material information as defined in Title 37, Code of Federal Regulations, § 1.56(a) which occurred between the filing date of the prior application and the national or PCT international filing date of this application.

SERIAL NUMBER	FILING DATE	STATUS

I/We hereby declare that all statements made herein of my/our own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under § 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

I/We hereby appoint the following attorneys and agents, with full power of substitution and revocation, to prosecute this application and to transact all business in the United States Patent and Trademark Office connected therewith and request that all correspondence and telephone calls with respect to this application be directed to Leslie A. Mooi, HYSEQ, INC., 670 Almanor Avenue, Sunnyvale, CA 94085, Telephone No. (408) 524-8100:

ATTORNEY	REGISTRATION NO.
Petrina S. His	38,496
Leslie A. Mooi	37,047

Full name of
first joint inventor: Y. Tom Tang

Inventor's signature: _____ Date: _____

Residence and Post
Office Address: 4230 Ranwick Court, San Jose, CA 95118

Citizenship: United States of America

Full name of
second joint inventor: Ping Zhou

Inventor's signature: _____ Date: _____

Residence and Post
Office Address: 1461 Japaur Lane, San Jose, CA 95132

Citizenship: People's Republic of China

Full name of
third joint inventor:

Ryle Goodrich

Inventor's signature: _____

Date: _____

Residence and Post
Office Address:

4896 Sandy Lane, San Jose, CA 95124

Citizenship:

United States of America

Full name of
fourth joint inventor:

Chenghua Liu

Inventor's signature: _____

Date: _____

Residence and Post
Office Address:

1125 Ranchero Way, Apt. # 14, San Jose, CA 95117

Citizenship:

People's Republic of China

Full name of
fifth joint inventor:

Vinod Asundi

Inventor's signature: _____

Date: _____

Residence and Post
Office Address:

709 Foster City Blvd., Foster City, CA 94404

Citizenship:

United States of America

Full name of
sixth joint inventor:

Feiyan Ren

Inventor's signature: _____

Date: _____

Residence and Post
Office Address:

20685 Garden Manor Court, Cupertino, CA 95014

Citizenship:

People's Republic of China

Full name of
seventh joint inventor: Jie Zhang

Inventor's signature: _____ Date: _____

Residence and Post
Office Address: 20800 Homestead Road, #38B, Cupertino, CA 95014

Citizenship: People's Republic of China

Full name of
eighth joint inventor: Qing A. Zhao

Inventor's signature: _____ Date: _____

Residence and Post
Office Address: 1028 S. de Anza Blvd., Apt. B-210, San Jose, CA 95129

Citizenship: People's Republic of China

Full name of
ninth joint inventor: Aidong J. Xue

Inventor's signature: _____ Date: _____

Residence and Post
Office Address: 1621 S. Mary Avenue, Sunnyvale, CA 94087

Citizenship: People's Republic of China

Full name of
tenth joint inventor: Yonghong Yang

Inventor's signature: _____ Date: _____

Residence and Post
Office Address: 4230 Ranwick Ct, San Jose, CA 95118

Citizenship: United States of America

U.S. Patent & Trademark Office

Full name of
eleventh joint inventor: Tom Wehrman

Inventor's signature: _____ Date: _____

Residence and Post
Office Address: 300 Pasteur Drive, Edwards R314, Stanford University Medical
Center, Stanford, CA 94305

Citizenship: United States of America

Full name of
twelfth joint inventor: Radoje T. Drmanac

Inventor's signature: _____ Date: _____

Residence and Post
Office Address: 850 East Greenwich Place, Palo Alto, CA 94303

Citizenship: Yugoslavia

Express Mail No.: EF415382545US

Docket No.: 797

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant(s): Tang, et al.

Serial No: Not Yet Assigned

Filed: Herewith

For: NOVEL NUCLEIC ACIDS
AND POLYPEPTIDES

CERTIFICATE OF MAILING
BY "EXPRESS MAIL" UNDER 37 CFR § 1.10

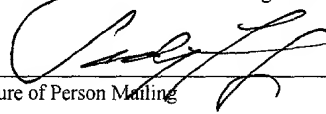
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Date of Deposit November 17, 2000

I hereby certify that this paper and all enclosures are being deposited with the United States Postal Service "Express Mail Post Office to Addressee" under 37 CFR § 1.10 on the date indicated above and is addressed to the Assistant Commissioner for Patents, Washington, D.C., 20231

Type or Print Name of Person Mailing: Sandy Fong

Signature of Person Mailing



STATEMENT REGARDING SEQUENCE LISTING UNDER 37 CFR §1.821(f)

BOX PATENT APPLICATION
Assistant Commissioner for Patents
Washington, D.C. 20231

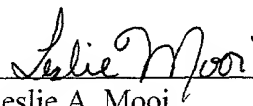
Dear Sir:

I hereby state that the content of the paper and computer readable copies of the Sequence Listing, submitted in accordance with 37 CFR §1.821(c) and (e), respectively, are the same.

Respectfully submitted,

Dated: November 17, 2000

By:


Leslie A. Mooi
Attorney for Applicants
Registration No.: 37,047
HYSEQ, INC.
670 Almanor Avenue
Sunnyvale, CA 94085

SEQUENCE LISTING

<110> Tang, Y. Tom
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 Goodrich, Ryle
 Liu, Chenghua
 Asundi, Vinod
 Ren, Feiyan
 Zhang, Jie
 Zhao, Qing A.
 Xue, Aidong J.
 Yang, Yonghong
 Wehrman, Tom
 Drmanac, Radoje T.

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gcg gcc tgc ggg ctg gcc ggg ggc tgc gcc gcc gtg ctc ttc tcg gcc	99	
Ala Ala Cys Gly Leu Ala Gly Gly Ser Ala Ala Val Leu Phe Ser Ala		
10 15 20 25		
gtg gcg gta ggg aag ccg cgc gca ggc ggg gac gcg gag cca cgc ccg	147	
Val Ala Val Gly Lys Pro Arg Ala Gly Gly Asp Ala Glu Pro Arg Pro		
30 35 40		
gct gag ccg ccg gcc tgg gcg ggg ggc gcg ccg ccg ggc ccc ggt gtc	195	
Ala Glu Pro Pro Ala Trp Ala Gly Gly Ala Arg Pro Gly Pro Gly Val		
45 50 55		
tgg gac ccc aac tgg gac agg cga gaa cca ctg tct ctg atc aac gtg	243	
Trp Asp Pro Asn Trp Asp Arg Arg Glu Pro Leu Ser Leu Ile Asn Val		
60 65 70		
cgg aag agg aac gtg gaa tct ggg gaa gaa gag ctg gcg tcc aag ctg	291	
Arg Lys Arg Asn Val Glu Ser Gly Glu Glu Glu Leu Ala Ser Lys Leu		
75 80 85		
gac cac tac aaa gcc aag gcc acg ccg cac atc ttc ctc atc agg cat	339	
Asp His Tyr Lys Ala Lys Ala Thr Arg His Ile Phe Leu Ile Arg His		
90 95 100 105		
tcc cag tac cac gtg gat ggc tcc ctg gag aag gac cgc act ctg acc	387	
Ser Gln Tyr His Val Asp Gly Ser Leu Glu Lys Asp Arg Thr Leu Thr		
110 115 120		
ccg ctg ggt ccg gag cag gct gaa ctc act ggg ctc cgc ctg gca agc	435	
Pro Leu Gly Arg Glu Gln Ala Glu Leu Thr Gly Leu Arg Leu Ala Ser		
125 130 135		
ttg ggg ttg aag ttt aat aaa atc gtc cat tcg tct atg acg cgc gcc	483	
Leu Gly Leu Lys Phe Asn Lys Ile Val His Ser Ser Met Thr Arg Ala		
140 145 150		
ata gag acc acc gat atc atc agc ccg cac ctg cca ggc gtc tgc aaa	531	
Ile Glu Thr Thr Asp Ile Ile Ser Arg His Leu Pro Gly Val Cys Lys		
155 160 165		

gtc agc aca gat ctg ctg cgg gaa ggc gcc ccc atc gag cca gac ccg	579
Val Ser Thr Asp Leu Leu Arg Glu Gly Ala Pro Ile Glu Pro Asp Pro	
170 175 180 185	
ccc gtg tct cat tgg aag ccg gaa gct gtg cag tat tac gaa gac gga	627
Pro Val Ser His Trp Lys Pro Glu Ala Val Gln Tyr Tyr Glu Asp Gly	
190 195 200	
gcc cgg atc gag gcc gcc ttc cgg aac tac atc cac cgc gca gat gcc	675
Ala Arg Ile Glu Ala Ala Phe Arg Asn Tyr Ile His Arg Ala Asp Ala	
205 210 215	
agg cag gag gag gac agt tac gag atc ttc atc tgt cac gcc aac gtc	723
Arg Gln Glu Glu Asp Ser Tyr Glu Ile Phe Ile Cys His Ala Asn Val	
220 225 230	
atc cgc tac atc gtg tgc aga gca ctg cag ttt cct cct gaa ggc tgg	771
Ile Arg Tyr Ile Val Cys Arg Ala Leu Gln Phe Pro Pro Glu Gly Trp	
235 240 245	
ctc cgg ctc tcc ctc aat aat ggc agc atc acc cac ctg gtg atc cga	819
Leu Arg Leu Ser Leu Asn Asn Gly Ser Ile Thr His Leu Val Ile Arg	
250 255 260 265	
ccc aac ggc cga gtt gcg ctc agg acc ctc ggg gac acg ggg ttc atg	867
Pro Asn Gly Arg Val Ala Leu Arg Thr Leu Gly Asp Thr Gly Phe Met	
270 275 280	
cct ccc gac aag atc act cga tcc tga gggct ccggcctctc cttccctctg	919
Pro Pro Asp Lys Ile Thr Arg Ser *	
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tcctccctgc acaggccgca cacacttaac gttttgttcc caaggagacc ggcggaaagt	979
agaaacctgc aatgctgcat ctgggaactg acttgtgacc aggctgagaa ggggagagtt	1039
gggatcagac agcctgactt ctctgcaggg ttttatacct gaccatgaac ccccaggatg	1099
gcgtgggggt taaggtgaaa gcgtctcacg cacaagtcag gcctgttgtg gggacttgaa	1159
agaggcctga cccagaccac catgttcgca cccacagctg acccgtgctg aggggccagg	1219
ctccattggc aaagccggtc aggcacgagg gcgactgagg cacgtggatg aggagggcac	1279
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aaa	1342

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aaggatttgc agcaag atg gat ttg gga aag gac caa tct cat ttg aag	169
Met Asp Leu Gly Lys Asp Gln Ser His Leu Lys	
1 5 10	
cac cat cag aca cct gac cct cat caa gaa gag aac cat tct cca gaa	217
His His Gln Thr Pro Asp Pro His Gln Glu Glu Asn His Ser Pro Glu	
15 20 25	
gtc att gga acc tgg agt ttg aga aac aga gaa cta ctt aga aaa aga	265
Val Ile Gly Thr Trp Ser Leu Arg Asn Arg Glu Leu Leu Arg Lys Arg	
30 35 40	
aaa gct gaa gtg cat gaa aag gaa aca tca caa tgg cta ttt gga gaa	313
Lys Ala Glu Val His Glu Lys Glu Thr Ser Gln Trp Leu Phe Gly Glu	
45 50 55	
cag aaa aaa cgc aag cag cag aga aca gga aaa gga aat cga aga ggc	361
Gln Lys Lys Arg Lys Gln Gln Arg Thr Gly Lys Gly Asn Arg Arg Gly	
60 65 70 75	
aga aag aga caa caa aac aca gaa ttg aag gtg gag cct cag cca cag	409
Arg Lys Arg Gln Gln Asn Thr Glu Leu Lys Val Glu Pro Gln Pro Gln	
80 85 90	
ata gaa aag gaa ata gtg gag aaa gca ctg gca cct ata gag aaa aaa	457
Ile Glu Lys Glu Ile Val Glu Lys Ala Leu Ala Pro Ile Glu Lys Lys	
95 100 105	
act gag cca cct ggg agc ata acc aaa gta ttt cct tca gta gcc tcc	505
Thr Glu Pro Pro Gly Ser Ile Thr Lys Val Phe Pro Ser Val Ala Ser	
110 115 120	
ccg caa aaa gtt gtg cct gag gaa cac ttt tct gaa ata tgt caa gaa	553
Pro Gln Lys Val Val Pro Glu Glu His Phe Ser Glu Ile Cys Gln Glu	
125 130 135	
agt aac ata tat cag gag aat ttt tct gag tac caa gaa ata gca gta	601
Ser Asn Ile Tyr Gln Glu Asn Phe Ser Glu Tyr Gln Glu Ile Ala Val	
140 145 150 155	
caa aac cat tct tct gaa aca tgc caa cat gtg tct gaa cct gaa gac	649
Gln Asn His Ser Ser Glu Thr Cys Gln His Val Ser Glu Pro Glu Asp	
160 165 170	
ctc tct cct aaa atg tac caa gaa ata tct gta ctt caa gac aat tct	697
Leu Ser Pro Lys Met Tyr Gln Glu Ile Ser Val Leu Gln Asp Asn Ser	
175 180 185	

tcc aaa ata tgc caa gac atg aag gaa cct gaa gac aac tct cct aac	745
Ser Lys Ile Cys Gln Asp Met Lys Glu Pro Glu Asp Asn Ser Pro Asn	
190 195 200	
aca tgc caa gta ata tct gta att caa gac cat cct ttc aaa atg tac	793
Thr Cys Gln Val Ile Ser Val Ile Gln Asp His Pro Phe Lys Met Tyr	
205 210 215	
caa gat atg gct aaa cga gaa gat ctg gct cct aaa atg tgc caa gaa	841
Gln Asp Met Ala Lys Arg Glu Asp Leu Ala Pro Lys Met Cys Gln Glu	
220 225 230 235	
gct gct gta ccc aaa atc ctt cct tgt cca aca tct gaa gac aca gct	889
Ala Ala Val Pro Lys Ile Leu Pro Cys Pro Thr Ser Glu Asp Thr Ala	
240 245 250	
gat ctg gca gga tgc tct ctt caa gca tat cca aaa cca gat gtg cct	937
Asp Leu Ala Gly Cys Ser Leu Gln Ala Tyr Pro Lys Pro Asp Val Pro	
255 260 265	
aaa ggc tat att ctt gac aca gac caa aat cca gca gaa cca gag gaa	985
Lys Gly Tyr Ile Leu Asp Thr Asp Gln Asn Pro Ala Glu Pro Glu Glu	
270 275 280	
tac aat gaa aca gat caa gga ata gct gag aca gaa ggc ctt ttt cct	1033
Tyr Asn Glu Thr Asp Gln Gly Ile Ala Glu Thr Glu Gly Leu Phe Pro	
285 290 295	
aaa ata caa gaa ata gct gag cct aaa gac ctt tct aca aaa aca cac	1081
Lys Ile Gln Glu Ile Ala Glu Pro Lys Asp Leu Ser Thr Lys Thr His	
300 305 310 315	
caa gaa tca gct gaa cct aaa tac ctt cct cat aaa aca tgt aac gaa	1129
Gln Glu Ser Ala Glu Pro Lys Tyr Leu Pro His Lys Thr Cys Asn Glu	
320 325 330	
att att gtg cct aaa gcc ccc tct cat aaa aca atc caa gaa aca cct	1177
Ile Ile Val Pro Lys Ala Pro Ser His Lys Thr Ile Gln Glu Thr Pro	
335 340 345	
cat tct gaa gac tat tca att gaa ata aac caa gaa act cct ggg tct	1225
His Ser Glu Asp Tyr Ser Ile Glu Ile Asn Gln Glu Thr Pro Gly Ser	
350 355 360	
gaa aaa tat tca cct gaa acg tat caa gaa ata cct ggg ctt gaa gaa	1273
Glu Lys Tyr Ser Pro Glu Thr Tyr Gln Glu Ile Pro Gly Leu Glu Glu	
365 370 375	
tat tca cct gaa ata tac caa gaa aca tcc cag ctt gaa gaa tat tca	1321
Tyr Ser Pro Glu Ile Tyr Gln Glu Thr Ser Gln Leu Glu Glu Tyr Ser	
380 385 390 395	
cct gaa ata tac caa gaa aca ccg ggg cct gaa gac ctc tct act gag	1369
Pro Glu Ile Tyr Gln Glu Thr Pro Gly Pro Glu Asp Leu Ser Thr Glu	
400 405 410	
aca tat aaa aat aag gat gtg cct aaa gaa tgc ttt cca gaa cca cac	1417

Thr	Tyr	Lys	Asn	Lys	Asp	Val	Pro	Lys	Glu	Cys	Phe	Pro	Glu	Pro	His	
			415					420					425			
caa	gaa	aca	ggg	ggg	ccc	caa	ggc	cag	gat	cct	aaa	gca	cac	cag	gaa	1465
Gln	Glu	Thr	Gly	Gly	Pro	Gln	Gly	Gln	Asp	Pro	Lys	Ala	His	Gln	Glu	
		430					435					440				
gat	gct	aaa	gat	gct	tat	act	ttt	cct	caa	gaa	atg	aaa	gaa	aaa	ccc	1513
Asp	Ala	Lys	Asp	Ala	Tyr	Thr	Phe	Pro	Gln	Glu	Met	Lys	Glu	Lys	Pro	
	445					450					455					
aaa	gaa	gag	cca	gga	ata	cca	gca	att	ctg	aat	gag	agt	cat	cca	gaa	1561
Lys	Glu	Glu	Pro	Gly	Ile	Pro	Ala	Ile	Leu	Asn	Glu	Ser	His	Pro	Glu	
460				465					470					475		
aat	gat	gtc	tat	agt	tat	gtt	ttg	ttt	taa	c	aatgctcaac	cataaagttg				1612
Asn	Asp	Val	Tyr	Ser	Tyr	Val	Leu	Phe	*							
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				Met Ala Ala Ser Leu												
				1	5											
cgg ctc ctc	gga gct gcc tcc	ggc ctc	cgg tac	tgg agc	cgg cgg ctg											162
Arg Leu Leu	Gly Ala Ala	Ser Gly	Leu Arg	Tyr Trp	Ser Arg Arg	Leu										
	10		15		20											
cgg ccg gca	gcc ggc agc ttt	gca gcg	gtg tgt	tct agg	tca gtg gct											210
Arg Pro Ala	Ala Gly Ser	Phe Ala	Ala Val	Cys Ser	Arg Ser	Val Ala										
	25		30		35											
tca aag act	cca gtt gga ttc	att gga	ctg ggc	aac atg	ggg aat cca											258
Ser Lys Thr	Pro Val Gly	Phe Ile	Gly Leu	Gly Asn	Met Gly	Asn Pro										
	40		45		50											
atg gca aaa	aat ctc atg	aaa cat	ggc tat	cca ctt	att att	tat gat										306
Met Ala Lys	Asn Leu Met	Lys His	Gly Tyr	Pro Leu	Ile Ile	Tyr Asp										
	55		60		65											
gtg ttc cct	gat gcc tgc	aaa gag	ttt caa	gat gca	ggg gaa	cag gta										354

Val	Phe	Pro	Asp	Ala	Cys	Lys	Glu	Phe	Gln	Asp	Ala	Gly	Glu	Gln	Val	
70					75					80					85	
gta tct tcc cca gca gat gtt gct gaa aaa gct gac aga att att aca																402
Val	Ser	Ser	Pro	Ala	Asp	Val	Ala	Glu	Lys	Ala	Asp	Arg	Ile	Ile	Thr	
				90					95					100		
atg ctg ccc acc agt atc aat gca ata gaa gct tat tcc gga gca aat																450
Met	Leu	Pro	Thr	Ser	Ile	Asn	Ala	Ile	Glu	Ala	Tyr	Ser	Gly	Ala	Asn	
			105					110					115			
ggg att cta aaa aaa gtg aag aag ggc tca tta tta ata gat tcc agc																498
Gly	Ile	Leu	Lys	Lys	Val	Lys	Lys	Gly	Ser	Leu	Leu	Ile	Asp	Ser	Ser	
		120					125					130				
act att gat cct gca gtt tca aaa gaa ttg gcc aaa gaa gtt gag aaa																546
Thr	Ile	Asp	Pro	Ala	Val	Ser	Lys	Glu	Leu	Ala	Lys	Glu	Val	Glu	Lys	
		135				140					145					
atg gga gca gtt ttc atg gat gcc cct gtt tct ggt ggt gta gga gct																594
Met	Gly	Ala	Val	Phe	Met	Asp	Ala	Pro	Val	Ser	Gly	Gly	Val	Gly	Ala	
150					155					160					165	
gca cga tct ggg aac ctc acg ttt atg gtg gga gga gtt gaa gat gaa																642
Ala	Arg	Ser	Gly	Asn	Leu	Thr	Phe	Met	Val	Gly	Gly	Val	Glu	Asp	Glu	
				170					175					180		
ttt gct gct gcc caa gag ttg ctg ggg tgc atg ggc tcc aac gtg gtg																690
Phe	Ala	Ala	Ala	Gln	Glu	Leu	Leu	Gly	Cys	Met	Gly	Ser	Asn	Val	Val	
			185					190					195			
tac tgt gga gct gtt ggg act ggg cag gcg gca aag atc tgc aac aac																738
Tyr	Cys	Gly	Ala	Val	Gly	Thr	Gly	Gln	Ala	Ala	Lys	Ile	Cys	Asn	Asn	
		200					205					210				
atg ctg tta gct att agt atg att gga act gct gaa gct atg aat ctt																786
Met	Leu	Leu	Ala	Ile	Ser	Met	Ile	Gly	Thr	Ala	Glu	Ala	Met	Asn	Leu	
		215				220					225					
gga atc agg tta ggg ctt gac cca aaa cta ctg gct aaa atc cta aat																834
Gly	Ile	Arg	Leu	Gly	Leu	Asp	Pro	Lys	Leu	Leu	Ala	Lys	Ile	Leu	Asn	
230					235				240					245		
atg agc tca gga cgg tgt tgg tca agt gac act tat aat cct gta cct																882
Met	Ser	Ser	Gly	Arg	Cys	Trp	Ser	Ser	Asp	Thr	Tyr	Asn	Pro	Val	Pro	
				250					255					260		
gga gtg atg gat ggc gtt ccc tcg gct aat aac tat cag ggt gga ttt																930
Gly	Val	Met	Asp	Gly	Val	Pro	Ser	Ala	Asn	Asn	Tyr	Gln	Gly	Gly	Phe	
			265					270					275			
gga aca aca ctc atg gct aag gat ctg gga ttg gca caa gac tct gct																978
Gly	Thr	Thr	Leu	Met	Ala	Lys	Asp	Leu	Gly	Leu	Ala	Gln	Asp	Ser	Ala	
		280					285					290				
acc agc aca aag agc cca atc ctt ctt ggc agt ctg gcc cat cag atc																1026
Thr	Ser	Thr	Lys	Ser	Pro	Ile	Leu	Leu	Gly	Ser	Leu	Ala	His	Gln	Ile	

295	300	305	
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Tyr Arg Met Met Cys Ala Lys Gly Tyr Ser Lys	Lys Asp Phe Ser Ser		
310	315 320 325		
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Val Phe Gln Phe Leu Arg Glu Glu Glu Thr Phe	*		
330	335		
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tccccaagca tcttcaacta aatcattgaa tacttcaatc	aggatattat ctgctttact	1424	
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gaattggtgt gaagagagaa gttagagaag ggaaatgcag	tgaattacta tctgtgtcca	1544	
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tccagggagc tgataaagca ggagaactgt tgctgcatgt	tttctatttg gactccgtca	1664	
caatatggta ggatatccct caccaactcc cgacactcag	cagacttggt tttatatattt	1724	
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atttcagagc caatgatgat atttgcttta gataattatt	atattattat aaatatagcc	1844	
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Lys Asn Ile Lys Ala Leu Val Ala Phe His Ser	Thr Ala Leu Asp Lys
5	10 15
	105

gaa att aca tca gca aat tat gct ggt gtc tgt aca tca tct gtg att Glu Ile Thr Ser Ala Asn Tyr Ala Gly Val Cys Thr Ser Ser Val Ile 20 25 30	153
aaa gaa gaa aac att gat caa cca gga tac tgt tat ctc tca cct gat Lys Glu Glu Asn Ile Asp Gln Pro Gly Tyr Cys Tyr Leu Ser Pro Asp 35 40 45	201
gga aag aga aaa act atg ctc tgc ttg gct tgt gga caa tcc atg aga Gly Lys Arg Lys Thr Met Leu Cys Leu Ala Cys Gly Gln Ser Met Arg 50 55 60 65	249
aca gag aaa gga ctg aaa caa ttg ctt cca ggg gtt cca ttc ctc tgt Thr Glu Lys Gly Leu Lys Gln Leu Leu Pro Gly Val Pro Phe Leu Cys 70 75 80	297
att tca ggc acc aag act cag aag ccc ttc tta caa ggg ccc ttc aag Ile Ser Gly Thr Lys Thr Gln Lys Pro Phe Leu Gln Gly Pro Phe Lys 85 90 95	345
gtc atc agt gtg gct gag gtt gat ttg tgc tgt gac aag gct gaa aaa Val Ile Ser Val Ala Glu Val Asp Leu Ser Cys Asp Lys Ala Glu Lys 100 105 110	393
act cta agt tac tac caa gca cgt cta ttg tct tta cgg atg aag acc Thr Leu Ser Tyr Tyr Gln Ala Arg Leu Leu Ser Leu Arg Met Lys Thr 115 120 125	441
tgc acg caa gct gca tct cac agt ggc atg gca gcc aca cac cag aag Cys Thr Gln Ala Ala Ser His Ser Gly Met Ala Ala Thr His Gln Lys 130 135 140 145	489
gca gtg aaa ata att gca tac aaa aat ggg gat ggg tat cgt aat ggg Ala Val Lys Ile Ile Ala Tyr Lys Asn Gly Asp Gly Tyr Arg Asn Gly 150 155 160	537
aag tta att gtg gct gga aca ttc ccc atg ctt ctt aca gaa tgc acg Lys Leu Ile Val Ala Gly Thr Phe Pro Met Leu Leu Thr Glu Cys Thr 165 170 175	585
gaa caa ctt ggg ctt gcc aga gca gcc tcc aaa gta tat acc aaa gat Glu Gln Leu Gly Leu Ala Arg Ala Ala Ser Lys Val Tyr Thr Lys Asp 180 185 190	633
gga acc cca atc ttt acc ttg cgt gat ttg gtt tta tgg gct cta gat Gly Thr Pro Ile Phe Thr Leu Arg Asp Leu Val Leu Trp Ala Leu Asp 195 200 205	681
gaa tcc ttt ctc cag aga gac tct gag aaa caa aag caa gat gca gct Glu Ser Phe Leu Gln Arg Asp Ser Glu Lys Gln Lys Gln Asp Ala Ala 210 215 220 225	729
cct gtt gga aaa gaa cag ata att gtt gaa agt atg gaa gaa aat cca Pro Val Gly Lys Glu Gln Ile Ile Val Glu Ser Met Glu Glu Asn Pro 230 235 240	777
aga atg aaa gtg aaa aac aga tta ttt gca aaa tct gtg aca tcc gat	825

Arg Met Lys Val Lys Asn Arg Leu Phe Ala Lys Ser Val Thr Ser Asp	
245 250 255	
agt ttg gat ggt ata gac aag tct ttg ctt acc ctc atc ctc aga aat	873
Ser Leu Asp Gly Ile Asp Lys Ser Leu Leu Thr Leu Ile Leu Arg Asn	
260 265 270	
cct att gcc atc tgg gtg tct tgt ggt gaa cca ttt cta cct cca aat	921
Pro Ile Ala Ile Trp Val Ser Cys Gly Glu Pro Phe Leu Pro Pro Asn	
275 280 285	
gct ttg cag aaa gca gaa aaa tta gag aaa cag aac tgg cta aaa aag	969
Ala Leu Gln Lys Ala Glu Lys Leu Glu Lys Gln Asn Trp Leu Lys Lys	
290 295 300 305	
gac aga att ttg gct gat cta gat acc atg aga cac aaa atg aga cag	1017
Asp Arg Ile Leu Ala Asp Leu Asp Thr Met Arg His Lys Met Arg Gln	
310 315 320	
tta aaa ggg cgg cga gta gcg gca tgt cag cca gcc acc atg gtt cct	1065
Leu Lys Gly Arg Arg Val Ala Ala Cys Gln Pro Ala Thr Met Val Pro	
325 330 335	
acc aag agc cct gtg cag ccc gtg gtg gtt gaa gga ggc tgg acc gaa	1113
Thr Lys Ser Pro Val Gln Pro Val Val Val Glu Gly Gly Trp Thr Glu	
340 345 350	
cag act caa cag gaa att aaa ctc atg gaa ctt ata aga cat aca gag	1161
Gln Thr Gln Gln Glu Ile Lys Leu Met Glu Leu Ile Arg His Thr Glu	
355 360 365	
gca cac ctt tct gaa atc caa gaa atg gaa tcc aaa ata aat ttt cca	1209
Ala His Leu Ser Glu Ile Gln Glu Met Glu Ser Lys Ile Asn Phe Pro	
370 375 380 385	
att gca acc aaa cgt ata gca gtc aag ccg agc aac ctg tat aag cag	1257
Ile Ala Thr Lys Arg Ile Ala Val Lys Pro Ser Asn Leu Tyr Lys Gln	
390 395 400	
ccc aac aca aaa cga gtg tgg att tat cta aat gga ggc aga cct gaa	1305
Pro Asn Thr Lys Arg Val Trp Ile Tyr Leu Asn Gly Gly Arg Pro Glu	
405 410 415	
gat ggc act tat gcc tgg ggc aaa act att tca gag ctg ctg caa gac	1353
Asp Gly Thr Tyr Ala Trp Gly Lys Thr Ile Ser Glu Leu Leu Gln Asp	
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Cys Ser Ser Arg Leu Lys Met Thr His Pro Ala Arg Ala Leu Tyr Thr	
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Pro Ser Gly Glu Pro Ile Gln Ser Trp Asp Asp Ile Glu Arg Asp Met	
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Val Ile Cys Val Ser Met Gly His Gly Phe Lys Thr Pro Lys Glu Leu	

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Lys Leu Gly Ser Ser Gly Gly Trp Phe Leu Arg Val Leu Gly Pro Gly			
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Gly Cys Asn Thr Lys Ala Ala Arg Pro Leu Ile Ser Ser Ala Val Tyr			
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Val Lys Asn Gln Leu Ser Gly Thr Leu Gln Ile Lys Pro Gly Val Phe			
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Cys Leu Asn Arg Ile Lys Ser Phe Arg Tyr Pro Trp Ala Arg Leu Tyr	
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Ser Thr Ser Gln Thr Thr Val Asp Ser Gly Glu Val Lys Thr Phe Leu	
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Ala Leu Ala His Lys Trp Trp Asp Glu Gln Gly Val Tyr Ala Pro Leu	
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His Ser Met Asn Asp Leu Arg Val Pro Phe Ile Arg Asp Asn Leu Leu	
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250 255 260	
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Leu Gly Ile Val Phe Ser Glu Gln Ile Ala Gly Ile Val Pro Lys Gly	
265 270 275	
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Leu	Glu	Ser	Asn	Gly	Leu	Ser	Val	Gln	Thr	Val	Val	Gly	Met	Leu	Tyr		
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Tyr	Ala	Ala	His	Ala	Val	Lys	Ser	Arg	Val	Gln	Glu	His	Pro	Ala	Ser		
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Cys	Thr	Asn	Pro	Ala	Val	His	Glu	Lys	Leu	Lys	Lys	*					
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Tyr	Tyr	Gln	Asn	Ser	Ile	Asp	Asp	Lys	Leu	Leu	Val	Glu	Lys	Ile	Phe		
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Leu	Asn	Glu	Met	Trp	Lys	Cys	Gln	Asn	Met	Leu	Arg	Ser	His	Val	Arg		
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Glu	Leu	Leu	Asp	Leu	His	Lys	Gln	Pro	Thr	Ser	Glu	Ala	Asn	Cys	Ser		
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Asp	Glu	Lys	Leu	Arg	Ser	Gln	Leu	Glu	Leu	Leu	Ile	Ser	Pro	Thr	Cys		
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Ser	Cys	Lys	Gln	Ala	Asp	Ile	Cys	Val	Arg	Glu	Ile	Ala	Arg	Lys	Leu		
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Leu	Leu	Glu	Arg	Ile	Ala	Pro	Val	His	Ile	Asp	Ser	Glu	Ala	Ile	Ser		
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Glu	Glu	Glu	Gly	Val	Ser	Pro	Asp	Thr	Ala	Ile	Arg	Ser	Gly	Leu	Glu		
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ctt	ctt	aag	gtt	ctg	tct	ttt	aca	cat	cct	acc	tcg	ttc	cac	tct	gca	944	
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Ser His Ala Phe Met Lys Lys Met Ala Glu Asn Ile Lys Leu Thr Arg	
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ctcaccaagc ctgctcctca ttccctggag tgcccctgag cccatgtgtc cgcctcctg 300
cagaac atg gag aac ttc acc ctg gca agg gac gag aag ggg aat gtc 348
Met Glu Asn Phe Thr Leu Ala Arg Asp Glu Lys Gly Asn Val
1 5 10

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ccc acc aag acc gag agc tcc ctc aac tgg ctg caa gac cca gct ttt Pro Thr Lys Thr Glu Ser Ser Leu Asn Trp Leu Gln Asp Pro Ala Phe 65 70 75	540
gtg gcc tca gcc tac att cct gag agc ctg ggc agc ttg caa ggc gat Val Ala Ser Ala Tyr Ile Pro Glu Ser Leu Gly Ser Leu Gln Gly Asp 80 85 90	588
gat gac aag atc tac ttt ttc ttc agc gag act ggc cag gaa ttt gag Asp Asp Lys Ile Tyr Phe Phe Phe Ser Glu Thr Gly Gln Glu Phe Glu 95 100 105 110	636
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Asp	Arg	Val	Leu	Asn	Phe	Leu	Lys	Asp	His	Phe	Leu	Met	Asp	Gly	Gln		
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Val	Arg	Ser	Arg	Met	Leu	Leu	Leu	Gln	Pro	Gln	Ala	Arg	Tyr	Gln	Arg		
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gtg	gct	gta	cac	cgc	gtc	cct	ggc	ctg	cac	cac	acc	tac	gat	gtc	ctc	1212	
Val	Ala	Val	His	Arg	Val	Pro	Gly	Leu	His	His	Thr	Tyr	Asp	Val	Leu		
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Phe	Leu	Gly	Thr	Gly	Asp	Gly	Arg	Leu	His	Lys	Ala	Val	Ser	Val	Gly		
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Pro	Arg	Val	His	Ile	Ile	Glu	Glu	Leu	Gln	Ile	Phe	Ser	Ser	Gly	Gln		
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Pro	Val	Gln	Asn	Leu	Leu	Leu	Asp	Thr	His	Arg	Gly	Leu	Leu	Tyr	Ala		
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Tyr	Arg	Ser	Cys	Gly	Asp	Cys	Leu	Leu	Ala	Arg	Asp	Pro	Tyr	Cys	Ala		
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Trp	Ser	Gly	Ser	Ser	Cys	Lys	His	Val	Ser	Leu	Tyr	Gln	Pro	Gln	Leu		
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Ala	Thr	Arg	Pro	Trp	Ile	Gln	Asp	Ile	Glu	Gly	Ala	Ser	Ala	Lys	Asp		
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Leu	Cys	Ser	Ala	Ser	Ser	Val	Val	Ser	Pro	Ser	Phe	Val	Pro	Thr	Gly		
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Glu	Lys	Pro	Cys	Glu	Gln	Val	Gln	Phe	Gln	Pro	Asn	Thr	Val	Asn	Thr		
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ttg	gcc	tgc	ccg	ctc	ctc	tcc	aac	ctg	gcg	acc	cga	ctc	tgg	cta	cgc	1692	
Leu	Ala	Cys	Pro	Leu	Leu	Ser	Asn	Leu	Ala	Thr	Arg	Leu	Trp	Leu	Arg		
			450					455					460				
aac	ggg	gcc	ccc	gtc	aat	gcc	tcg	gcc	tcc	tgc	cac	gtg	cta	ccc	act	1740	
Asn	Gly	Ala	Pro	Val	Asn	Ala	Ser	Ala	Ser	Cys	His	Val	Leu	Pro	Thr		

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Pro	Thr	Lys	Lys	Leu	Ala	Asn	Lys	Pro	Asp	Lys	Asn	Ser	Ser	Ser	Glu		
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Gln	Leu	Phe	Ser	Ser	Ala	Arg	Leu	Gln	Asn	Glu	Lys	Lys	Thr	Ile	Leu		
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Ala	Leu	Leu	Lys	Arg	Thr	Met	Asn	Ile	Lys	Glu	Asn	Lys	Ala	Met	Leu		
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Ala	Gln	Leu	Leu	Ala	Glu	Leu	Asn	Ser	Met	Pro	Asp	Phe	Phe	Pro	Val		
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Val	Glu	Asp	Ile	Thr	Glu	Glu	Asp	Leu	Glu	Asn	Val	Ala	Ile	Thr	Val		
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Arg	Asp	Lys	Ile	Tyr	Asp	Lys	Val	Leu	Gly	Asn	Thr	Cys	His	Gln	Cys		

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Arg Gln Lys Thr Ile Asp Thr Lys Thr Val Cys Arg Asn Gln Gly Cys			
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Cys Gly Val Arg Gly Gln Phe Cys Gly Pro Cys Leu Arg Asn Arg Tyr			
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Gly Glu Asp Val Arg Ser Ala Leu Leu Asp Pro Asp Trp Val Cys Pro			
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ccc tgt cgt ggg atc tgc aat tgc agc tac tgt cgg aag cgt gac ggc			1063
Pro Cys Arg Gly Ile Cys Asn Cys Ser Tyr Cys Arg Lys Arg Asp Gly			
325	330	335	340
cgc tgt gcc aca gga atc ctc att cat ctg gcc aag ttt tat ggt tat			1111
Arg Cys Ala Thr Gly Ile Leu Ile His Leu Ala Lys Phe Tyr Gly Tyr			
345	350	355	
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Asp Asn Val Lys Glu Tyr Leu Glu Ser Leu Gln Lys Glu Leu Val Glu			
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Asp Asn *			
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Met Thr Thr Asp
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gac aca gaa gtg ccc gct atg act cta gca ccg ggc cac gcc gct ctg 461
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gaa act caa acg ctg agc gct gag acc tct tct agg gcc tca acc cca 509
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gcc ggc ccc att cca gaa gca gag acc agg gga gcc aag aga att tcc 557
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Pro Ala Arg Glu Thr Arg Ser Phe Thr Lys Thr Ser Pro Asn Phe Met	
55 60 65	
gtg ctg atc gcc acc tcc gtg gag aca tca gcc gcc agt ggc agc ccc	653
Val Leu Ile Ala Thr Ser Val Glu Thr Ser Ala Ala Ser Gly Ser Pro	
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gag gga gct gga atg acc aca gtt cag acc atc aca ggc agt gat ccc	701
Glu Gly Ala Gly Met Thr Thr Val Gln Thr Ile Thr Gly Ser Asp Pro	
85 90 95 100	
gag gaa gcc atc ttt gac acc ctt tgc acc gat gac agc tct gaa gag	749
Glu Glu Ala Ile Phe Asp Thr Leu Cys Thr Asp Asp Ser Ser Glu Glu	
105 110 115	
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Ala Lys Thr Leu Thr Met Asp Ile Leu Thr Leu Ala His Thr Ser Thr	
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Glu Ala Lys Gly Leu Ser Ser Glu Ser Ser Ala Ser Ser Asp Gly Pro	
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His Pro Val Ile Thr Pro Ser Arg Ala Ser Glu Ser Ser Ala Ser Ser	
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Asp Gly Pro His Pro Val Ile Thr Pro Ser Arg Ala Ser Glu Ser Ser	
165 170 175 180	
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Ala Ser Ser Asp Gly Pro His Pro Val Ile Thr Pro Ser Arg Ala Ser	
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Thr Pro Ser Arg Ala Ser Glu Ser Ser Ala Ser Ser Asp Gly Pro His	
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cca gtc atc acc ccc tca tgg tcc ccg gga tct gac gtc act ctc ctc	1181
Pro Val Ile Thr Pro Ser Trp Ser Pro Gly Ser Asp Val Thr Leu Leu	
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gct gaa gcc ctg gtg act gtc aca aac atc gag gtt att aat tgc agc	1229
Ala Glu Ala Leu Val Thr Val Thr Asn Ile Glu Val Ile Asn Cys Ser	

265								270								275								
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Thr	Asp	Leu	Ile	Pro	Thr	Glu	Gly	Val	Lys	Ala	Ser	Ser	Thr	Ser	Asp									
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Pro	Pro	Ala	Leu	Pro	Asp	Ser	Thr	Glu	Ala	Lys	Pro	His	Ile	Thr	Glu									
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Val	Thr	Ala	Ser	Ala	Glu	Thr	Leu	Ser	Thr	Ala	Gly	Thr	Thr	Glu	Ser									
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Ala	Ala	Pro	His	Ala	Thr	Val	Gly	Thr	Pro	Leu	Pro	Thr	Asn	Ser	Ala									
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Thr	Glu	Arg	Glu	Val	Thr	Ala	Pro	Gly	Ala	Thr	Thr	Leu	Ser	Gly	Ala									
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Leu	Val	Thr	Val	Ser	Arg	Asn	Pro	Leu	Glu	Glu	Thr	Ser	Ala	Leu	Ser									
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Val	Glu	Thr	Pro	Ser	Tyr	Val	Lys	Val	Ser	Gly	Ala	Ala	Pro	Val	Ser									
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Ser	Ala	Ser	Ser	Tyr	Ser	Pro	Ser	Glu	Ala	Ala	Leu	Lys	Asn	Phe	Thr									
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Ser	Arg	Gly	Thr	Asn	Ser	Thr	Leu	Ala	Lys	Ile	Thr	Thr	Ser	Ala	Lys									
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Glu Arg Leu Met Gln Gln Leu His Arg Glu Leu His Ala His Ala Pro	
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His Phe Gln Val Ser Leu Leu Arg Val Arg Arg Gly *	
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Met Thr Thr Asp	
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gac aca gaa gtg ccc gct atg act cta gca ccg ggc cac gcc gct ctg	461

230	235	240	
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gcc aca gaa aga gaa gtg aca gca ccc ggg gcc acg acc ctc agt gga Ala Thr Glu Arg Glu Val Thr Ala Pro Gly Ala Thr Thr Leu Ser Gly 265 270 275			1229
gct ctg gtc aca gtt agc agg aat ccc ctg gaa gaa acc tca gcc ctc Ala Leu Val Thr Val Ser Arg Asn Pro Leu Glu Glu Thr Ser Ala Leu 280 285 290			1277
tct gtt gag aca cca agt tac gtc aaa gtc tca gga gca gct ccg gtc Ser Val Glu Thr Pro Ser Tyr Val Lys Val Ser Gly Ala Ala Pro Val 295 300 305			1325
tcc ata gag gct ggg tca gca gtg ggc aaa aca act tcc ttt gct ggg Ser Ile Glu Ala Gly Ser Ala Val Gly Lys Thr Thr Ser Phe Ala Gly 310 315 320			1373
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acc cct tca gag aca ccg acc atg gac atc gca acc aag ggg ccc ttc Thr Pro Ser Glu Thr Pro Thr Met Asp Ile Ala Thr Lys Gly Pro Phe 345 350 355			1469
ccc acc agc agg gac cct ctt cct tct gtc cct ccg act aca acc aac Pro Thr Ser Arg Asp Pro Leu Pro Ser Val Pro Pro Thr Thr Thr Asn 360 365 370			1517
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gca gaa agg ctg atg cag cag ctc cac cgg gaa ctc cac gcc cac gcg Ala Glu Arg Leu Met Gln Gln Leu His Arg Glu Leu His Ala His Ala 440 445 450			1757
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455 460 465			

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Met Gln Val Trp Leu Leu Thr
1 5
ctg gaa agg ctg agg gtt ctg ccc aaa cct agg agt gaa ttc gac ttc 462
Leu Glu Arg Leu Arg Val Leu Pro Lys Pro Arg Ser Glu Phe Asp Phe
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Phe Pro Ile Ser His Thr His Pro Arg Arg His Pro Asn Pro Arg Ile
25 30 35
tcc cac gtt cgg ctg cca ctg cct ccc agg tgg gct ttg cag gac cca 558
Ser His Val Arg Leu Pro Leu Pro Pro Arg Trp Ala Leu Gln Asp Pro
40 45 50 55
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Pro Cys His *
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caggcctgat gtc      atg acc ctg tat cct ctc cac tgg cag gaa gag atg      349
                   Met Thr Leu Tyr Pro Leu His Trp Gln Glu Glu Met
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tca gga gaa agt gtg gtg agc tca gcg gtg cca gcg gct gct acc cgc      397
Ser Gly Glu Ser Val Val Ser Ser Ala Val Pro Ala Ala Ala Thr Arg
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acc act tcc ttc aag ggc acg agc ccc agc tcc aaa tac gtg aag ctg      445
Thr Thr Ser Phe Lys Gly Thr Ser Pro Ser Ser Lys Tyr Val Lys Leu
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aat gtg ggt gga gcc ctc tac tat acc acc atg cag acg ctg acc aag      493
Asn Val Gly Gly Ala Leu Tyr Tyr Thr Thr Met Gln Thr Leu Thr Lys
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cag gac acc atg ctg aag gcc atg ttc agc ggg cgc atg gaa gtg ctc      541
Gln Asp Thr Met Leu Lys Ala Met Phe Ser Gly Arg Met Glu Val Leu
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acc gac agt gaa ggc tgg atc ctc att gac cgc tgt ggg aag cac ttt      589
Thr Asp Ser Glu Gly Trp Ile Leu Ile Asp Arg Cys Gly Lys His Phe
                   80              85              90

ggt acg ata ctc aac tac ctt cga gac ggg gcg gtg cct tta ccc gag      637
Gly Thr Ile Leu Asn Tyr Leu Arg Asp Gly Ala Val Pro Leu Pro Glu
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Ser Arg Arg Glu Ile Glu Glu Leu Leu Ala Glu Ala Lys Tyr Tyr Leu
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110	115	120	
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tac aac aga agt aac aac aaa tac tca tat acc agc aat tct gac gac Tyr Asn Arg Ser Asn Asn Lys Tyr Ser Tyr Thr Ser Asn Ser Asp Asp 175 180 185			877
aat atg ttg aaa aac att gaa ctg ttt gat aag ctg tct ctg cgc ttt Asn Met Leu Lys Asn Ile Glu Leu Phe Asp Lys Leu Ser Leu Arg Phe 190 195 200			925
aac gga agg gtc ctg ttc ata aag gat gtt att ggg gat gaa atc tgc Asn Gly Arg Val Leu Phe Ile Lys Asp Val Ile Gly Asp Glu Ile Cys 205 210 215 220			973
tgc tgg tcc ttt tat ggt cag ggc cgg aag att gct gaa gtc tgt tgt Cys Trp Ser Phe Tyr Gly Gln Gly Arg Lys Ile Ala Glu Val Cys Cys 225 230 235			1021
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gcc cac ctc cac cag tga gcaggc aagagaccga gccgccctcc tctcaccgcc Ala His Leu His Gln *			1315
			320
cccactccct gccgtgctac acccagatcc tgtgcaggct gccgggcccc ttctgcttcc			1375
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<222> (287)..(1924)

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                                     Met Pro Pro
                                     1

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Phe Leu Leu Leu Thr Cys Leu Phe Ile Thr Gly Thr Ser Val Ser Pro
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gtg gcc cta gat cct tgt tct gct tac atc agc ctg aat gag ccc tgg      391
Val Ala Leu Asp Pro Cys Ser Ala Tyr Ile Ser Leu Asn Glu Pro Trp
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agg aac act gac cac cag ttg gat gag tct caa ggt cct cct cta tgt      439
Arg Asn Thr Asp His Gln Leu Asp Glu Ser Gln Gly Pro Pro Leu Cys
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gac aac cat gtg aat ggg gag tgg tac cac ttc acg ggc atg gcg gga      487
Asp Asn His Val Asn Gly Glu Trp Tyr His Phe Thr Gly Met Ala Gly
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gat gcc atg cct acc ttc tgc ata cca gaa aac cac tgt gga acc cac      535
Asp Ala Met Pro Thr Phe Cys Ile Pro Glu Asn His Cys Gly Thr His
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gca cct gtc tgg ctc aat ggc agc cac ccc cta gaa ggc gac ggc att      583
Ala Pro Val Trp Leu Asn Gly Ser His Pro Leu Glu Gly Asp Gly Ile
      85                      90                      95

gtg caa cgc cag gct tgt gcc agc ttc aat ggg aac tgc tgt ctc tgg      631
Val Gln Arg Gln Ala Cys Ala Ser Phe Asn Gly Asn Cys Cys Leu Trp
      100                      105                      110                      115

aac acc acg gtg gaa gtc aag gct tgc cct gga ggc tac tat gtg tat      679
Asn Thr Thr Val Glu Val Lys Ala Cys Pro Gly Gly Tyr Tyr Val Tyr
                        120                      125                      130

cgt ctg acc aag ccc agc gtc tgc ttc cac gtc tac tgt ggt cat ttt      727
Arg Leu Thr Lys Pro Ser Val Cys Phe His Val Tyr Cys Gly His Phe
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tat gac atc tgc gac gag gac tgc cat ggc agc tgc tca gat acc agc      775
Tyr Asp Ile Cys Asp Glu Asp Cys His Gly Ser Cys Ser Asp Thr Ser
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atc tgt gtg aac ctc aaa aac tcc tac cgc tgt gag tgt ggg gtt ggc Ile Cys Val Asn Leu Lys Asn Ser Tyr Arg Cys Glu Cys Gly Val Gly 200 205 210			919
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ggc tac cag tgt gaa tgt ccc cgg ggc ctg gtg ctg tct gag gat aac Gly Tyr Gln Cys Glu Cys Pro Arg Gly Leu Val Leu Ser Glu Asp Asn 245 250 255			1063
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Arg Glu Ala Leu Pro Thr Leu Lys Leu Arg Asp Ser Leu Tyr Phe Gly	
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Ile Glu Pro Val Val His Val Ser Gly Leu Glu Ser Leu Val Glu Ser	
420 425 430 435	
tgc ttt gcc acc ccc acc tcc aag atc gac gag gtc ctg aaa tac tac	1639
Cys Phe Ala Thr Pro Thr Ser Lys Ile Asp Glu Val Leu Lys Tyr Tyr	
440 445 450	
ctc atc cgg gat ggc tgt gtt tca gat gac tcg gta aag cag tac aca	1687
Leu Ile Arg Asp Gly Cys Val Ser Asp Asp Ser Val Lys Gln Tyr Thr	
455 460 465	
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Ser Arg Asp His Leu Ala Lys His Phe Gln Val Pro Val Phe Lys Phe	
470 475 480	
gtg ggc aaa gac cac aag gaa gtg ttt ctg cac tgc cgg gtt ctt gtc	1783
Val Gly Lys Asp His Lys Glu Val Phe Leu His Cys Arg Val Leu Val	
485 490 495	
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Cys Gly Val Leu Asp Glu Arg Ser Arg Cys Ala Gln Gly Cys His Arg	
500 505 510 515	
cga atg cgt cgt ggg gca gga gga gag gac tca gcc ggt cta cag ggc	1879
Arg Met Arg Arg Gly Ala Gly Gly Glu Asp Ser Ala Gly Leu Gln Gly	
520 525 530	
cag acg cta aca ggc ggc ccg atc cgc atc gac tgg gag gac tag ttc	1927
Gln Thr Leu Thr Gly Gly Pro Ile Arg Ile Asp Trp Glu Asp *	
535 540 545	
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2444

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<213> Homo sapiens

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<400> 15

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atg ggg gca aag gat cca agc att gag cct tca tcc tct att ccc cat 165
Met Gly Ala Lys Asp Pro Ser Ile Glu Pro Ser Ser Ser Ile Pro His
1 5 10 15

cca gtg ggg tgc cga ggc tca ggc agc atg acg acg gag acc ttt gtg 213
Pro Val Gly Cys Arg Gly Ser Gly Ser Met Thr Thr Glu Thr Phe Val
20 25 30

aag gat atc aag cct ggg ctc aag aat ctg aac ctt atc ttc att gtg 261
Lys Asp Ile Lys Pro Gly Leu Lys Asn Leu Asn Leu Ile Phe Ile Val
35 40 45

ctg gag aca ggc cga gtg acc aag aca aag gac ggg cat gag gtt cgg 309
Leu Glu Thr Gly Arg Val Thr Lys Thr Lys Asp Gly His Glu Val Arg
50 55 60

acc tgc aaa gtg gcg gac aaa aca ggc agc atc aat atc tct gtc tgg 357
Thr Cys Lys Val Ala Asp Lys Thr Gly Ser Ile Asn Ile Ser Val Trp
65 70 75 80

gac gat gtt ggc aat ctg atc cag cct ggg gac att atc cgg ctc acc 405
Asp Asp Val Gly Asn Leu Ile Gln Pro Gly Asp Ile Ile Arg Leu Thr
85 90 95

aaa ggg tac gct tca gtt ttc aaa ggt tgt ctg aca cta tat act ggc 453
Lys Gly Tyr Ala Ser Val Phe Lys Gly Cys Leu Thr Leu Tyr Thr Gly
100 105 110

cgt ggg ggt gat ctg cag aag att gga gaa ttc tgt atg gtt tat tct 501
Arg Gly Gly Asp Leu Gln Lys Ile Gly Glu Phe Cys Met Val Tyr Ser
115 120 125

gag gtt cct aac ttc agt gag cca aac cca gag tac agc acc cag cag 549
Glu Val Pro Asn Phe Ser Glu Pro Asn Pro Glu Tyr Ser Thr Gln Gln
130 135 140

gca ccc aac aag gcg gtg cag aac gac agc aac cct tca gct tcc cag 597
Ala Pro Asn Lys Ala Val Gln Asn Asp Ser Asn Pro Ser Ala Ser Gln
145 150 155 160

gcgccccaat ttcgattttc aaacgcaact cctacaggat tctgagaccc cgtcccatct	120
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Met Ala Gln Lys Pro Lys Val Asp Pro His Val Gly Arg Leu Gly Tyr	
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Leu Gln Ala Leu Val Thr Glu Phe Gln Glu Thr Gln Ser Gln Asp Ala	
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aag gag caa gtc ctc gcc aac ctc gcc aac ttc gct tat gac ccc agc	444
Lys Glu Gln Val Leu Ala Asn Leu Ala Asn Phe Ala Tyr Asp Pro Ser	
35 40 45	
aac tac gag tat ctg cgg cag ctg cag gtc ctg gat tta ttt ctc gat	492
Asn Tyr Glu Tyr Leu Arg Gln Leu Gln Val Leu Asp Leu Phe Leu Asp	
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tcg ctg tcg gag gag aat gag acc ctg gtg gag ttt gct att gga ggc	540
Ser Leu Ser Glu Glu Asn Glu Thr Leu Val Glu Phe Ala Ile Gly Gly	
65 70 75 80	
ctg tgc aac ctg tgc cca gac agg gcc aac aag gag cac atc ctg cac	588
Leu Cys Asn Leu Cys Pro Asp Arg Ala Asn Lys Glu His Ile Leu His	
85 90 95	
gca gga ggt gtc cca ctc atc atc aac tgc cta tcc agc ccc aat gag	636
Ala Gly Gly Val Pro Leu Ile Ile Asn Cys Leu Ser Ser Pro Asn Glu	
100 105 110	
gag acg gtg ctg tct gcc atc acc acg ctc atg cac ctg agc ccg ccg	684
Glu Thr Val Leu Ser Ala Ile Thr Thr Leu Met His Leu Ser Pro Pro	
115 120 125	
ggc cgc agc ttt ctc cca gag ctg acc gcc acg ccc gtg gtg cag tgc	732
Gly Arg Ser Phe Leu Pro Glu Leu Thr Ala Thr Pro Val Val Gln Cys	
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Met Leu Arg Phe Ser Leu Ser Ala Ser Ala Arg Leu Arg Asn Leu Ala	
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cag atc ttc ctg gag gac ttc tgc tcc ccc cgc cag gtg gcc gag gcc	828
Gln Ile Phe Leu Glu Asp Phe Cys Ser Pro Arg Gln Val Ala Glu Ala	
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Arg Ser Arg Gln Ala His Ser Ala Leu Gly Ile Pro Leu Pro Arg Ser	
180 185 190	

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Val Ala Pro Arg Gln Arg *	
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ggtgcctttt cagccatctg aaaggcgggt tctttcagca ggacaggcat ttacactgat	1049
gaaacgccac tgggagttag gaagccagac tccagagaca cggagaagat caaactggag	1109
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<210> 17
<211> 2099
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (119) .. (580)

<400> 17

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atg aat gtg ggc aca gcg cac agc gag gtg aac ccc aac acg cgg gtg	166
Met Asn Val Gly Thr Ala His Ser Glu Val Asn Pro Asn Thr Arg Val	
1 5 10 15	
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Met Asn Ser Arg Gly Ile Trp Leu Ser Tyr Val Leu Ala Ile Gly Leu	
20 25 30	
ctc cac atc gtg ctg ctg agc atc ccg ttt gtg agt gtc cct gtc gtc	262
Leu His Ile Val Leu Leu Ser Ile Pro Phe Val Ser Val Pro Val Val	
35 40 45	
tgg acc ctc acc aac ctc att cac aac atg ggc atg tat atc ttc ctg	310
Trp Thr Leu Thr Asn Leu Ile His Asn Met Gly Met Tyr Ile Phe Leu	
50 55 60	
cac acg gtg aag ggg aca ccc ttt gag acc ccg gac cag ggc aag gcg	358
His Thr Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala	
65 70 75 80	
agg ctg cta acc cac tgg gag cag atg gat tat ggg gtc cag ttc acg	406
Arg Leu Leu Thr His Trp Glu Gln Met Asp Tyr Gly Val Gln Phe Thr	
85 90 95	
gcc tct cgg aag ttc ttg acc atc aca ccc atc gtg ctg tac ttc ctc	454
Ala Ser Arg Lys Phe Leu Thr Ile Thr Pro Ile Val Leu Tyr Phe Leu	
100 105 110	
acc agc ttc tac act aag tac gac cag atc cat ttt gtg ctc aac acc	502
Thr Ser Phe Tyr Thr Lys Tyr Asp Gln Ile His Phe Val Leu Asn Thr	
115 120 125	
gtg tcc ctg atg agc gtg ctt atc ccc aag ctg ccc cag ctc cac gga	550
Val Ser Leu Met Ser Val Leu Ile Pro Lys Leu Pro Gln Leu His Gly	
130 135 140	
gtc cgg att ttt gga atc aat aag tac tga g agtgcagccc cttcccctgc	601
Val Arg Ile Phe Gly Ile Asn Lys Tyr *	
145 150	
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gggaactttc accttaaaat ctttctaagc aaagtgtgaa taggattttt actccctttg 2041
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<210> 18
 <211> 1605
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (535) .. (1050)

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gctggtaact ttggcgctc cgccaagccc tgccagactc ccctggctgt gatggcattc 180
tgtgccatcc tccttgtccc cagcctctgc aggatgcct ccctaccac ctctccctgg 240

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gccttccctg tccactgggc tggattcatg ttcaaaccac tggactggca gggcaacgac 300

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gcatgagcca tgtgtcttctt tgcccttctc tgtcctgttc caatcttctg cctcccagtc 420

actccctggg gactatggga tcaactgtccc cccacctgtg tggccacacc atgtgtcctg 480

tcaatccaga actgcctctg agctccaggc tgaccacaga tcagccacag cctg atg 537
Met
1

cct gca gcc cca ctt tgc tca ccc ttc ccc tcc cct cct cct tcc ttc 585
Pro Ala Ala Pro Leu Cys Ser Pro Phe Pro Ser Pro Pro Pro Ser Phe
5 10 15

cac aca gca agc cta cct ttc tcc atc cat gct cac cat agc ccc ctt 633
His Thr Ala Ser Leu Pro Phe Ser Ile His Ala His His Ser Pro Leu
20 25 30

cct tgt gac ttg gac cct cca ttg tac ctg gct gag act gtc agc ctc 681
Pro Cys Asp Leu Asp Pro Pro Leu Tyr Leu Ala Glu Thr Val Ser Leu
35 40 45

ctg gag gag tgg ggt cca cct tct tct tgc cct atg cag tgc aag ctc 729
Leu Glu Glu Trp Gly Pro Pro Ser Ser Cys Pro Met Gln Cys Lys Leu
50 55 60 65

act tct cac cca gca agg ttg act cat ctg cct cca tgt ctc tgg ggc 777
Thr Ser His Pro Ala Arg Leu Thr His Leu Pro Pro Cys Leu Trp Gly
70 75 80

ttt gct gtt gcc ctg aaa cct agc tgg gct ggt ctt gct ccc agc ttg 825
Phe Ala Val Ala Leu Lys Pro Ser Trp Ala Gly Leu Ala Pro Ser Leu
85 90 95

ctt ccc cct cct cgg atg tcc ctt tgc agg ccc ctg tcg ttc ctc cgg 873
Leu Pro Pro Pro Arg Met Ser Leu Cys Arg Pro Leu Ser Phe Leu Arg
100 105 110

cac cag tgt cct tgg ctg cca tgg caa gct cat cag ggg ctt gta ccc 921
His Gln Cys Pro Trp Leu Pro Trp Gln Ala His Gln Gly Leu Val Pro
115 120 125

tgg tca cca agc atg gta gca gct gcc tgc att gta tct cca tct ggt 969
Trp Ser Pro Ser Met Val Ala Ala Ala Cys Ile Val Ser Pro Ser Gly
130 135 140 145

cac tgc agg tgc caa ccc ttc atc ccc cat gtt ttc ctg ggc cat gga 1017
His Cys Arg Cys Gln Pro Phe Ile Pro His Val Phe Leu Gly His Gly
150 155 160

ggg ctg acc tcc gtt tct ggg gaa tgt ggc tga gctgtggt aaccagctac 1068
Gly Leu Thr Ser Val Ser Gly Glu Cys Gly *
165 170

accccagggtg ctctttccat ggtgggtgcct gctcatcttg ctgatgcaaa ctaggaagtt 1128

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<210> 19
<211> 1497
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (210)..(1172)

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tgggcgggag cccttgtctg ggtctcgcgg ggggctgcca gatgcgtagg ccacactgac 180
tagttccttc ttgtcgcttt tcccagcaa atg gcg gat gac gcc ggt gca gcg 233
Met Ala Asp Asp Ala Gly Ala Ala
1 5

ggg ggg ccc ggg ggc cct ggt ggc cct ggg atg ggg aac cgc ggt ggc 281
Gly Gly Pro Gly Gly Pro Gly Gly Pro Gly Met Gly Asn Arg Gly Gly
10 15 20

ttc cgc gga ggt ttc ggc agt ggc atc cgg ggc cgg ggt cgc ggc cgt 329
Phe Arg Gly Gly Phe Gly Ser Gly Ile Arg Gly Arg Gly Arg Gly Arg
25 30 35 40

gga cgg ggc cgg ggc cga ggc cgc gga gct cgc gga ggc aag gcc gag 377
Gly Arg Gly Arg Gly Arg Gly Arg Gly Ala Arg Gly Gly Lys Ala Glu
45 50 55

gat aag gag tgg atg ccc gtc acc aag ttg ggc cgc ttg gtc aag gac 425
Asp Lys Glu Trp Met Pro Val Thr Lys Leu Gly Arg Leu Val Lys Asp
60 65 70

atg aag atc aag tcc ctg gag gag atc tat ctc ttc tcc ctg ccc att 473

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Lys	Glu	Ser	Glu	Ile	Ile	Asp	Phe	Phe	Leu	Gly	Ala	Ser	Leu	Lys	Asp		
	90					95				100							
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Glu	Val	Leu	Lys	Ile	Met	Pro	Val	Gln	Lys	Gln	Thr	Arg	Ala	Gly	Gln		
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Arg	Thr	Arg	Phe	Lys	Ala	Phe	Val	Ala	Ile	Gly	Asp	Tyr	Asn	Gly	His		
			125						130					135			
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Val	Gly	Leu	Gly	Val	Lys	Cys	Ser	Lys	Glu	Val	Ala	Thr	Ala	Ile	Arg		
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Gly	Ala	Ile	Ile	Leu	Ala	Lys	Leu	Ser	Ile	Val	Pro	Val	Arg	Arg	Gly		
	155						160					165					
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Tyr	Trp	Gly	Asn	Lys	Ile	Gly	Lys	Pro	His	Thr	Val	Pro	Cys	Lys	Val		
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Thr	Ala	Trp	Gly	His	His	Pro	Gly	Gln	Ala	Leu	His	Arg	Pro	Arg	Ala		
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Gln	Arg	Leu	Leu	Gly	Glu	Gln	Asp	Arg	Gln	Ala	Pro	His	Cys	His	Leu		
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Ala	His	Gly	Asp	Asp	Gly	Glu	Leu	Gly	Gln	Asp	Asp	Gly	Pro	Thr	Asp		
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Gly	Gly	Gly	His	Leu	Leu	Gly	Ala	Leu	Asn	Thr	Gln	Thr	Asp	Val	Ala		
	250					255					260						
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Ile	Val	Val	Pro	Asp	Ser	Asn	Lys	Cys	Leu	Glu	Pro	Gly	Ala	Leu	Ala		
265					270					275					280		
ggc	acg	ggt	ctg	ctt	ctg	cac	tgg	cat	aat	ctt	caa	aac	ctc	atc	ctt	1097	
Gly	Thr	Gly	Leu	Leu	Leu	His	Trp	His	Asn	Leu	Gln	Asn	Leu	Ile	Leu		
				285				290						295			
gag	aga	ggg	cac	cac	aca	gtg	aac	gaa	agt	caa	atg	agt	gct	gct	gat	1145	
Glu	Arg	Gly	His	His	Thr	Val	Asn	Glu	Ser	Gln	Met	Ser	Ala	Ala	Asp		

300	305	310	
tcc tta ata ggc agg gag aag aga tag atcac cactccaggg acttagatct			1197
Ser Leu Ile Gly Arg Glu Lys Arg *			
315	320		
tcattgtcctt ggaccaagcg gccacaactt cgggtgacggg gcatccactc cttatcgctc			1257
ggccttgcgc tccagcgagc tccgcaggca catcggccca caggccacac agtcacacag			1317
gccgcagacc accaggccac cagagtgcac agcatgcaca gaaacactgc cgcaggaagc			1377
acacacagcg gcttcccaca tcacaagggc cacaatgggc ccccaggggc caccgccgtg			1437
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 <213> Homo sapiens

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		Met	
		1	
acg aac gtg tac tcc ttg gat ggg att ctg gtg ttt ggt ttg ctc ttt			164
Thr Asn Val Tyr Ser Leu Asp Gly Ile Leu Val Phe Gly Leu Leu Phe			
5 10 15			
gtt tgc acc tgt gcc tac ttc aag aaa gta cct cgt ctc aaa acc tgg			212
Val Cys Thr Cys Ala Tyr Phe Lys Lys Val Pro Arg Leu Lys Thr Trp			
20 25 30			
ctg cta tca gag aag aag ggt gtt tgg ggt gtg ttt tac aaa gcc gct			260
Leu Leu Ser Glu Lys Lys Gly Val Trp Gly Val Phe Tyr Lys Ala Ala			
35 40 45			
gtg att gga acc agg ctg cat gct gct gtg gca att gct tgt gtt gta			308
Val Ile Gly Thr Arg Leu His Ala Ala Val Ala Ile Ala Cys Val Val			
50 55 60 65			
atg gcc ttt tac gtc ctg ttt ata aaa tga a ttccaaagca cccaagtcac			359
Met Ala Phe Tyr Val Leu Phe Ile Lys *			
70 75			
caactgccaa ccaaggggac ggggatgaag aacctgttgg agacctgaac ccagtgtagg			419

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agagttcagc tgaaatcatc ggtccccagg atgacaccac agcatctgcc cctgctatat 479
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ttcctttgat ctatgtgtaa atcagtcctt ggcagagtgc atataatgtc cggataaatt 599
acaccctcgc gtgataagat tacatacctc cttcataaaa acctgtcatc ctgtttgttc 659
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ttcagacttc tttgagagcg agaatttcca gactttcttt cctccttgat tggctctggca 779
ttggggcggg gatgctgggt gggaacccgt ttgaattgcc aggaaattct tgggttagaa 839
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ttggccgcg 907

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<212> DNA
<213> Homo sapiens

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<220>
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<222> (103)..(1116)

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tcttcttttg cgtcgccagc cgagccacat cgctcagaca cc atg ggg aag gtg 114
Met Gly Lys Val
1

aag gtc gga gtc aac gga ttt ggt cgt att ggg cgc ctg gtc acc agg 162
Lys Val Gly Val Asn Gly Phe Gly Arg Ile Gly Arg Leu Val Thr Arg
5 10 15 20

gct gct ttt aac tct ggt aaa gtg gat att gtt gcc atc aat gac ccc 210
Ala Ala Phe Asn Ser Gly Lys Val Asp Ile Val Ala Ile Asn Asp Pro
25 30 35

ttc att gac ctc aac tac atg gtt tac atg ttc caa tat gat tcc acc 258
Phe Ile Asp Leu Asn Tyr Met Val Tyr Met Phe Gln Tyr Asp Ser Thr
40 45 50

cat ggc aaa ttc cat ggc acc gtc aag gct gag aac ggg aag ctt gtc 306
His Gly Lys Phe His Gly Thr Val Lys Ala Glu Asn Gly Lys Leu Val
55 60 65

atc aat gga aat ccc atc acc atc ttc cag gag cga gat ccc tcc aaa 354
Ile Asn Gly Asn Pro Ile Thr Ile Phe Gln Glu Arg Asp Pro Ser Lys
70 75 80

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atc aag tgg ggc gat gct ggc gct gag tac gtc gtg gag tcc act ggc Ile Lys Trp Gly Asp Ala Gly Ala Glu Tyr Val Val Glu Ser Thr Gly 85 90 95 100	402
gtc ttc acc acc atg gag aag gct ggg gct cat ttg cag ggg gga gcc Val Phe Thr Thr Met Glu Lys Ala Gly Ala His Leu Gln Gly Gly Ala 105 110 115	450
aaa agg gtc atc atc tct gcc ccc tct gct gat gcc ccc atg ttc gtc Lys Arg Val Ile Ile Ser Ala Pro Ser Ala Asp Ala Pro Met Phe Val 120 125 130	498
atg ggt gtg aac cat gag aag tat gac aac agc ctc aag atc atc agc Met Gly Val Asn His Glu Lys Tyr Asp Asn Ser Leu Lys Ile Ile Ser 135 140 145	546
aat gcc tcc tgc acc acc aac tgc tta gca ccc ctg gcc aag gtc atc Asn Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Leu Ala Lys Val Ile 150 155 160	594
cat gac aac ttt ggt atc gtg gaa gga ctc atg acc aca gtc cat gcc His Asp Asn Phe Gly Ile Val Glu Gly Leu Met Thr Thr Val His Ala 165 170 175 180	642
atc act gcc acc cag aag act gtg gga tgg ccc ctt ccg gga aac tgt Ile Thr Ala Thr Gln Lys Thr Val Gly Trp Pro Leu Pro Gly Asn Cys 185 190 195	690
ggc gtg atg gcc gcg ggg gcg tct gcc aga aac atc atc cct gcc tct Gly Val Met Ala Ala Gly Ala Ser Ala Arg Asn Ile Ile Pro Ala Ser 200 205 210	738
act ggc gct gcc aag gct gtg ggc aag gtc atc cct gag ctg aac ggg Thr Gly Ala Ala Lys Ala Val Gly Lys Val Ile Pro Glu Leu Asn Gly 215 220 225	786
aag ctc act ggc atg gcc ttc cgt gtc ccc act gcc aac gtg tca gtg Lys Leu Thr Gly Met Ala Phe Arg Val Pro Thr Ala Asn Val Ser Val 230 235 240	834
gtg gac ctg acc tgc cgt cta gaa aaa cct gcc aaa tat gat gac atc Val Asp Leu Thr Cys Arg Leu Glu Lys Pro Ala Lys Tyr Asp Asp Ile 245 250 255 260	882
aag aag gtg gtg aag cag gcg tcg gag ggc ccc ctc aag ggc atc ctg Lys Lys Val Val Lys Gln Ala Ser Glu Gly Pro Leu Lys Gly Ile Leu 265 270 275	930
ggc tac act gag cac cag gtg gtc tcc tct gac ttc aac agc gac acc Gly Tyr Thr Glu His Gln Val Val Ser Ser Asp Phe Asn Ser Asp Thr 280 285 290	978
cac tcc tcc acc ttt gac gct ggg gct ggc att gcc ctc aac gac cac His Ser Ser Thr Phe Asp Ala Gly Ala Gly Ile Ala Leu Asn Asp His 295 300 305	1026
ttt gtc aag ctc att tcc tgg tat gac aac gaa ttt ggc tac agc aac	1074

Phe Val Lys Leu Ile Ser Trp Tyr Asp Asn Glu	Phe Gly Tyr Ser Asn	
310	315	320
agg gtg gtg gac ctc atg gcc cac atg gcc tcc aag gag taa gacccct		1123
Arg Val Val Asp Leu Met Ala His Met Ala Ser	Lys Glu *	
325	330	335
ggaccaccag cccagcaag agcacaagag gaagagagag accctcactg ctggggagtc		1183
cctgccacac tcagtcccc accacactga atctcccctc ctcacagttg ccatgtagac		1243
cccttgaaga ggggaggggc ctaggagacc gcacctgtgc atgtaccatc aataaagtac		1303
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (532) .. (930)

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gctccagtcg gtggaaagaa aaggcagaga cgttgcagag gccaggtctg ctcaggggaa	180
gacagttctg ggtgtagagg actcacatcc cagagaggct gaggaagggg ttaccaccgc	240
aagctttctc aggcgggctc ttgaggggtg gctgggggtc tcttggcgac gggcctgcgg	300
cactggaagc cctactggag tttggcctgt ctccggcaca ggtttggacg gagctgtttt	360
gtgctgaaag gttttctcgg ggtccgtggt gtccccaaa ggtgccaccg tgcggtgtctc	420
ctagctccct gccagcttcc tgtccctgtg ctactgccc ccacgcctcc tgccaaggcc	480
gagccacaca cccgctccac ctgcatttcc tctaccgact cgccagccca a atg ccg	537
	Met Pro
	1
ctc ttc act ctg gcc tcg ctg agc ggc tgc ccg agg agg agc tct agg	585
Leu Phe Thr Leu Ala Ser Leu Ser Gly Cys Pro Arg Arg Ser Ser Arg	
5	10
ccg acg ccc acc gca ggc ctt aca gtc ttc tct gga cgc tcc ctt gca	633
Pro Thr Pro Thr Ala Gly Leu Thr Val Phe Ser Gly Arg Ser Leu Ala	
20	25
gat gca ccg tgg cct ggc ggc gag ccc ccg gtc acc ttc ctc cgc acg	681

Asp	Ala	Pro	Trp	Pro	Gly	Gly	Glu	Pro	Pro	Val	Thr	Phe	Leu	Arg	Thr	
35					40					45					50	
gaa gag ggg ccg gac gcc acc ttc ccc agg acc att ccc ctg atc caa																729
Glu	Glu	Gly	Pro	Asp	Ala	Thr	Phe	Pro	Arg	Thr	Ile	Pro	Leu	Ile	Gln	
			55						60					65		
cag ttg cta aac gcc acg gag ctc acg cag gac ccg gcc gcc tac tcc																777
Gln	Leu	Leu	Asn	Ala	Thr	Glu	Leu	Thr	Gln	Asp	Pro	Ala	Ala	Tyr	Ser	
			70					75					80			
cag ctg gtg gcc gtg ctg gtc tac acc gcc gag cgg gcc aag ttc gcc																825
Gln	Leu	Val	Ala	Val	Leu	Val	Tyr	Thr	Ala	Glu	Arg	Ala	Lys	Phe	Ala	
		85					90					95				
acc ggg gta gag cgg cag gac tgg atg gag ctg ttc att gac acc ttt																873
Thr	Gly	Val	Glu	Arg	Gln	Asp	Trp	Met	Glu	Leu	Phe	Ile	Asp	Thr	Phe	
	100					105					110					
aag ctg gtg cac agg gac atc gtg ggg gac ccc gag acc gcg ctg gcc																921
Lys	Leu	Val	His	Arg	Asp	Ile	Val	Gly	Asp	Pro	Glu	Thr	Ala	Leu	Ala	
	115				120				125					130		
ctc tgc taa agcccg gcacccgcc agccgggctg ggccctccct gccacactag																977
Leu	Cys	*														
cttcccaggg ctgccccga caggctggct ctcagtggag gccagagatc tggaatcggg																1037
gtcagcgggg ctacagtctt tccaggggct ctggggcagc tccagcctc ttcccatgct																1097
ggtggccacc gtgtcccttg ctgcggctgc atcttccagt ctctcctcgg tcttccagt																1157
gccgctctct ttataagaac cctggtcatt gaatttaagg cccaccccaa gtccagaatg																1217
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 <213> Homo sapiens

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tcacgtgtcc	gctgcagtcg	cgaaacagtt	ccggtggtga	ggagaccttt	ccaaatataa											120
gaggaataaa	gaagtcacct	cccagctgt	catcatcttc	cagcagattg	agcaagaata											180
ttttgagcac	tacaggaaag	acagtccatc	aaacccgaga	tgatgatcag	ccacgtgatt											240

ttttcaagaa gaggaatagg gtgaatgaat ctcatcagaa aagcagcaat	atg aat Met Asn 1	296
gct ggc cca tct tgg aat aaa gtg caa cat tca aag aat tct tca gga Ala Gly Pro Ser Trp Asn Lys Val Gln His Ser Lys Asn Ser Ser Gly 5 10 15		344
aaa agg cag agt aaa tcc caa gta ccc cac gct tct tcc cag ccg aga Lys Arg Gln Ser Lys Ser Gln Val Pro His Ala Ser Ser Gln Pro Arg 20 25 30		392
agc agc ctc aca gct gtc acc cag cct act gaa gaa aaa ctt aaa gaa Ser Ser Leu Thr Ala Val Thr Gln Pro Thr Glu Glu Lys Leu Lys Glu 35 40 45 50		440
agc att tcc ccg gaa gca aga cgc aaa agg aat cca ctc ggt tcc agg Ser Ile Ser Pro Glu Ala Arg Arg Lys Arg Asn Pro Leu Gly Ser Arg 55 60 65		488
tgt cag ggg gcc tca ggg aat aaa ctg ttt ctt gat ttt cag tca atg Cys Gln Gly Ala Ser Gly Asn Lys Leu Phe Leu Asp Phe Gln Ser Met 70 75 80		536
aaa att att aaa gag aat gct gat gag gac agt gca agt gat ctc tct Lys Ile Ile Lys Glu Asn Ala Asp Glu Asp Ser Ala Ser Asp Leu Ser 85 90 95		584
gat tcg gaa aga att ccc att cct cct tct ccc ctc aca cct cca gat Asp Ser Glu Arg Ile Pro Ile Pro Pro Ser Pro Leu Thr Pro Pro Asp 100 105 110		632
ctc aat ctt cga gct gaa gaa att gat cca gtt tac ttt gat ctt cac Leu Asn Leu Arg Ala Glu Glu Ile Asp Pro Val Tyr Phe Asp Leu His 115 120 125 130		680
cct ggt cag ggc cat aca aaa cct gaa tac tat tat cct aat ttc ctt Pro Gly Gln Gly His Thr Lys Pro Glu Tyr Tyr Tyr Pro Asn Phe Leu 135 140 145		728
cca tcc cct ttc agc tcc tgg gac cta cga gat atg gcc ctg ctt ctg Pro Ser Pro Phe Ser Ser Trp Asp Leu Arg Asp Met Ala Leu Leu Leu 150 155 160		776
aac gca gag aac aaa acg gaa gcc gtg ccc cga gtg gga gga ctt ctt Asn Ala Glu Asn Lys Thr Glu Ala Val Pro Arg Val Gly Gly Leu Leu 165 170 175		824
ggg aag tat atc gat aga ctt att cag ctt gag tgg ctg caa gtc cag Gly Lys Tyr Ile Asp Arg Leu Ile Gln Leu Glu Trp Leu Gln Val Gln 180 185 190		872
act gta cag tgt gaa aaa gca aag ggg ggc aaa gca agg ccc ccc act Thr Val Gln Cys Glu Lys Ala Lys Gly Gly Lys Ala Arg Pro Pro Thr 195 200 205 210		920

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gcc cct ggg acc tca ggg gca ctg aaa agc cct ggg aga agt aag cta      968
Ala Pro Gly Thr Ser Gly Ala Leu Lys Ser Pro Gly Arg Ser Lys Leu
                215                      220                      225

att gct agt gct ctg tcc aag cca cta cct cac cag gaa ggg gct tca      1016
Ile Ala Ser Ala Leu Ser Lys Pro Leu Pro His Gln Glu Gly Ala Ser
                230                      235                      240

aag tca ggc cct tcc cga aag aaa gct ttt cac cat gaa gaa atc cac      1064
Lys Ser Gly Pro Ser Arg Lys Lys Ala Phe His His Glu Glu Ile His
                245                      250                      255

cca tca cat tat gca ttt gag act tcc cct aga ccc att gat gtg ctt      1112
Pro Ser His Tyr Ala Phe Glu Thr Ser Pro Arg Pro Ile Asp Val Leu
                260                      265                      270

ggg ggt acc agg ttt tgt tct cag agg caa acc ctt gaa atg agg aca      1160
Gly Gly Thr Arg Phe Cys Ser Gln Arg Gln Thr Leu Glu Met Arg Thr
                275                      280                      285                      290

gaa gaa aaa aaa aaa aaa tca agt aag agt acg aag ctg cag cgc tgg      1208
Glu Glu Lys Lys Lys Lys Ser Ser Lys Ser Thr Lys Leu Gln Arg Trp
                295                      300                      305

gat ctg tcc ggc agt gga agc agc tct aag gtg gaa acc agc ggt cac      1256
Asp Leu Ser Gly Ser Gly Ser Ser Ser Lys Val Glu Thr Ser Gly His
                310                      315                      320

att cga gtt ccc aaa cag gca gct gtg att ctg gac tca gca gat tcc      1304
Ile Arg Val Pro Lys Gln Ala Ala Val Ile Leu Asp Ser Ala Asp Ser
                325                      330                      335

tgt aag gcc tcc aaa aca caa gca cat gca cat cct agg aaa aag gga      1352
Cys Lys Ala Ser Lys Thr Gln Ala His Ala His Pro Arg Lys Lys Gly
                340                      345                      350

aag gca gag agc tgt ggt cat gcc act gta tcg agt gag aaa aaa ctg      1400
Lys Ala Glu Ser Cys Gly His Ala Thr Val Ser Ser Glu Lys Lys Leu
                355                      360                      365                      370

aaa aca aac gga gta aag caa aac aca tat aaa cta aaa taa atatcta      1449
Lys Thr Asn Gly Val Lys Gln Asn Thr Tyr Lys Leu Lys *
                375                      380

aaatgctgaa ttgccaaagac ctgcaggtac ctcaatgtta gagcgcttcc aaaagtcaaa      1509

atactgtgaa ttttaaggaa ttttacaaat actgacathtt aagtaaaaaa aaaaaaa      1566

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<210> 24
 <211> 2851
 <212> DNA
 <213> Homo sapiens
 <220>

<221> CDS
 <222> (70)..(2322)

<400> 24

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             Met Leu Ser Leu Glu Leu Leu Ser Gln Val Val Gly Phe
               1             5             10

cat cag cca ggt agt atc aga ctt gct acc acc cct gta agg gta gat      156
His Gln Pro Gly Ser Ile Arg Leu Ala Thr Thr Pro Val Arg Val Asp
             15             20             25

gaa ttt aaa tat caa atg act cgg act ggc tgg cat gca aca gaa cag      204
Glu Phe Lys Tyr Gln Met Thr Arg Thr Gly Trp His Ala Thr Glu Gln
             30             35             40             45

tat ctc att gaa cct gaa aaa att caa gag atg ttc cct tta ctc aac      252
Tyr Leu Ile Glu Pro Glu Lys Ile Gln Glu Met Phe Pro Leu Leu Asn
             50             55             60

atg aat aag gtt tta gct gga ttg tat aat cct gga gat ggt cac att      300
Met Asn Lys Val Leu Ala Gly Leu Tyr Asn Pro Gly Asp Gly His Ile
             65             70             75

gat cct tat tct cta act atg gca ctg gct gct ggg gct agg aaa tgt      348
Asp Pro Tyr Ser Leu Thr Met Ala Leu Ala Ala Gly Ala Arg Lys Cys
             80             85             90

ggg gcc ctt tta aaa tat cct gca cca gta act tct ctg aaa gcc agg      396
Gly Ala Leu Leu Lys Tyr Pro Ala Pro Val Thr Ser Leu Lys Ala Arg
             95             100             105

tca gat gga aca tgg gac gtt gaa aca cca cag ggg tct atg aga gca      444
Ser Asp Gly Thr Trp Asp Val Glu Thr Pro Gln Gly Ser Met Arg Ala
            110             115             120             125

aat aga att gtg aat gct gca gga ttt tgg gct cgt gaa gta ggt aaa      492
Asn Arg Ile Val Asn Ala Ala Gly Phe Trp Ala Arg Glu Val Gly Lys
            130             135             140

atg att gga cta gaa cat cct ctc att ccg gtt caa cat caa tat gtt      540
Met Ile Gly Leu Glu His Pro Leu Ile Pro Val Gln His Gln Tyr Val
            145             150             155

gtt aca tcg act ata tct gaa gtg aaa gct ttg aaa cga gaa ctg cct      588
Val Thr Ser Thr Ile Ser Glu Val Lys Ala Leu Lys Arg Glu Leu Pro
            160             165             170

gtg ctc cgt gac ctg gaa gga tca tat tat ctc cga cag gaa agg gat      636
Val Leu Arg Asp Leu Glu Gly Ser Tyr Tyr Leu Arg Gln Glu Arg Asp
            175             180             185

ggg ctt ttg ttt ggt cca tat gaa agt caa gag aaa atg aaa gtt cag      684
Gly Leu Leu Phe Gly Pro Tyr Glu Ser Gln Glu Lys Met Lys Val Gln
            190             195             200             205

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gac tcc tgg gtc acc aat gga gtt cct cca ggt ttt gga aag gaa ctc	732
Asp Ser Trp Val Thr Asn Gly Val Pro Pro Gly Phe Gly Lys Glu Leu	
210 215 220	
ttt gag tct gat cta gat cga atc atg gaa cac atc aaa gct gcc atg	780
Phe Glu Ser Asp Leu Asp Arg Ile Met Glu His Ile Lys Ala Ala Met	
225 230 235	
gaa atg gtt cct gtc ttg aaa aag gct gac atc atc aat gtt gtc aat	828
Glu Met Val Pro Val Leu Lys Lys Ala Asp Ile Ile Asn Val Val Asn	
240 245 250	
ggg cct atc acg tat tct cct gac att ctg cct atg gtg ggg ccc cat	876
Gly Pro Ile Thr Tyr Ser Pro Asp Ile Leu Pro Met Val Gly Pro His	
255 260 265	
cag ggg gtc aga aac tac tgg gtg gct ata ggc ttt gga tat ggc ata	924
Gln Gly Val Arg Asn Tyr Trp Val Ala Ile Gly Phe Gly Tyr Gly Ile	
270 275 280 285	
atc cac gct ggt ggg gta ggg aaa tat ctc agt gac tgg atc ctg cat	972
Ile His Ala Gly Gly Val Gly Lys Tyr Leu Ser Asp Trp Ile Leu His	
290 295 300	
gga gaa cct cct ttt gat ctg ata gaa ttg gat cct aat cgc tat ggc	1020
Gly Glu Pro Pro Phe Asp Leu Ile Glu Leu Asp Pro Asn Arg Tyr Gly	
305 310 315	
aaa tgg aca aca acc cag tac act gag gcc aaa gca aga gaa tca tat	1068
Lys Trp Thr Thr Thr Gln Tyr Thr Glu Ala Lys Ala Arg Glu Ser Tyr	
320 325 330	
gga ttc aac aat att gtt ggt tat cct aaa gaa gaa cgg ttt gct ggg	1116
Gly Phe Asn Asn Ile Val Gly Tyr Pro Lys Glu Glu Arg Phe Ala Gly	
335 340 345	
agg ccg act caa cga gtc agt ggg ctc tat caa agg ctg gag tct aag	1164
Arg Pro Thr Gln Arg Val Ser Gly Leu Tyr Gln Arg Leu Glu Ser Lys	
350 355 360 365	
tgt tcc atg ggg ttc cat gct ggc tgg gag cag ccg cac tgg ttc tac	1212
Cys Ser Met Gly Phe His Ala Gly Trp Glu Gln Pro His Trp Phe Tyr	
370 375 380	
aaa cca ggc cag gac act cag tac agg cca agt ttt cgc cac aca aac	1260
Lys Pro Gly Gln Asp Thr Gln Tyr Arg Pro Ser Phe Arg His Thr Asn	
385 390 395	
tgg ttt gag cct gtg ggc tcg gag tat aaa cag gtt atg caa aga gta	1308
Trp Phe Glu Pro Val Gly Ser Glu Tyr Lys Gln Val Met Gln Arg Val	
400 405 410	
ggg gta act gac cta tca cca ttt ggc aag ttt aac atc aaa ggc caa	1356
Gly Val Thr Asp Leu Ser Pro Phe Gly Lys Phe Asn Ile Lys Gly Gln	
415 420 425	

gat tcc att aga cta ctg gac cat ctc ttt gca aat gtc att cca aag Asp Ser Ile Arg Leu Leu Asp His Leu Phe Ala Asn Val Ile Pro Lys 430 435 440 445	1404
gtg ggt ttt aca aat ata agt cac atg tta aca ccc aag ggt cga gtg Val Gly Phe Thr Asn Ile Ser His Met Leu Thr Pro Lys Gly Arg Val 450 455 460	1452
tat gct gag ctg act gtt tct cac caa tct cct ggg gag ttt ctt tta Tyr Ala Glu Leu Thr Val Ser His Gln Ser Pro Gly Glu Phe Leu Leu 465 470 475	1500
att act ggc tct gga tca gaa ctt cat gat ctt aga tgg att gaa gaa Ile Thr Gly Ser Gly Ser Glu Leu His Asp Leu Arg Trp Ile Glu Glu 480 485 490	1548
gaa gca gtc aaa ggt gga tat gat gtt gaa att aaa aac ata act gat Glu Ala Val Lys Gly Gly Tyr Asp Val Glu Ile Lys Asn Ile Thr Asp 495 500 505	1596
gag ctt gga gtt ctt gga gtt gct ggg cca cag gca aga aag gtc ctt Glu Leu Gly Val Leu Gly Val Ala Gly Pro Gln Ala Arg Lys Val Leu 510 515 520 525	1644
cag aaa ctg acc cct gaa gat ctt agt gat gat gtt ttc aag ttt ctt Gln Lys Leu Thr Pro Glu Asp Leu Ser Asp Asp Val Phe Lys Phe Leu 530 535 540	1692
caa acc aag tcc tta aag gtt tcc aac att cct gtc act gct att agg Gln Thr Lys Ser Leu Lys Val Ser Asn Ile Pro Val Thr Ala Ile Arg 545 550 555	1740
ata tct tat act ggt gag ctg ggt tgg gag ctg tat cac aga aga gaa Ile Ser Tyr Thr Gly Glu Leu Gly Trp Glu Leu Tyr His Arg Arg Glu 560 565 570	1788
gat tct gtg gcg ctg tat gac gct atc atg aat gca ggc cag gag gag Asp Ser Val Ala Leu Tyr Asp Ala Ile Met Asn Ala Gly Gln Glu Glu 575 580 585	1836
gga atc gac aat ttt gga acc tat gcc atg aat gcc tta cgc ctg gag Gly Ile Asp Asn Phe Gly Thr Tyr Ala Met Asn Ala Leu Arg Leu Glu 590 595 600 605	1884
aaa gcc ttc aga gcc tgg ggg tta gag atg aac tgt gat aca aat cct Lys Ala Phe Arg Ala Trp Gly Leu Glu Met Asn Cys Asp Thr Asn Pro 610 615 620	1932
ttg gaa gct gga ctg gaa tat ttt gtg aag tta aat aag cca gca gac Leu Glu Ala Gly Leu Glu Tyr Phe Val Lys Leu Asn Lys Pro Ala Asp 625 630 635	1980
ttc ata gga aag caa gca ctg aaa cag att aaa gcc aag ggg ctg aaa Phe Ile Gly Lys Gln Ala Leu Lys Gln Ile Lys Ala Lys Gly Leu Lys 640 645 650	2028
cga aga ctg gtc tgc ctc acc ttg gca acg gat gat gtt gat cca gag	2076

Arg	Arg	Leu	Val	Cys	Leu	Thr	Leu	Ala	Thr	Asp	Asp	Val	Asp	Pro	Glu	
655						660					665					
gga	aat	gaa	agc	atc	tgg	tac	aat	ggc	aag	gtg	gtt	ggc	aac	acg	aca	2124
Gly	Asn	Glu	Ser	Ile	Trp	Tyr	Asn	Gly	Lys	Val	Val	Gly	Asn	Thr	Thr	
670					675					680					685	
tct	gga	agc	tat	agc	tac	agc	atc	cag	aag	agt	ctg	gct	ttc	gca	tat	2172
Ser	Gly	Ser	Tyr	Ser	Tyr	Ser	Ile	Gln	Lys	Ser	Leu	Ala	Phe	Ala	Tyr	
				690					695					700		
gtc	cct	gta	caa	cta	agt	gaa	gtg	gga	cag	caa	gtg	gaa	gtt	gaa	cta	2220
Val	Pro	Val	Gln	Leu	Ser	Glu	Val	Gly	Gln	Gln	Val	Glu	Val	Glu	Leu	
			705					710					715			
tta	ggc	aaa	aat	tac	cca	gca	gtc	atc	ata	caa	gaa	cct	ttg	gta	ttg	2268
Leu	Gly	Lys	Asn	Tyr	Pro	Ala	Val	Ile	Ile	Gln	Glu	Pro	Leu	Val	Leu	
		720					725					730				
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Thr	Glu	Pro	Thr	Arg	Asn	Arg	Leu	Gln	Lys	Lys	Gly	Gly	Lys	Asp	Lys	
		735				740					745					
act	tga	aaaaagac	ctt	tcagcag	tca	actgaattag	agttgctaat	gactgtcctt								2372
Thr	*															
750																
gaaattatta	taactggctc	ccagggggaat	agaggaaacc	aggaattcat	ttcaaaatca											2432
tcaaagtcta	aatttagaat	cttaatgaaa	cctttctggt	aagtgttttc	taagcaagac											2492
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cattggatgt	ccagaatccc	ctgtagttga	taatgttggg	aataagctct	gcaactttct	540
ttggcattca	gttgttaaaa	acaaatagga	tgcaaattcc	tcaactccag	gttatgaaaa	600
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			Met Ile Val Phe Gly Trp Ala Val			
			1	5		
ttc tta gcg agc aga agc ctt ggc cag ggt ctg ttg ttg act ctc gaa						701
Phe Leu Ala Ser Arg Ser Leu Gly Gln Gly Leu Leu Leu Thr Leu Glu						
10			15		20	
gag cac ata gcc cac ttc cta ggg act gga ggt gcc gct act acc atg						749
Glu His Ile Ala His Phe Leu Gly Thr Gly Gly Ala Ala Thr Thr Met						
25		30		35	40	
ggt aat tcc tgt atc tgc cga gat gac agt gga aca gat gac agt gtt						797
Gly Asn Ser Cys Ile Cys Arg Asp Asp Ser Gly Thr Asp Asp Ser Val						
		45		50	55	
gac acc caa cag caa cag gcc gag aac agt gca gta ccc act gct gac						845
Asp Thr Gln Gln Gln Gln Ala Glu Asn Ser Ala Val Pro Thr Ala Asp						
		60		65	70	
aca agg agc caa cca cgg gac cct gtt cgg cca cca agg agg ggc cga						893
Thr Arg Ser Gln Pro Arg Asp Pro Val Arg Pro Pro Arg Arg Gly Arg						
		75		80	85	
gga cct cat gag cca agg aga aag aaa caa aat gtg gat ggg cta gtg						941
Gly Pro His Glu Pro Arg Arg Lys Lys Gln Asn Val Asp Gly Leu Val						
	90		95		100	
ttg gac aca ctg gca gta ata cgg act ctt gta gat aat gat cag gaa						989
Leu Asp Thr Leu Ala Val Ile Arg Thr Leu Val Asp Asn Asp Gln Glu						
105		110		115	120	
cct ccc tat tca atg ata aca tta cac gaa atg gca gaa aca gat gaa						1037
Pro Pro Tyr Ser Met Ile Thr Leu His Glu Met Ala Glu Thr Asp Glu						
		125		130	135	
gga tgg ttg gat gtt gtc cag tct tta att aga gtt att cca ctg gaa						1085
Gly Trp Leu Asp Val Val Gln Ser Leu Ile Arg Val Ile Pro Leu Glu						

140	145	150	
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ttg ccc act aaa gat gca ctc cag aaa ttg act gaa att ctc aat tta Leu Pro Thr Lys Asp Ala Leu Gln Lys Leu Thr Glu Ile Leu Asn Leu 170 175 180			1181
aat gga gaa gta gct tgc cag gac tca agc cat cct gcc aaa cac agg Asn Gly Glu Val Ala Cys Gln Asp Ser Ser His Pro Ala Lys His Arg 185 190 195 200			1229
aac aca tct gca gtc cta ggc tgc ttg gcc gag aaa cta gca ggt cct Asn Thr Ser Ala Val Leu Gly Cys Leu Ala Glu Lys Leu Ala Gly Pro 205 210 215			1277
gca agt ata ggt tta ctt agc cca gga ata ctg gaa tac ttg cta cag Ala Ser Ile Gly Leu Leu Ser Pro Gly Ile Leu Glu Tyr Leu Leu Gln 220 225 230			1325
tgt ctg aag tta cag tcc cac ccc aca gtc atg ctt ttt gca ctt atc Cys Leu Lys Leu Gln Ser His Pro Thr Val Met Leu Phe Ala Leu Ile 235 240 245			1373
gca ctg gaa aag ttt gca cag aca agt gaa aat aaa ttg act att tct Ala Leu Glu Lys Phe Ala Gln Thr Ser Glu Asn Lys Leu Thr Ile Ser 250 255 260			1421
gaa tcc agt att agt gac cgg ctt gtc aca ttg gag tcc tgg gct aat Glu Ser Ser Ile Ser Asp Arg Leu Val Thr Leu Glu Ser Trp Ala Asn 265 270 275 280			1469
gat cct gat tat ctg aaa cgt caa gtt ggt ttc tgt gcc cag tgg agc Asp Pro Asp Tyr Leu Lys Arg Gln Val Gly Phe Cys Ala Gln Trp Ser 285 290 295			1517
tta gac aat ctc ttt tta aaa gaa ggt aga cag ctg acc tat gag aaa Leu Asp Asn Leu Phe Leu Lys Glu Gly Arg Gln Leu Thr Tyr Glu Lys 300 305 310			1565
gtg aac ttg agt agc att agg gcc atg ctg aat agc aat gat gtc agc Val Asn Leu Ser Ser Ile Arg Ala Met Leu Asn Ser Asn Asp Val Ser 315 320 325			1613
gag tac ctg aag atc tca cct cat ggc tta gag gct cgc tgt gat gcc Glu Tyr Leu Lys Ile Ser Pro His Gly Leu Glu Ala Arg Cys Asp Ala 330 335 340			1661
tcc tct ttt gaa agt gtg cgt tgc acc ttt tgt gtg gat gcc ggg gta Ser Ser Phe Glu Ser Val Arg Cys Thr Phe Cys Val Asp Ala Gly Val 345 350 355 360			1709
tgg tac tat gaa gta aca gtg gtc act tct ggc gtc atg cag att ggc Trp Tyr Tyr Glu Val Thr Val Val Thr Ser Gly Val Met Gln Ile Gly 365 370 375			1757

tgg gcc act cga gac agc aaa ttc ctc aat cat gaa ggc tac ggc att Trp Ala Thr Arg Asp Ser Lys Phe Leu Asn His Glu Gly Tyr Gly Ile 380 385 390	1805
ggg gat gat gaa tac tcc tgt gcg tat gat ggc tgc cgg cag ctg att Gly Asp Asp Glu Tyr Ser Cys Ala Tyr Asp Gly Cys Arg Gln Leu Ile 395 400 405	1853
tgg tac aat gcc aga agt aag cct cac ata cac cca tgc tgg aaa gaa Trp Tyr Asn Ala Arg Ser Lys Pro His Ile His Pro Cys Trp Lys Glu 410 415 420	1901
gga gat aca gta gga ttt ctg tta gac ttg aat gaa aag caa atg atc Gly Asp Thr Val Gly Phe Leu Leu Asp Leu Asn Glu Lys Gln Met Ile 425 430 435 440	1949
ttc ttt tta aat ggc aac cag ctg cct cct gaa aag caa gtc ttt tca Phe Phe Leu Asn Gly Asn Gln Leu Pro Pro Glu Lys Gln Val Phe Ser 445 450 455	1997
tct act gta tct gga ttt ttt gct gca gct agt ttc atg tca tat caa Ser Thr Val Ser Gly Phe Phe Ala Ala Ser Phe Met Ser Tyr Gln 460 465 470	2045
caa tgt gag ttc aat ttt gga gca aaa cca ttc aaa tac cca cca tct Gln Cys Glu Phe Asn Phe Gly Ala Lys Pro Phe Lys Tyr Pro Pro Ser 475 480 485	2093
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aaa atc att ttg cca agg cac agg cgt ctt gct ctg ttg aag caa gtc Lys Ile Ile Leu Pro Arg His Arg Arg Leu Ala Leu Leu Lys Gln Val 505 510 515 520	2189
agt atc cga gaa aac tgc tgt tcc ctt tgt tgt gat gag gta gca gac Ser Ile Arg Glu Asn Cys Cys Ser Leu Cys Cys Asp Glu Val Ala Asp 525 530 535	2237
aca caa ttg aag cca tgt gga cac agt gac ctg tgc atg gat tgt gcc Thr Gln Leu Lys Pro Cys Gly His Ser Asp Leu Cys Met Asp Cys Ala 540 545 550	2285
ttg cag ctg gag acc tgc cca ttg tgt cgt aaa gaa ata gta tct aga Leu Gln Leu Glu Thr Cys Pro Leu Cys Arg Lys Glu Ile Val Ser Arg 555 560 565	2333
atc aga cag att tct cat att tca tga cacat gtgaagaggc atcgtggact Ile Arg Gln Ile Ser His Ile Ser *	2385
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 <222> (14)..(475)

<400> 26

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                   1             5             10

tcg gac cct gag cag gag acg cga acc aac atg ctg ctg gag ctc gca   97
Ser Asp Pro Glu Gln Glu Thr Arg Thr Asn Met Leu Leu Glu Leu Ala
      15             20             25

agg tca ctt ttc aat agg atg gac ttt gaa gac ttg ggg ttg gta gta   145
Arg Ser Leu Phe Asn Arg Met Asp Phe Glu Asp Leu Gly Leu Val Val
      30             35             40

gat tgg gac cac cac ctg cct cca cca gct gcc aag act gtg gtt gag   193
Asp Trp Asp His His Leu Pro Pro Pro Ala Ala Lys Thr Val Val Glu
      45             50             55             60

aac ctc ccc agg aca gtc atc aga ggc tct cag gct gag ctc aag tgc   241
Asn Leu Pro Arg Thr Val Ile Arg Gly Ser Gln Ala Glu Leu Lys Cys
      65             70             75

ccc gtg tgt ctt ttg gaa ttt gag gag gag gag act gcc att gag atg   289
Pro Val Cys Leu Leu Glu Phe Glu Glu Glu Glu Thr Ala Ile Glu Met
      80             85             90

cct tgc cat cac ctt ttc cat tcc agc tgc att ctg ccc tgg cta agc   337
Pro Cys His His Leu Phe His Ser Ser Cys Ile Leu Pro Trp Leu Ser
      95             100            105

aag aca aat tcc tgt ccc ttg tgc cgc cat gag ctg ccc act gat gac   385
Lys Thr Asn Ser Cys Pro Leu Cys Arg His Glu Leu Pro Thr Asp Asp
     110             115             120

gac act tat gag gag cac aga cga gat aag gct cga aaa cag cag cag   433
Asp Thr Tyr Glu Glu His Arg Arg Asp Lys Ala Arg Lys Gln Gln Gln
     125             130             135             140

caa cac cga ctg gag aac ctc cat gga gcc atg tac acg tga ggaggtt   482
Gln His Arg Leu Glu Asn Leu His Gly Ala Met Tyr Thr  *
     145             150

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ctttaccac aaaaaaaaaa aa   564

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Pro Ser Asp Pro Glu Gln Glu Thr Arg Thr Asn Met Leu Leu Glu Leu		
	15 20 25	
gca agg tca ctt ttc aat agg atg gac ttt gaa gac ttg ggg ttg gta		146
Ala Arg Ser Leu Phe Asn Arg Met Asp Phe Glu Asp Leu Gly Leu Val		
	30 35 40	
gta gat tgg gac cac cac ctg cct cca cca gct gcc aag act gtg gtt		194
Val Asp Trp Asp His His Leu Pro Pro Pro Ala Ala Lys Thr Val Val		
	45 50 55	
gag aac ctc ccc agg aca gtc atc aga ggc tct cag gct gct ctc acc		242
Glu Asn Leu Pro Arg Thr Val Ile Arg Gly Ser Gln Ala Ala Leu Thr		
	60 65 70 75	
gtg ccc tgg gcc cag tac tca agc ttc ttt ctg ttc atg gac tgc tgg		290
Val Pro Trp Ala Gln Tyr Ser Ser Phe Phe Leu Phe Met Asp Cys Trp		
	80 85 90	
ggg atg gaa gaa gag tgg cag ttg gga gca ggg gag ggt ggt tat cag		338
Gly Met Glu Glu Glu Trp Gln Leu Gly Ala Gly Glu Gly Gly Tyr Gln		
	95 100 105	
ctt atg aag atc aga cca agg cta gaa cac tac tct act ttt ctc aga		386
Leu Met Lys Ile Arg Pro Arg Leu Glu His Tyr Ser Thr Phe Leu Arg		
	110 115 120	
caa att cct gtc cct tgt gcc gct atg agc tgc cca ctg atg acg aca		434
Gln Ile Pro Val Pro Cys Ala Ala Met Ser Cys Pro Leu Met Thr Thr		
	125 130 135	
ctt atg agg agc aca gac gag ata agg ctc gaa aac agc agc agc aac		482
Leu Met Arg Ser Thr Asp Glu Ile Arg Leu Glu Asn Ser Ser Ser Asn		
	140 145 150 155	
acc gac tgg aga acc tcc atg gag cca tgt aca cgt gag gag gtt ggg		530
Thr Asp Trp Arg Thr Ser Met Glu Pro Cys Thr Arg Glu Glu Val Gly		
	160 165 170	
gct gag tgc tgg ccc tct gcg tct tcc tta tta acc ttg aat cct cat		578
Ala Glu Cys Trp Pro Ser Ala Ser Ser Leu Leu Thr Leu Asn Pro His		

175

180

185

taa aggtttcttt acccacaataa aaaaaaaaa

609

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<210> 28

<211> 1291

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	1 5	

cgc tcc cgc gcg ggt ctc cgg gcc ctg ttc cgt agc cgc gat gct gcg	100
Arg Ser Arg Ala Gly Leu Arg Ala Leu Phe Arg Ser Arg Asp Ala Ala	
10 15 20 25	

cta ttt cca ggc tgc gag cgg gga ctt cac tgc tct gct gtc tcc tgc	148
Leu Phe Pro Gly Cys Glu Arg Gly Leu His Cys Ser Ala Val Ser Cys	
30 35 40	

aag aac tgg ctc aag aaa ttt gcc tcg aaa acc aaa aaa aag gtt tgg	196
Lys Asn Trp Leu Lys Lys Phe Ala Ser Lys Thr Lys Lys Lys Val Trp	
45 50 55	

tat gaa agt cct tcc ttg ggt tct cac tcg act tac aaa cca tcc aag	244
Tyr Glu Ser Pro Ser Leu Gly Ser His Ser Thr Tyr Lys Pro Ser Lys	
60 65 70	

ttg gaa ttc ctc atg agg agc acc tca aag aaa acc agg aag gaa gac	292
Leu Glu Phe Leu Met Arg Ser Thr Ser Lys Lys Thr Arg Lys Glu Asp	
75 80 85	

cat gcg cgc ctg agg gcc ctg aac ggc ctc ctc tat aag gca ctg aca	340
His Ala Arg Leu Arg Ala Leu Asn Gly Leu Leu Tyr Lys Ala Leu Thr	
90 95 100 105	

gac ctg ctg tgt acc cct gaa gtg agt cag gag ctg tat gac ctt aac	388
Asp Leu Leu Cys Thr Pro Glu Val Ser Gln Glu Leu Tyr Asp Leu Asn	
110 115 120	

gtg gag ctc tcc aag gtt tcc ctg act cca gac ttc tca gcc tgc cga	436
Val Glu Leu Ser Lys Val Ser Leu Thr Pro Asp Phe Ser Ala Cys Arg	
125 130 135	

gcg tac tgg aag aca acg ctc tct gct gag cag aac gca cac atg gag	484
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Ala Tyr Trp Lys Thr Thr Leu Ser Ala Glu Gln Asn Ala His Met Glu	
140 145 150	
gct gtc ctg cag aga agt gcc gcg cac atg agg cac ctt ttg atg tcc	532
Ala Val Leu Gln Arg Ser Ala Ala His Met Arg His Leu Leu Met Ser	
155 160 165	
cag cag acc ctg agg aat gtg cca ccg ata gtg ttt gtt caa gac aag	580
Gln Gln Thr Leu Arg Asn Val Pro Pro Ile Val Phe Val Gln Asp Lys	
170 175 180 185	
gga aat gca gct cta gct gag ctt gat cag tta ctg gca gtc gca gac	628
Gly Asn Ala Ala Leu Ala Glu Leu Asp Gln Leu Leu Ala Val Ala Asp	
190 195 200	
ttt gga ccc cgg gat gaa aga gac aac ttt gta caa aat gat ttc agg	676
Phe Gly Pro Arg Asp Glu Arg Asp Asn Phe Val Gln Asn Asp Phe Arg	
205 210 215	
gac cct gat gcc cca caa ccc tgc ggc acc aca gag ccg acc aca agc	724
Asp Pro Asp Ala Pro Gln Pro Cys Gly Thr Thr Glu Pro Thr Thr Ser	
220 225 230	
tcc agt ctg tgt ggg atc gat cat gag gcg ctc cac aag cag att atg	772
Ser Ser Leu Cys Gly Ile Asp His Glu Ala Leu His Lys Gln Ile Met	
235 240 245	
gag tac aaa agg agg aaa gat aaa ggg ctc ggg ggc ctg gtg tgg cag	820
Glu Tyr Lys Arg Arg Lys Asp Lys Gly Leu Gly Gly Leu Val Trp Gln	
250 255 260 265	
ggg cag gtg gct gag ctg aca acg cag atg aaa aag gga agg aag agg	868
Gly Gln Val Ala Glu Leu Thr Thr Gln Met Lys Lys Gly Arg Lys Arg	
270 275 280	
gcc aag ccc cgc ctg gag cag gac agc tcc ctc aag agt tac ctg tca	916
Ala Lys Pro Arg Leu Glu Gln Asp Ser Ser Leu Lys Ser Tyr Leu Ser	
285 290 295	
ggc gag gag gtt gaa gat gac ctg gac ctg gtt ggt gcc ccg gag tac	964
Gly Glu Glu Val Glu Asp Asp Leu Asp Leu Val Gly Ala Pro Glu Tyr	
300 305 310	
gaa tgc tat gcc ccg gac aca gag gag ttg gag gca gag aga gga ggt	1012
Glu Cys Tyr Ala Pro Asp Thr Glu Glu Leu Glu Ala Glu Arg Gly Gly	
315 320 325	
ggc aga aca gag gat ggc cac agc tgc gga gca agc agg gag tag atg	1060
Gly Arg Thr Glu Asp Gly His Ser Cys Gly Ala Ser Arg Glu *	
330 335 340	
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gcttcattga ggcagttgat ggagttaaac catctgctct tctgctactt caacattttc 1180	
tagcttttcc gtgtatctaa acacaatttg ctacacaagt cactgttttt ttttccatgc 1240	

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1291

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<211> 766
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Met Ser Glu Lys
1

gag aac aac ttc ccg cca ctg ccc aag ttc atc cct gtg aag ccc tgc 162
Glu Asn Asn Phe Pro Pro Leu Pro Lys Phe Ile Pro Val Lys Pro Cys
5 10 15 20

ttc tac cag aac ttc tcc gac gag atc cca gtg gag cac cag gtc ctg 210
Phe Tyr Gln Asn Phe Ser Asp Glu Ile Pro Val Glu His Gln Val Leu
25 30 35

gtg aag agg atc tac ccg ctg tgg atg ttt tac tgc gcc acc ctc ggc 258
Val Lys Arg Ile Tyr Arg Leu Trp Met Phe Tyr Cys Ala Thr Leu Gly
40 45 50

gtc aac ctc att gcc tgc ctg gcc tgg tgg atc ggc gga ggc tcg ggg 306
Val Asn Leu Ile Ala Cys Leu Ala Trp Trp Ile Gly Gly Gly Ser Gly
55 60 65

acc aac ttc ggc ctg gcc ttc gtg tgg ctg ctc ctg ttc acg cct tgc 354
Thr Asn Phe Gly Leu Ala Phe Val Trp Leu Leu Phe Thr Pro Cys
70 75 80

ggc tac gtg tgc tgg ttc ccg cct gtc tac aag gcc ttc cga gcc gac 402
Gly Tyr Val Cys Trp Phe Arg Pro Val Tyr Lys Ala Phe Arg Ala Asp
85 90 95 100

agc tcc ttt aat ttc atg gcg ttt ttc ttc atc ttc gga gcc cag ttt 450
Ser Ser Phe Asn Phe Met Ala Phe Phe Phe Ile Phe Gly Ala Gln Phe
105 110 115

gtc ctg acc gtc atc cag gcg att ggc ttc tcc ggc tgg ggc gcg tgc 498
Val Leu Thr Val Ile Gln Ala Ile Gly Phe Ser Gly Trp Gly Ala Cys
120 125 130

ggc tgg ctg tcg gca att gga ttc ttc cag tac agc ccg ggc gct gcc 546
Gly Trp Leu Ser Ala Ile Gly Phe Phe Gln Tyr Ser Pro Gly Ala Ala
135 140 145

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gtg gtc atg ctg ctt cca gcc atc atg ttc tcc gtg tcg gct gcc atg      594
Val Val Met Leu Leu Pro Ala Ile Met Phe Ser Val Ser Ala Ala Met
      150                      155                      160

atg gcc atc gcg atc atg aag gtg cac agg atc tac cga ggg ggc tgg      642
Met Ala Ile Ala Ile Met Lys Val His Arg Ile Tyr Arg Gly Gly Trp
      165                      170                      175                      180

cgg aag ctt cca gaa ggc cag acg gag tgg cac acg ggc ctt ggc gga      690
Arg Lys Leu Pro Glu Gly Gln Thr Glu Trp His Thr Gly Leu Gly Gly
      185                      190                      195

acc ccc cgc gac ggg ggc ccc gtc aac atc ttt cgg cga agc ttg ccc      738
Thr Pro Arg Asp Gly Gly Pro Val Asn Ile Phe Arg Arg Ser Leu Pro
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gaggtacggc ctgtggtc  atg gcg ctg ttc cca gcc ttt gcg ggg ctt agt      171
                    Met Ala Leu Phe Pro Ala Phe Ala Gly Leu Ser
                      1                      5                      10

gag gct ccc gat ggc ggg agc tcc agg aaa gag tta gac tgg ctg agc      219
Glu Ala Pro Asp Gly Gly Ser Ser Arg Lys Glu Leu Asp Trp Leu Ser
      15                      20                      25

aac cca agc ttt tgt gtt gga tcc ata acg tcc ctg agc caa caa act      267
Asn Pro Ser Phe Cys Val Gly Ser Ile Thr Ser Leu Ser Gln Gln Thr
      30                      35                      40

gaa gca gct cca gcc cat gtt tct gaa ggg tta ccg ctg aca agg agt      315
Glu Ala Ala Pro Ala His Val Ser Glu Gly Leu Pro Leu Thr Arg Ser
      45                      50                      55

cat ctg aaa tca gag tct tca gat gaa agt gac act aac aaa aag ctc      363
His Leu Lys Ser Glu Ser Ser Asp Glu Ser Asp Thr Asn Lys Lys Leu
      60                      65                      70                      75

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aaa caa aca agt aga aaa aag aag aaa gag aaa aag aaa aaa agg aag	411
Lys Gln Thr Ser Arg Lys Lys Lys Lys Glu Lys Lys Lys Lys Arg Lys	
80 85 90	
cat cag cat cat aag aaa aca aag agg aag cat ggg ccg tcg agt agc	459
His Gln His His Lys Lys Thr Lys Arg Lys His Gly Pro Ser Ser Ser	
95 100 105	
agc agg tct gag aca gac acc gat tct gaa aag gac aaa cct tcc aga	507
Ser Arg Ser Glu Thr Asp Thr Asp Ser Glu Lys Asp Lys Pro Ser Arg	
110 115 120	
ggc gtt gga ggc agt aaa aag gaa tct gag gaa ccg aat caa gga aat	555
Gly Val Gly Gly Ser Lys Lys Glu Ser Glu Glu Pro Asn Gln Gly Asn	
125 130 135	
aat gct gca gct gat act gga cat cgc ttt gtt tgg ctt gag gac att	603
Asn Ala Ala Ala Asp Thr Gly His Arg Phe Val Trp Leu Glu Asp Ile	
140 145 150 155	
cag gct gtg acg gga gaa acc ttc aga aca gat aag aaa cca gat cct	651
Gln Ala Val Thr Gly Glu Thr Phe Arg Thr Asp Lys Lys Pro Asp Pro	
160 165 170	
gcg aac tgg gag tac aag tct ctc tac cga ggg gat ata gca aga tac	699
Ala Asn Trp Glu Tyr Lys Ser Leu Tyr Arg Gly Asp Ile Ala Arg Tyr	
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Lys Arg Lys Gly Asp Ser Cys Leu Gly Ile Asn Pro Lys Lys Gln Cys	
190 195 200	
ata tct tgg gaa ggg act tcc aca gag aag aag cat tca cgc aag cag	795
Ile Ser Trp Glu Gly Thr Ser Thr Glu Lys Lys His Ser Arg Lys Gln	
205 210 215	
gtt gaa cgc tat ttt act aag aag agt gtg gga tta atg aac atc gat	843
Val Glu Arg Tyr Phe Thr Lys Lys Ser Val Gly Leu Met Asn Ile Asp	
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gga gtt gcc att agc agt aaa act gaa cct ccc tca tct gag ccc atc	891
Gly Val Ala Ile Ser Ser Lys Thr Glu Pro Pro Ser Ser Glu Pro Ile	
240 245 250	
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Ser Phe Ile Pro Val Lys Asp Leu Glu Asp Ala Ala Pro Val Thr Thr	
255 260 265	
tgg ttg aat cct ctg ggg att tat gat cag tca acc aca cat tgg cta	987
Trp Leu Asn Pro Leu Gly Ile Tyr Asp Gln Ser Thr Thr His Trp Leu	
270 275 280	
caa gga cag ggt cct cca gag cag gaa tca aag cag cca gac gca cag	1035
Gln Gly Gln Gly Pro Pro Glu Gln Glu Ser Lys Gln Pro Asp Ala Gln	
285 290 295	

Asp	Ser	Gly	Glu	Pro	Arg	Ala	Gly	Glu	Lys	Gly	Ala	Arg	Gly	Trp	Lys		
525						530					535						
gcg	tgg	atg	cac	cag	cag	gaa	cga	ggt	ggc	tgg	gtg	gtc	atc	aac	cca	1803	
Ala	Trp	Met	His	Gln	Gln	Glu	Arg	Gly	Gly	Trp	Val	Val	Ile	Asn	Pro		
540					545					550					555		
gat	gag	gat	gac	gat	gaa	cca	gaa	gag	gat	gac	cag	gaa	ata	aaa	gat	1851	
Asp	Glu	Asp	Asp	Asp	Glu	Pro	Glu	Glu	Asp	Asp	Gln	Glu	Ile	Lys	Asp		
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aag	act	ctg	ccc	agg	tgg	cag	atc	tgg	ctt	gct	gct	gag	cgt	tcc	cgt	1899	
Lys	Thr	Leu	Pro	Arg	Trp	Gln	Ile	Trp	Leu	Ala	Ala	Glu	Arg	Ser	Arg		
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gac	cag	agg	cac	tgg	cgg	ccc	tgg	cgc	cct	gat	aag	acc	aag	aag	caa	1947	
Asp	Gln	Arg	His	Trp	Arg	Pro	Trp	Arg	Pro	Asp	Lys	Thr	Lys	Lys	Gln		
			590				595					600					
acc	gag	gaa	gac	tgt	gag	gat	ccc	gag	aga	cag	ggg	gtg	ttt	gat	gat	1995	
Thr	Glu	Glu	Asp	Cys	Glu	Asp	Pro	Glu	Arg	Gln	Gly	Val	Phe	Asp	Asp		
			605				610					615					
att	ggg	caa	tct	ttg	atc	aga	ctt	tcc	agc	cat	gat	ctt	cag	ttc	cag	2043	
Ile	Gly	Gln	Ser	Leu	Ile	Arg	Leu	Ser	Ser	His	Asp	Leu	Gln	Phe	Gln		
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ctg	gtg	gag	gcc	ttc	ctg	cag	ttc	ttg	ggt	gtg	cct	tct	ggc	ttt	act	2091	
Leu	Val	Glu	Ala	Phe	Leu	Gln	Phe	Leu	Gly	Val	Pro	Ser	Gly	Phe	Thr		
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cct	cca	gcc	tcc	tgt	ctt	tat	ctg	gcc	atg	gat	gag	aac	agc	atc	ttt	2139	
Pro	Pro	Ala	Ser	Cys	Leu	Tyr	Leu	Ala	Met	Asp	Glu	Asn	Ser	Ile	Phe		
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gat	aat	gga	ctt	tat	gat	gaa	aag	ccc	ttg	act	ttt	ttc	aac	cct	ttg	2187	
Asp	Asn	Gly	Leu	Tyr	Asp	Glu	Lys	Pro	Leu	Thr	Phe	Phe	Asn	Pro	Leu		
			670				675					680					
ttt	tct	ggg	gct	agc	tgt	gtt	ggc	cgc	atg	gat	agg	ttg	ggc	tat	cct	2235	
Phe	Ser	Gly	Ala	Ser	Cys	Val	Gly	Arg	Met	Asp	Arg	Leu	Gly	Tyr	Pro		
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cgc	tgg	acc	agg	ggt	cag	aac	cga	gag	ggc	gag	gag	ttc	atc	cgc	aat	2283	
Arg	Trp	Thr	Arg	Gly	Gln	Asn	Arg	Glu	Gly	Glu	Glu	Phe	Ile	Arg	Asn		
					705				710						715		
gtc	ttc	cac	ctt	gtc	atg	cct	tta	ttt	tca	ggc	aaa	gag	aag	tcc	cag	2331	
Val	Phe	His	Leu	Val	Met	Pro	Leu	Phe	Ser	Gly	Lys	Glu	Lys	Ser	Gln		
				720					725					730			
ctc	tgc	ttc	tcc	tgg	tta	cag	tat	gag	att	gca	aag	gtc	att	tgg	tgc	2379	
Leu	Cys	Phe	Ser	Trp	Leu	Gln	Tyr	Glu	Ile	Ala	Lys	Val	Ile	Trp	Cys		
				735				740					745				
ctg	cac	act	aaa	aac	aag	aag	aga	tta	aag	tct	caa	ggg	aag	aac	tgc	2427	
Leu	His	Thr	Lys	Asn	Lys	Lys	Arg	Leu	Lys	Ser	Gln	Gly	Lys	Asn	Cys		

750	755	760	
aaa aaa cta gcc aag aat ctc ctt aag gag cca gaa aac tgc aac aac			2475
Lys Lys Leu Ala Lys Asn Leu Leu Lys Glu Pro Glu Asn Cys Asn Asn			
765	770	775	
ttt tgc ctg tgg aag cag tat gca cat ctg gag tgg ttg ctt ggc aac			2523
Phe Cys Leu Trp Lys Gln Tyr Ala His Leu Glu Trp Leu Leu Gly Asn			
780	785	790	795
acg gag gat gcc aga aaa gtt ttt gac aca gca ctt ggc atg gca gga			2571
Thr Glu Asp Ala Arg Lys Val Phe Asp Thr Ala Leu Gly Met Ala Gly			
	800	805	810
agc aga gaa ctg aaa gac tct gac ctc tgt gag ctc agt ctg ctc tat			2619
Ser Arg Glu Leu Lys Asp Ser Asp Leu Cys Glu Leu Ser Leu Leu Tyr			
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gct gag ctg gag gtg gag ctg tcg cca gaa gtg aga agg gct gcc aca			2667
Ala Glu Leu Glu Val Glu Leu Ser Pro Glu Val Arg Arg Ala Ala Thr			
	830	835	840
gct cga gct gtt cac ata tta acc aag ctg act gag agc agc ccc tat			2715
Ala Arg Ala Val His Ile Leu Thr Lys Leu Thr Glu Ser Ser Pro Tyr			
	845	850	855
ggg ccc tac act gga cag gtg ttg gct gtt cac att ttg aaa gcg cga			2763
Gly Pro Tyr Thr Gly Gln Val Leu Ala Val His Ile Leu Lys Ala Arg			
	860	865	870
aag gct tat gag cac gca ctg cag gac tgt ttg ggt gac agc tgt gtc			2811
Lys Ala Tyr Glu His Ala Leu Gln Asp Cys Leu Gly Asp Ser Cys Val			
	880	885	890
tcc aat cca gct ccc acc gat tcc tgt agc cgc cta att agc ctg gct			2859
Ser Asn Pro Ala Pro Thr Asp Ser Cys Ser Arg Leu Ile Ser Leu Ala			
	895	900	905
aaa tgc ttc atg ctc ttc cag tat ttg acc ata ggg att gat gct gct			2907
Lys Cys Phe Met Leu Phe Gln Tyr Leu Thr Ile Gly Ile Asp Ala Ala			
	910	915	920
gtg cag ata tac gaa cag gtg ttt gca aaa ctg aac agt tct gtt ttc			2955
Val Gln Ile Tyr Glu Gln Val Phe Ala Lys Leu Asn Ser Ser Val Phe			
	925	930	935
cca gaa ggc tct ggc gag ggg gac agt gcc agc tcc cag agt tgg acc			3003
Pro Glu Gly Ser Gly Glu Gly Asp Ser Ala Ser Ser Gln Ser Trp Thr			
	940	945	950
agt gtt ctc gaa gcc atc aca ctg atg cac acg agc ctg ctg aga ttc			3051
Ser Val Leu Glu Ala Ile Thr Leu Met His Thr Ser Leu Leu Arg Phe			
	960	965	970
cac atg aaa gtg agt gtt tac ccg ctg gcc cct ctg cga gag gca ctc			3099
His Met Lys Val Ser Val Tyr Pro Leu Ala Pro Leu Arg Glu Ala Leu			
	975	980	985

tca cag gct tta aag ttg tat cca ggc aac cag gtt ctt tgg agg tcc	3147
Ser Gln Ala Leu Lys Leu Tyr Pro Gly Asn Gln Val Leu Trp Arg Ser	
990 995 1000	
tat gta cag att cag aat aag tcc cac agt gcc agc aaa acc agg aga	3195
Tyr Val Gln Ile Gln Asn Lys Ser His Ser Ala Ser Lys Thr Arg Arg	
1005 1010 1015	
ttt ttt gac aca atc acc agg tct gcc aaa ccc ttg gag cct tgg ttg	3243
Phe Phe Asp Thr Ile Thr Arg Ser Ala Lys Pro Leu Glu Pro Trp Leu	
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ttt gca att gaa gct gag aaa ctg agg aag aga ctg gtg gaa act gtc	3291
Phe Ala Ile Glu Ala Glu Lys Leu Arg Lys Arg Leu Val Glu Thr Val	
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cag agg tta gac ggt aga gag atc cac gcc aca att cct gag acc ggc	3339
Gln Arg Leu Asp Gly Arg Glu Ile His Ala Thr Ile Pro Glu Thr Gly	
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tta atg cat cgg atc caa gcc ctg ttt gaa aat gcc atg cgc agc gac	3387
Leu Met His Arg Ile Gln Ala Leu Phe Glu Asn Ala Met Arg Ser Asp	
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Ser Gly Ser Gln Cys Pro Leu Leu Trp Arg Met Tyr Leu Asn Phe Leu	
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gtt tcc tta gga aat aaa gaa aga agc aaa ggt gta ttc tac aaa gca	3483
Val Ser Leu Gly Asn Lys Glu Arg Ser Lys Gly Val Phe Tyr Lys Ala	
1100 1105 1110 1115	
ctt cag aat tgc cct tgg gca aag gtg ttg tac ctg gac gcc gtg gag	3531
Leu Gln Asn Cys Pro Trp Ala Lys Val Leu Tyr Leu Asp Ala Val Glu	
1120 1125 1130	
tat ttc ccc gat gag atg cag gag atc ctg gac ctg atg act gag aag	3579
Tyr Phe Pro Asp Glu Met Gln Glu Ile Leu Asp Leu Met Thr Glu Lys	
1135 1140 1145	
gag ctc cgg gtg cgc ctg ccg ctg gag gag ctg gag ctg ctg ctg gag	3627
Glu Leu Arg Val Arg Leu Pro Leu Glu Glu Leu Glu Leu Leu Leu Glu	
1150 1155 1160	
gat tag agagcagtgg gaaaacgggc tgtgcctgcg aggccaagtt gccaccctg	3683
Asp *	
1165	
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gcc gcg gcg gcg aat ctg aat gcg gtg cgg gag acc atg gac gtt ctg   97
Ala Ala Ala Ala Asn Leu Asn Ala Val Arg Glu Thr Met Asp Val Leu
                   15                   20                   25

ctt gag att tca aga att ttg aat act ggc tta gat atg gaa act ctg   145
Leu Glu Ile Ser Arg Ile Leu Asn Thr Gly Leu Asp Met Glu Thr Leu
                   30                   35                   40

tct att tgt gta cgg ctt tgt gaa caa gga att aac cca gaa gct tta   193
Ser Ile Cys Val Arg Leu Cys Glu Gln Gly Ile Asn Pro Glu Ala Leu
                   45                   50                   55                   60

tca tcg gtt att aag gag ctt cgc aag gct act gaa gca ctg aag gct   241
Ser Ser Val Ile Lys Glu Leu Arg Lys Ala Thr Glu Ala Leu Lys Ala
                   65                   70                   75

gct gaa aat atg aca agc tga ct ttctggagaa attctgatga gatatgtcaa   294
Ala Glu Asn Met Thr Ser *
                   80

gctctgcaag agggttagaa gattgcattg tagttgagaa tgtacaatga aattactgca   354

tgcagcagtg tagaaaaatt ttacttttta aaagaattat aaaaccatag ctttataaat   414

cagtggaaag tggcttacag agagaactat cagatgtggt tacatcacat cttattcact   474

ttttttaaca gctctaattgc ttgggcattg ctatgttcat atttatgtat tccttattta   534

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ccaggttgaa gtatagtgga acccatcagt agtaatgtgt agtagttatg acttggtgac   654

atttccatta taaactttta ttttgaattg tttatgcatt ataactgtgg atttatattg   714

tattgggctg aaagttgaca ggatttcagc caccacttgt gaatttttat ttagattcat   774

tatgtatatc agaatcttgt tttttgaaat aagagcatgg aaaacatttc ttgtaatcta   834

ctcttgaaca aagaatattt agtttttcaa acagtttggt gggcagctaa tagtgtgaac   894

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atgacaatgc ttaggttagt attatttgta atttgaatca tttacatcta atgagaatgt 1014
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acctcgcgat agctactggc cctgggagcag ccgttgggat tgcgcttgcg cacagcgtgt 180
cttctggatc gccataccta ccctgtggtc ctcatcttcc tggcctcata gctcctctc 240
tccaagc atg tct tcc ccg ttg caa aga gct gtg gga gat acc aag agg 289
Met Ser Ser Pro Leu Gln Arg Ala Val Gly Asp Thr Lys Arg
1 5 10
gcc ttt tct gca tct tct agt tcc tct gcc agt cta ccc ttt gat gac 337
Ala Phe Ser Ala Ser Ser Ser Ser Ser Ala Ser Leu Pro Phe Asp Asp
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agg gac tca aac cat acc tca gag ggg aat ggc gac tct ttg tta gct 385
Arg Asp Ser Asn His Thr Ser Glu Gly Asn Gly Asp Ser Leu Leu Ala
35 40 45
gat gaa gac act gac ttt gaa gac agc ttg aat cgc aat gtg aag aag 433
Asp Glu Asp Thr Asp Phe Glu Asp Ser Leu Asn Arg Asn Val Lys Lys
50 55 60
aga gca gca aaa cga cca ccg aaa aca aca ccg gtg gca aaa cat cca 481
Arg Ala Ala Lys Arg Pro Pro Lys Thr Thr Pro Val Ala Lys His Pro
65 70 75
aag aaa ggg tcc cga gtg gta cat cgt cat agc cgg aaa cag tca gag 529
Lys Lys Gly Ser Arg Val Val His Arg His Ser Arg Lys Lys Ser Glu
80 85 90
cca cca gcc aat gat ctt ttc aat gct gtg aaa gcc gcc aaa agt gac 577
Pro Pro Ala Asn Asp Leu Phe Asn Ala Val Lys Ala Ala Lys Ser Asp
95 100 105 110

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gag atc atc cag cac cta aca gag cag ttt aat gag gac tcg ggg gac Glu Ile Ile Gln His Leu Thr Glu Gln Phe Asn Glu Asp Ser Gly Asp 160 165 170	769
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ctc tca gac tca caa gtc cgc gcc ttc cgt cac act agc acc ctg gct Leu Ser Asp Ser Gln Val Arg Ala Phe Arg His Thr Ser Thr Leu Ala 225 230 235	961
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gtg cac caa gat aac aat cag cgt cag tat gag gct gaa aga aac aag Val His Gln Asp Asn Asn Gln Arg Gln Tyr Glu Ala Glu Arg Asn Lys 255 260 265 270	1057
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cgc aaa gag ctc caa gag cat caa gag gag att gag ggg atg atg aat Arg Lys Glu Leu Gln Glu His Gln Glu Glu Ile Glu Gly Met Met Asn 290 295 300	1153
gcc ctc ttc agg ggt gtc ttt gtt cat cgg tac agg gat gtc ctt cct Ala Leu Phe Arg Gly Val Phe Val His Arg Tyr Arg Asp Val Leu Pro 305 310 315	1201
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tac agc acg tct ttc ctc acc gac agc tat tta aaa tat att ggt tgg	1297

Tyr	Ser	Thr	Ser	Phe	Leu	Thr	Asp	Ser	Tyr	Leu	Lys	Tyr	Ile	Gly	Trp	
335					340					345					350	
act	ctg	cat	gat	aag	cac	cga	gaa	gtc	cgc	gtg	aag	tgc	gtg	aag	gct	1345
Thr	Leu	His	Asp	Lys	His	Arg	Glu	Val	Arg	Val	Lys	Cys	Val	Lys	Ala	
				355					360					365		
ctg	aaa	ggg	ctg	tac	ggg	aac	cgg	gac	ctg	acc	gca	cgc	ctg	gag	ctc	1393
Leu	Lys	Gly	Leu	Tyr	Gly	Asn	Arg	Asp	Leu	Thr	Ala	Arg	Leu	Glu	Leu	
			370					375					380			
ttc	acc	agc	cgc	ttc	aag	gac	cgg	atg	gtt	tcc	atg	atc	atg	gac	aga	1441
Phe	Thr	Ser	Arg	Phe	Lys	Asp	Arg	Met	Val	Ser	Met	Ile	Met	Asp	Arg	
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Glu	Tyr	Ser	Val	Ala	Val	Glu	Ala	Val	Arg	Leu	Leu	Ile	Leu	Ile	Leu	
	400					405				410						
aag	aac	atg	gaa	ggg	ttg	ctg	acg	gac	gcg	gat	tgt	gag	agc	gtc	tac	1537
Lys	Asn	Met	Glu	Gly	Leu	Leu	Thr	Asp	Ala	Asp	Cys	Glu	Ser	Val	Tyr	
415					420				425					430		
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Pro	Val	Val	Tyr	Pro	Ser	Asn	Arg	Gly	Leu	Ala	Ser	Ala	Ala	Gly	Glu	
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ttt	ctg	tac	tgg	aaa	ctt	ttc	tac	cct	gag	tgc	gag	ata	aga	acg	atg	1633
Phe	Leu	Tyr	Trp	Lys	Leu	Phe	Tyr	Pro	Glu	Cys	Glu	Ile	Arg	Thr	Met	
			450					455					460			
ggg	gga	aga	gag	caa	cgc	cag	agc	cca	ggc	gcc	cag	agg	act	ttc	ttc	1681
Gly	Gly	Arg	Glu	Gln	Arg	Gln	Ser	Pro	Gly	Ala	Gln	Arg	Thr	Phe	Phe	
		465				470						475				
cag	ctt	ctg	ctg	tcc	ttc	ttt	gtg	gag	agc	gag	ctc	cat	gac	cac	gct	1729
Gln	Leu	Leu	Leu	Ser	Phe	Phe	Val	Glu	Ser	Glu	Leu	His	Asp	His	Ala	
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Arg	Gln	Ala	Ser	Glu	Gly	His	Pro	Pro	Val	Gly	Arg	Val	Thr	Gly	Arg	
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575	580	585	590
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Phe Ser Ala Asp Ala Glu Lys Val Thr Pro Leu Leu Gln Leu Leu Ser			
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Cys Phe Asp Leu His Ile Tyr Cys Thr Gly Arg Leu Glu Lys His Leu			
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Glu Leu Phe Leu Gln Gln Leu Gln Glu Val Val Val Lys His Ala Glu			
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Pro Glu Phe Thr Phe Phe Ser Arg Ala Asp Phe Ala Arg Ser Gln Leu			
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Val Asp Leu Leu Thr Asp Arg Phe Gln Gln Glu Leu Glu Glu Leu Leu			
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Gln Ser Ser Phe Leu Asp Glu Asp Glu Val Tyr Asn Leu Ala Ala Thr			
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Leu Lys Arg Leu Ser Ala Phe Tyr Asn Thr His Asp Leu Thr Arg Trp			
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Gln Lys Gln Leu Ser Ser Leu Arg Asp Arg Met Val Ala Phe Cys Glu			
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Leu Cys Gln Ser Cys Leu Ser Asp Val Asp Thr Glu Ile Gln Glu Gln			
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10 15 20

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Phe Leu Ala Arg Asp Ala Leu Arg Ser Leu Ala Val Leu Glu Gly Ala
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Ser Leu Val Val Gly Lys Asp Gly Phe Ile Lys Ala Ile Gly Pro Ala
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Asp Val Ile Gln Arg Gln Phe Ser Gly Glu Thr Phe Glu Glu Leu Ile
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Asp Cys Ser Gly Lys Cys Ile Leu Pro Gly Leu Val Asp Ala His Thr
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His Pro Val Trp Ala Gly Glu Arg Val His Glu Phe Ala Met Lys Leu
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Ala Gly Ala Thr Tyr Met Glu Ile His Gln Ala Gly Gly Gly Ile His
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Phe Thr Val Glu Arg Thr Arg Gln Ala Thr Glu Glu Glu Leu Phe Arg
125 130 135

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Lys Thr *	
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ggagaatttg ctaaactcag caaaattgaa ctctcgaag ccaactgaaaa gtcaattggt	240
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Met His Lys Tyr His Cys Glu Leu Lys Asn Leu Arg Glu	
1 5 10	
aaa gaa aaa cag ctc gag acc tca tgc aaa gag aaa act gag tat cta	336
Lys Glu Lys Gln Leu Glu Thr Ser Cys Lys Glu Lys Thr Glu Tyr Leu	
15 20 25	

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 Met Pro His Leu
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 Gly Leu Pro Arg Phe His Ser Val Ser Thr Gln Ser Glu Pro His Gly
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 Ser Pro Ile Ser Arg Arg Asn Arg Glu Ala Lys Gln Lys Arg Leu Arg
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 Glu Lys Gln Ala Thr Leu Glu Ala Glu Ile Ala Gly Glu Ser Lys Ser
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 gaa atc cct acg aaa ccc ggt gaa aag aaa gat gtc tct ggg ccc ctg 402
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 Pro Pro Ala Tyr Ser Pro Arg Tyr Val Glu Ala Ala Trp Tyr Pro Trp
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 Trp Val Arg Glu Gly Phe Phe Lys Pro Glu Tyr Gln Ala Arg Leu Pro
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 Gln Ala Thr Gly Glu Thr Phe Ser Met Cys Ile Pro Pro Pro Asn Val
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 Thr Gly Ser Leu His Ile Gly His Ala Leu Thr Val Ala Ile Gln Asp
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Pro	Met	Val	Leu	Pro	Ile	Cys	Ser	Arg	Ser	Gly	Asp	Val	Ile	Glu	Tyr		
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Lys Phe Val Pro Gln Pro Ala Glu Glu Leu Ser Pro Ser Ser Pro Met	
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855 860 865	
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Gln Leu Glu Leu Ser Lys Leu Asp Lys Ala Ala Ser His Leu Gln Gln
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Thr Ser Asn Asp Thr Thr Val Leu Leu Pro Pro Tyr Asp Asp Ala Thr	
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Asp	His	Leu	Gly	Phe	Gln	Val	Thr	Trp	Pro	Asp	Glu	Ser	Lys	Ala	Gly		
450					455					460					465		
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Gly	Ser	Trp	Asp	Leu	Ala	Val	Gln	Glu	Arg	Ala	Ala	Arg	Ser	Gln	Cys		

gtattttctta aatgtatttg attgatgcct cattcctccc taaaatgtat aaaaccaagc 2886
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 Met Asn His Ile Val Gln Thr Phe Ser Pro Val Asn Ser Gly
 1 5 10
 cag cct ccc aac tac gag atg ctc aag gag gag cag gaa gtg gct atg 157
 Gln Pro Pro Asn Tyr Glu Met Leu Lys Glu Glu Gln Glu Val Ala Met
 15 20 25 30
 ctg ggg gtg ccc cac aac cct gct ccc ccg atg tcc acc gtg atc cac 205
 Leu Gly Val Pro His Asn Pro Ala Pro Pro Met Ser Thr Val Ile His
 35 40 45
 atc cgc agc gag acc tcc gtg cct gac cat gtg gtc tgg tcc ctg ttc 253
 Ile Arg Ser Glu Thr Ser Val Pro Asp His Val Val Trp Ser Leu Phe
 50 55 60
 aac acc ctc ttc atg aac acc tgc tgc ctg ggc ttc ata gca ttc gcg 301
 Asn Thr Leu Phe Met Asn Thr Cys Cys Leu Gly Phe Ile Ala Phe Ala
 65 70 75
 tac tcc gtg aag tct agg gac agg aag atg gtt ggc gac gtg acc ggg 349
 Tyr Ser Val Lys Ser Arg Asp Arg Lys Met Val Gly Asp Val Thr Gly
 80 85 90
 gcc cag gcc tat gcc tcc acc gcc aag tgc ctg aac atc tgg gcc ctg 397
 Ala Gln Ala Tyr Ala Ser Thr Ala Lys Cys Leu Asn Ile Trp Ala Leu
 95 100 105 110
 att ttg ggc atc ttc atg acc att ctg ctc atc atc atc cca gtg ttg 445
 Ile Leu Gly Ile Phe Met Thr Ile Leu Leu Ile Ile Ile Pro Val Leu
 115 120 125
 gtc gtc cag gcc cag cga tag at caggaggcat cattgaggcc aggagctctg 498
 Val Val Gln Ala Gln Arg *
 130

cccgtgagct gtatccacgt actctatctt ccattcttcg cctgccccca gaggccagag 558
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gctgcctcgg cggcccgccc cggtcgcagc cca atg gtg gag gcc ata gtg gag 294
Met Val Glu Ala Ile Val Glu
1 5
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Phe Asp Tyr Gln Ala Gln His Asp Asp Glu Leu Thr Ile Ser Val Gly
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Glu Ile Ile Thr Asn Ile Arg Lys Glu Asp Gly Gly Trp Trp Glu Gly
25 30 35
cag atc aac ggc agg aga ggt ttg ttc cct gac aac ttt gta aga gaa 438
Gln Ile Asn Gly Arg Arg Gly Leu Phe Pro Asp Asn Phe Val Arg Glu
40 45 50 55
ata aag aaa gag atg aag aaa gac cct ctg acc aac aaa gct cca gaa 486
Ile Lys Lys Glu Met Lys Lys Asp Pro Leu Thr Asn Lys Ala Pro Glu
60 65 70
aag ccc ctg cac gaa gtg ccc agt gga aac tct ttg ctg tct tct gaa 534
Lys Pro Leu His Glu Val Pro Ser Gly Asn Ser Leu Leu Ser Ser Glu
75 80 85
acg att tta aga acc aat aag aga ggc gag cga cgg agg cgc cgg tgc 582
Thr Ile Leu Arg Thr Asn Lys Arg Gly Glu Arg Arg Arg Arg Arg Cys
90 95 100
cag gtg gca ttc agc tac ctg ccc cag aat gac gat gaa ctt gag ctg 630

Gln Val Ala Phe Ser Tyr Leu Pro Gln Asn Asp Asp Glu Leu Glu Leu	
105 110 115	
aaa gtt ggc gac atc ata gag gtg gta gga gag gta gag gaa gga tgg	678
Lys Val Gly Asp Ile Ile Glu Val Val Gly Glu Val Glu Glu Gly Trp	
120 125 130 135	
tgg gaa ggt gtt ctc aac ggg aag act gga atg ttt cct tcc aac ttc	726
Trp Glu Gly Val Leu Asn Gly Lys Thr Gly Met Phe Pro Ser Asn Phe	
140 145 150	
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Ile Lys Glu Leu Ser Gly Glu Ser Asp Glu Leu Gly Ile Ser Gln Asp	
155 160 165	
gag cag cta tcc aag tca agt tta agg gaa acc aca ggc tcc gag agt	822
Glu Gln Leu Ser Lys Ser Ser Leu Arg Glu Thr Thr Gly Ser Glu Ser	
170 175 180	
gat ggg ggt gac tca agc agc acc aag tct gaa ggt gcc aac ggg aca	870
Asp Gly Gly Asp Ser Ser Ser Thr Lys Ser Glu Gly Ala Asn Gly Thr	
185 190 195	
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Val Ala Thr Ala Ala Ile Gln Pro Lys Lys Val Lys Gly Val Gly Phe	
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Gly Asp Ile Phe Lys Asp Lys Pro Ile Lys Leu Arg Pro Arg Ser Ile	
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gaa gta gaa aat gac ttt ctg ccg gta gaa aag act att ggg aag aag	1014
Glu Val Glu Asn Asp Phe Leu Pro Val Glu Lys Thr Ile Gly Lys Lys	
235 240 245	
tta cct gca act aca gca act cca gac tca tca aaa aca gaa atg gac	1062
Leu Pro Ala Thr Thr Ala Thr Pro Asp Ser Ser Lys Thr Glu Met Asp	
250 255 260	
agc agg aca aag agc aag gat tac tgc aaa gta ata ttt cca tat gag	1110
Ser Arg Thr Lys Ser Lys Asp Tyr Cys Lys Val Ile Phe Pro Tyr Glu	
265 270 275	
gca cag aat gat gat gaa ttg aca atc aaa gaa gga gat ata gtc act	1158
Ala Gln Asn Asp Asp Glu Leu Thr Ile Lys Glu Gly Asp Ile Val Thr	
280 285 290 295	
ctc atc aat aag gac tgc atc gac gta ggc tgg tgg gaa gga gag ctg	1206
Leu Ile Asn Lys Asp Cys Ile Asp Val Gly Trp Trp Glu Gly Glu Leu	
300 305 310	
aac ggc aga cga ggc gtg ttc ccc gat aac ttc gtg aag tta ctt cca	1254
Asn Gly Arg Arg Gly Val Phe Pro Asp Asn Phe Val Lys Leu Leu Pro	
315 320 325	
ccg gac ttt gaa aag gaa ggg aat aga ccc aag aag cca ccg cct cca	1302
Pro Asp Phe Glu Lys Glu Gly Asn Arg Pro Lys Lys Pro Pro Pro Pro	

330	335	340	
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aag ccc tcc gtt cct gcc ata ccg cca aaa aag cct cgg cca cct aag Lys Pro Ser Val Pro Ala Ile Pro Pro Lys Lys Pro Arg Pro Pro Lys 395 400 405			1494
acc aat tct ctc agc aga cct ggc gca ctg ccc ccg aga agg ccg gag Thr Asn Ser Leu Ser Arg Pro Gly Ala Leu Pro Pro Arg Arg Pro Glu 410 415 420			1542
aga ccg gtg ggt ccg ctg aca cac acc agg ggt gac agt cca aag att Arg Pro Val Gly Pro Leu Thr His Thr Arg Gly Asp Ser Pro Lys Ile 425 430 435			1590
gac ttg gcc ggc agt tcg cta tct ggc atc ctg gac aaa gat ctc tcg Asp Leu Ala Gly Ser Ser Leu Ser Gly Ile Leu Asp Lys Asp Leu Ser 440 445 450 455			1638
gac cgc agc aat gac att gac tta gaa ggt ttt gac tcc gtg gta tca Asp Arg Ser Asn Asp Ile Asp Leu Glu Gly Phe Asp Ser Val Val Ser 460 465 470			1686
tct act gag aaa ctc agt cat ccg acc aca agc aga cca aaa gct aca Ser Thr Glu Lys Leu Ser His Pro Thr Thr Ser Arg Pro Lys Ala Thr 475 480 485			1734
ggg agg cgg cct ccg tcc cag tcc ctc aca tct tca tcc ctt tca agc Gly Arg Arg Pro Pro Ser Gln Ser Leu Thr Ser Ser Ser Leu Ser Ser 490 495 500			1782
cct gat atc ttc gac tcc cca agt ccc gaa gag gat aag gag gaa cac Pro Asp Ile Phe Asp Ser Pro Ser Pro Glu Glu Asp Lys Glu Glu His 505 510 515			1830
att tca ctt gcg cac aga gga gtg gac gcg tca aag aaa act tcc aag Ile Ser Leu Ala His Arg Gly Val Asp Ala Ser Lys Lys Thr Ser Lys 520 525 530 535			1878
act gtt acc ata tcc caa gtg tct gac aac aaa gca tcc ctg ccg ccc Thr Val Thr Ile Ser Gln Val Ser Asp Asn Lys Ala Ser Leu Pro Pro 540 545 550			1926
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cgccgccgcc actgaggaag aagccggccc agccgccgcc gcgtccggac cctcgcgccct      180
ggatcccagc gccccgatcc cggcgccccca acccccacgc ccgcctccgc caactttcac      240
gctgcctcgg cggcccggcc cggctcgacg cca atg gtg gag gcc ata gtg gag      294
                               Met Val Glu Ala Ile Val Glu
                               1                               5

ttt gac tac cag gcc cag cac gat gat gag ctg acg atc agc gtg ggt      342
Phe Asp Tyr Gln Ala Gln His Asp Asp Glu Leu Thr Ile Ser Val Gly
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gaa atc atc acc aac atc agg aag gag gat gga ggc tgg tgg gag gga      390
Glu Ile Ile Thr Asn Ile Arg Lys Glu Asp Gly Gly Trp Trp Glu Gly
                               25                               30                               35

cag atc aac ggc agg aga ggt ttg ttc cct gac aac ttt gta aga gaa      438
Gln Ile Asn Gly Arg Arg Gly Leu Phe Pro Asp Asn Phe Val Arg Glu
                               40                               45                               50                               55

ata aag aaa gag atg aag aaa gac cct ctc acc aac aaa gct cca gaa      486
Ile Lys Lys Glu Met Lys Lys Asp Pro Leu Thr Asn Lys Ala Pro Glu
                               60                               65                               70

aag ccc ctg cac gaa gtg ccc agt gga aac tct ttg ctg tct tct gaa      534
Lys Pro Leu His Glu Val Pro Ser Gly Asn Ser Leu Leu Ser Ser Glu
                               75                               80                               85

acg att tta aga acc aat aag aga ggc gag cga cgg agg cgc cgg tgc      582
Thr Ile Leu Arg Thr Asn Lys Arg Gly Glu Arg Arg Arg Arg Arg Cys
                               90                               95                               100

cag gtg gca ttc agc tac ctg ccc cag aat gac gat gaa ctt gag ctg      630
Gln Val Ala Phe Ser Tyr Leu Pro Gln Asn Asp Asp Glu Leu Glu Leu
                               105                               110                               115

aaa gtt ggc gac atc ata gag gtg gta gga gag gta gag gaa gga tgg      678
Lys Val Gly Asp Ile Ile Glu Val Val Gly Glu Val Glu Glu Gly Trp
                               120                               125                               130                               135

tgg gaa ggt gtt ctc aac ggg aag act gga atg ttt cct tcc aac ttc      726
Trp Glu Gly Val Leu Asn Gly Lys Thr Gly Met Phe Pro Ser Asn Phe
                               140                               145                               150

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gaa gta gaa aat gac ttt ctg ccg gta gaa aag act att ggg aag aag Glu Val Glu Asn Asp Phe Leu Pro Val Glu Lys Thr Ile Gly Lys Lys 235 240 245	1014
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agc agg aca aag agc aag gat tac tgc aaa gta ata ttt cca tat gag Ser Arg Thr Lys Ser Lys Asp Tyr Cys Lys Val Ile Phe Pro Tyr Glu 265 270 275	1110
gca cag aat gat gat gaa ttg aca atc aaa gaa gga gat ata gtc act Ala Gln Asn Asp Asp Glu Leu Thr Ile Lys Glu Gly Asp Ile Val Thr 280 285 290 295	1158
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ccg gac ttt gaa aag gaa ggg aat aga ccc aag aag cca ccg cct cca Pro Asp Phe Glu Lys Glu Gly Asn Arg Pro Lys Lys Pro Pro Pro Pro 330 335 340	1302
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gaa att aaa aag ata cct cct gaa aga cca gaa atg ctt cca aac aga Glu Ile Lys Lys Ile Pro Pro Glu Arg Pro Glu Met Leu Pro Asn Arg 360 365 370 375	1398
aca gaa gaa aaa gaa aga cca gag aga gag cca aaa ctg gat tta cag	1446

Thr	Glu	Glu	Lys	Glu	Arg	Pro	Glu	Arg	Glu	Pro	Lys	Leu	Asp	Leu	Gln	
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aag	ccc	tcc	gtt	cct	gcc	ata	ccg	cca	aaa	aag	cct	cgg	cca	cct	aag	1494
Lys	Pro	Ser	Val	Pro	Ala	Ile	Pro	Pro	Lys	Lys	Pro	Arg	Pro	Pro	Lys	
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acc	aat	tct	ctc	agc	aga	cct	ggc	gca	ctg	ccc	ccg	aga	agg	ccg	gag	1542
Thr	Asn	Ser	Leu	Ser	Arg	Pro	Gly	Ala	Leu	Pro	Pro	Arg	Arg	Pro	Glu	
		410					415					420				
aga	ccg	gtg	ggc	ccg	ctg	aca	cac	acc	agg	ggc	gac	agt	cca	aag	att	1590
Arg	Pro	Val	Gly	Pro	Leu	Thr	His	Thr	Arg	Gly	Asp	Ser	Pro	Lys	Ile	
	425					430				435						
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Asp	Leu	Ala	Gly	Ser	Ser	Leu	Ser	Gly	Ile	Leu	Asp	Lys	Asp	Leu	Ser	
440				445				450						455		
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Asp	Arg	Ser	Asn	Asp	Ile	Asp	Leu	Glu	Gly	Phe	Asp	Ser	Val	Val	Ser	
			460					465					470			
tct	act	gag	aaa	ctc	agt	cat	ccg	acc	aca	agc	aga	cca	aaa	gct	aca	1734
Ser	Thr	Glu	Lys	Leu	Ser	His	Pro	Thr	Thr	Ser	Arg	Pro	Lys	Ala	Thr	
		475					480						485			
ggg	agg	cgg	cct	ccg	tcc	cag	tcc	ctc	aca	tct	gtg	tct	gac	aac	aaa	1782
Gly	Arg	Arg	Pro	Pro	Ser	Gln	Ser	Leu	Thr	Ser	Val	Ser	Asp	Asn	Lys	
	490					495					500					
gca	tcc	ctg	ccg	ccc	aag	ccg	ggg	acc	atg	gca	gca	ggc	ggc	ggc	ggg	1830
Ala	Ser	Leu	Pro	Pro	Lys	Pro	Gly	Thr	Met	Ala	Ala	Gly	Gly	Gly	Gly	
	505					510				515						
cca	gcc	cct	ctg	tcc	tca	gcg	gcg	ccc	tcc	ccc	ctg	tca	tcc	tct	ttg	1878
Pro	Ala	Pro	Leu	Ser	Ser	Ala	Ala	Pro	Ser	Pro	Leu	Ser	Ser	Ser	Leu	
520				525				530							535	
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Gly	Thr	Ala	Gly	His	Arg	Ala	Asn	Ser	Pro	Ser	Leu	Phe	Gly	Thr	Glu	
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Gly	Lys	Pro	Lys	Met	Glu	Pro	Ala	Ala	Ser	Ser	Gln	Ala	Ala	Val	Glu	
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gag	cta	agg	aca	cag	gtc	cgc	gag	ctg	agg	agc	atc	atc	gag	acc	atg	2022
Glu	Leu	Arg	Thr	Gln	Val	Arg	Glu	Leu	Arg	Ser	Ile	Ile	Glu	Thr	Met	
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Lys	Asp	Gln	Gln	Lys	Arg	Glu	Ile	Lys	Gln	Leu	Leu	Ser	Glu	Leu	Asp	
	585					590				595						
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Glu	Glu	Lys	Lys	Ile	Arg	Leu	Arg	Leu	Gln	Met	Glu	Val	Asn	Asp	Ile	

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ggcccagcaa ggtcccaggt cttccctctc ctacgcgcct aagagagagg ccagtgccg 360
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                Met Phe Arg Lys

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Lys Lys Lys Lys Arg Pro Glu Ile Ser Ala Pro Gln Asn Phe Gln His	
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cgt gtc cac acc tcc ttc gag ccc aaa gaa ggc aag ttt gtg ggc ctc	511
Arg Val His Thr Ser Phe Asp Pro Lys Glu Gly Lys Phe Val Gly Leu	
25 30 35	
ccc cca caa tgg cag aac atc ctg gag aca ctg cgg cgc ccc aag ccc	559
Pro Pro Gln Trp Gln Asn Ile Leu Asp Thr Leu Arg Arg Pro Lys Pro	
40 45 50	
gtg gtg gag cct tcg cga atc aca cgg gtg cag ctc cag ccc atg aag	607
Val Val Asp Pro Ser Arg Ile Thr Arg Val Gln Leu Gln Pro Met Lys	
55 60 65	
aca gtg gtg cgg ggc agc gcg atg cct gtg gat ggc tac atc tcg ggg	655
Thr Val Val Arg Gly Ser Ala Met Pro Val Asp Gly Tyr Ile Ser Gly	
70 75 80	
ctg ctc aac gag atc cag aag ttg tca gtc atc agc tcc aac acc ctg	703
Leu Leu Asn Asp Ile Gln Lys Leu Ser Val Ile Ser Ser Asn Thr Leu	
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Arg Gly Arg Ser Pro Thr Ser Arg Arg Arg Ala Gln Ser Leu Gly Leu	
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Leu Gly Asp Glu His Trp Ala Thr Asp Pro Asp Met Tyr Leu Gln Ser	
120 125 130	
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Pro Gln Ser Glu Arg Thr Asp Pro His Gly Leu Tyr Leu Ser Cys Asn	
135 140 145	
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Gly Gly Thr Pro Ala Gly His Lys Gln Met Pro Trp Pro Glu Pro Gln	
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Ser Pro Arg Val Leu Pro Asn Gly Leu Ala Ala Lys Ala Gln Ser Leu	
165 170 175 180	
ggc ccc gcc gag ttt cag ggt gcc tcg cag cgc tgt ctg cag ctg ggt	991
Gly Pro Ala Glu Phe Gln Gly Ala Ser Gln Arg Cys Leu Gln Leu Gly	
185 190 195	
gcc tgc ctg cag agc tcc cca cca gga gcc tcg ccc ccc acg ggc acc	1039
Ala Cys Leu Gln Ser Ser Pro Pro Gly Ala Ser Pro Pro Thr Gly Thr	
200 205 210	
aat agg cat gga atg aag gct gcc aag cat ggc tct gag gag gcc cgg	1087
Asn Arg His Gly Met Lys Ala Ala Lys His Gly Ser Glu Glu Ala Arg	
215 220 225	

cca cag tcc tgc ctg gtg ggc tca gcc aca ggc agg cca ggt ggg gaa	1135
Pro Gln Ser Cys Leu Val Gly Ser Ala Thr Gly Arg Pro Gly Gly Glu	
230 235 240	
ggc agc cct agc cct aag acc cgg gag agc agc ctg aag cgc agg cta	1183
Gly Ser Pro Ser Pro Lys Thr Arg Glu Ser Ser Leu Lys Arg Arg Leu	
245 250 255 260	
ttc cga agc atg ttc ctg tcc act gct gcc aca gcc cct cca agc agc	1231
Phe Arg Ser Met Phe Leu Ser Thr Ala Ala Thr Ala Pro Pro Ser Ser	
265 270 275	
agc aag cca ggc cct cca cca cag agc aag ccc aac tcc tct ttc cga	1279
Ser Lys Pro Gly Pro Pro Pro Gln Ser Lys Pro Asn Ser Ser Phe Arg	
280 285 290	
ccg ccg cag aaa gac aac ccc cca agc ctg gtg gcc aag gcc cag tcc	1327
Pro Pro Gln Lys Asp Asn Pro Pro Ser Leu Val Ala Lys Ala Gln Ser	
295 300 305	
ttg ccc tcg gac cag ccg gtg ggg acc ttc agc cct ctg acc act tcg	1375
Leu Pro Ser Asp Gln Pro Val Gly Thr Phe Ser Pro Leu Thr Thr Ser	
310 315 320	
gat acc agc agc ccc cag aag tcc ctc cgc aca gcc ccg gcc aca ggc	1423
Asp Thr Ser Ser Pro Gln Lys Ser Leu Arg Thr Ala Pro Ala Thr Gly	
325 330 335 340	
cag ctt cca ggc cgg tct tcc cca gcg gga tcc ccc cgc acc tgg cac	1471
Gln Leu Pro Gly Arg Ser Ser Pro Ala Gly Ser Pro Arg Thr Trp His	
345 350 355	
gcc cag atc agc acc agc aac ctg tac ctg ccc cag gac ccc acg gtt	1519
Ala Gln Ile Ser Thr Ser Asn Leu Tyr Leu Pro Gln Asp Pro Thr Val	
360 365 370	
gcc aag ggt gcc ctg gct ggt gag gac aca ggt gtt gtg aca cat gag	1567
Ala Lys Gly Ala Leu Ala Gly Glu Asp Thr Gly Val Val Thr His Glu	
375 380 385	
cag ttc aag gct gcg ctc agg atg gtg gtg gac cag ggt gac ccc cgg	1615
Gln Phe Lys Ala Ala Leu Arg Met Val Val Asp Gln Gly Asp Pro Arg	
390 395 400	
ctg ctg ctg gac agc tac gtg aag att ggc gag ggc tcc acc ggc atc	1663
Leu Leu Leu Asp Ser Tyr Val Lys Ile Gly Glu Gly Ser Thr Gly Ile	
405 410 415 420	
gtc tgc ttg gcc cgg gag aag cac tcg ggc cgc cag gtg gcc gtc aag	1711
Val Cys Leu Ala Arg Glu Lys His Ser Gly Arg Gln Val Ala Val Lys	
425 430 435	
atg atg gac ctc agg aag cag cag cgc agg gag ctg ctc ttc aac gag	1759
Met Met Asp Leu Arg Lys Gln Gln Arg Arg Glu Leu Leu Phe Asn Glu	
440 445 450	

gtg gtg atc atg cgg gac tac cag cac ttc aac gtg gtg gag atg tac Val Val Ile Met Arg Asp Tyr Gln His Phe Asn Val Val Glu Met Tyr 455 460 465	1807
aag agc tac ctg gtg gga gag gag ctg tgg gtg ctc atg gag ttc ctg Lys Ser Tyr Leu Val Gly Glu Glu Leu Trp Val Leu Met Glu Phe Leu 470 475 480	1855
cag gga gga gcc ctc aca gac atc gtc tcc caa gtc agg ctg aat gag Gln Gly Gly Ala Leu Thr Asp Ile Val Ser Gln Val Arg Leu Asn Glu 485 490 495 500	1903
gag cag att gcc act gtg tgt gag gct gtg ctg cag gcc ctg gcc tac Glu Gln Ile Ala Thr Val Cys Glu Ala Val Leu Gln Ala Leu Ala Tyr 505 510 515	1951
ctg cat gct cag ggt gtc atc cac cgg gac atc aag agt gac tcc atc Leu His Ala Gln Gly Val Ile His Arg Asp Ile Lys Ser Asp Ser Ile 520 525 530	1999
ctg ctg acc ctc gat ggc agg gtg aag ctc tcg gac ttc gga ttc tgt Leu Leu Thr Leu Asp Gly Arg Val Lys Leu Ser Asp Phe Gly Phe Cys 535 540 545	2047
gct cag atc agc aaa gac gtc cct aag agg aag tcc ctg gtg gga acc Ala Gln Ile Ser Lys Asp Val Pro Lys Arg Lys Ser Leu Val Gly Thr 550 555 560	2095
ccc tac tgg atg gct cct gaa gtg atc tcc agg tct ttg tat gcc act Pro Tyr Trp Met Ala Pro Glu Val Ile Ser Arg Ser Leu Tyr Ala Thr 565 570 575 580	2143
gag gtg gat atc tgg tct ctg ggc atc atg gtg att gag atg gta gat Glu Val Asp Ile Trp Ser Leu Gly Ile Met Val Ile Glu Met Val Asp 585 590 595	2191
ggg gag cca ccg tac ttc agt gac tcc cca gtg caa gcc atg aag agg Gly Glu Pro Pro Tyr Phe Ser Asp Ser Pro Val Gln Ala Met Lys Arg 600 605 610	2239
ctc cgg gac agc ccc cca ccc aag ctg aaa aac tct cac aag gtc tcc Leu Arg Asp Ser Pro Pro Pro Lys Leu Lys Asn Ser His Lys Val Ser 615 620 625	2287
cca gtg ctg cga gac ttc ctg gag cgg atg ctg gtg cgg gac ccc caa Pro Val Leu Arg Asp Phe Leu Glu Arg Met Leu Val Arg Asp Pro Gln 630 635 640	2335
gag aga gcc aca gcc cag gag ctc cta gac cac ccc ttc ctg ctg cag Glu Arg Ala Thr Ala Gln Glu Leu Leu Asp His Pro Phe Leu Leu Gln 645 650 655 660	2383
aca ggg cta cct gag tgc ctg gtg ccc ctg atc cag ctc tac cga aag Thr Gly Leu Pro Glu Cys Leu Val Pro Leu Ile Gln Leu Tyr Arg Lys 665 670 675	2431
cag acc tcc acc tgc tga gccac cccaagtatg cctgccacct acgcccacag	2485

Gln Thr Ser Thr Cys *
680

gcagggcaca ctgggcagcc agcctgccgg caggacttgc ctgcctcctc ctctcagtat 2545
tctctccaaa gattgaaatg tgaagcccca gccccaccct ctgcccttca gcctactggg 2605
ccaggccgga cctgccccct cagtgtctct cctcccgag tccccagatg gagacccctt 2665
tctacaggat gacccttga tatttgcaca gggatatttc taagaaacgc agaggccagc 2725
gttcttggcc tctgcagcca acacagtaga aaaggctgct gtgggttttt aaaggcagtt 2785
gtccactagt gtcctaggcc actgcagagg gcagactgct ggtctccaca gatacctgct 2845
gttctcagct ccagcttcaa acctcgagtc tcgagagggc cacggggtgg ttttatgac 2905
cggaatcccg cttcctccct cacgtctgat gtcctgaagg tgcagtccca cctgtacagc 2965
ccctccccgc ccagaactgt gaatggcctg ctccaggcca tggctggggg cagggagtga 3025
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acagaatgga gaga 3099

<210> 42
<211> 1968
<212> DNA
<213> Homo sapiens

<220>
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<222> (154)..(1968)

<400> 42

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ggtgacaggc gttgagacca ccgaagggaa ccc atg gct agg atc agt ttt tcc 174
Met Ala Arg Ile Ser Phe Ser
1 5
tac ctc tgc cca gcc tcc tgg tac ttc act gtg ccc aca gtg agt cca 222
Tyr Leu Cys Pro Ala Ser Trp Tyr Phe Thr Val Pro Thr Val Ser Pro
10 15 20
ttt ctc cgt cag cgg gtg gca ttc ctg gga ctc ttc ttc ata tcc tgt 270
Phe Leu Arg Gln Arg Val Ala Phe Leu Gly Leu Phe Phe Ile Ser Cys
25 30 35
ctc ctt tta ctt atg tta atc ata gac ttt cga cat tgg agt gct tca 318
Leu Leu Leu Leu Met Leu Ile Ile Asp Phe Arg His Trp Ser Ala Ser
40 45 50 55

tta cca cga gat agg caa tac gaa agg tat ttg gct cga gta ggg gag Leu Pro Arg Asp Arg Gln Tyr Glu Arg Tyr Leu Ala Arg Val Gly Glu	366
60 65 70	
ctt gaa gct act gac act gaa gac cca aat ctg aat tat gga ctt gtt Leu Glu Ala Thr Asp Thr Glu Asp Pro Asn Leu Asn Tyr Gly Leu Val	414
75 80 85	
gtt gac tgt ggc agc agt ggt tcc cgg att ttt gtt tat ttc tgg cca Val Asp Cys Gly Ser Ser Gly Ser Arg Ile Phe Val Tyr Phe Trp Pro	462
90 95 100	
aga cat aat ggg aac ccc cat gac ttg ctg gac atc aaa cag atg aga Arg His Asn Gly Asn Pro His Asp Leu Leu Asp Ile Lys Gln Met Arg	510
105 110 115	
gac cgc aac agc caa cca gtg gtt aaa aaa atc aag cca gga atc tct Asp Arg Asn Ser Gln Pro Val Val Lys Lys Ile Lys Pro Gly Ile Ser	558
120 125 130 135	
gca atg gca gac act cca gaa cat gcc agt gat tac ctt cgt cct ctg Ala Met Ala Asp Thr Pro Glu His Ala Ser Asp Tyr Leu Arg Pro Leu	606
140 145 150	
ctg agc ttt gct gct gct cat gtg cct gtg aag aag cac aag gag acc Leu Ser Phe Ala Ala Ala His Val Pro Val Lys Lys His Lys Glu Thr	654
155 160 165	
cct ctt tac atc ctc tgc aca gca ggc atg agg ctt ctc cct gag agg Pro Leu Tyr Ile Leu Cys Thr Ala Gly Met Arg Leu Leu Pro Glu Arg	702
170 175 180	
aag cag ttg gct atc ttg gct gac cta gtg aaa gat tta cca ctg gag Lys Gln Leu Ala Ile Leu Ala Asp Leu Val Lys Asp Leu Pro Leu Glu	750
185 190 195	
ttt gac ttc ctc ttt tca cag tct caa gca gaa gtg atc tct ggg aag Phe Asp Phe Leu Phe Ser Gln Ser Gln Ala Glu Val Ile Ser Gly Lys	798
200 205 210 215	
cag gaa ggg gtt tat gca tgg att gga atc aac ttt gtt ttg gga aga Gln Glu Gly Val Tyr Ala Trp Ile Gly Ile Asn Phe Val Leu Gly Arg	846
220 225 230	
ttc gac cac gag gat gaa tca gat gct gag gct acc cag gaa ttg gca Phe Asp His Glu Asp Glu Ser Asp Ala Glu Ala Thr Gln Glu Leu Ala	894
235 240 245	
gca gga cgg aga agg aca gta ggg ata ctg gat atg gga gga gcc tct Ala Gly Arg Arg Arg Thr Val Gly Ile Leu Asp Met Gly Gly Ala Ser	942
250 255 260	
ctc caa att gct tat gaa gtt cct acc tca acc tct gtc ctt cct gca Leu Gln Ile Ala Tyr Glu Val Pro Thr Ser Thr Ser Val Leu Pro Ala	990
265 270 275	

aag cag gaa gaa gct gcc aag atc ctg ctg gct gag ttc aac ctg ggc	1038
Lys Gln Glu Glu Ala Ala Lys Ile Leu Leu Ala Glu Phe Asn Leu Gly	
280 285 290 295	
tgt gat gtg caa cac act gaa cac gtg tac agg gtt tat gtc aca act	1086
Cys Asp Val Gln His Thr Glu His Val Tyr Arg Val Tyr Val Thr Thr	
300 305 310	
ttt ctg ggt ttc gga ggc aac ttt gcc cgg cag cgc tac gaa gac ctt	1134
Phe Leu Gly Phe Gly Gly Asn Phe Ala Arg Gln Arg Tyr Glu Asp Leu	
315 320 325	
gtt ctg aat gaa act ctt aac aaa aac aga ttg ctt ggt cag aag aca	1182
Val Leu Asn Glu Thr Leu Asn Lys Asn Arg Leu Leu Gly Gln Lys Thr	
330 335 340	
ggt ctg agt ccc gac aat cca ttt ctg gat ccc tgc ctg cca gtg gga	1230
Gly Leu Ser Pro Asp Asn Pro Phe Leu Asp Pro Cys Leu Pro Val Gly	
345 350 355	
ctc aca gat gtg gtg gag agg aac agc caa gtc tta cat gtc cga gga	1278
Leu Thr Asp Val Val Glu Arg Asn Ser Gln Val Leu His Val Arg Gly	
360 365 370 375	
aga gga gac tgg gtg tct tgt ggg gca atg ctg agc ccc ctg ctg gct	1326
Arg Gly Asp Trp Val Ser Cys Gly Ala Met Leu Ser Pro Leu Leu Ala	
380 385 390	
cgc tcc aac acc agc cag gcc tca ctc aat ggc ata tat caa tcg cct	1374
Arg Ser Asn Thr Ser Gln Ala Ser Leu Asn Gly Ile Tyr Gln Ser Pro	
395 400 405	
att gac ttc aac aac agc gag ttc tac ggc ttc tct gag ttt ttt tat	1422
Ile Asp Phe Asn Asn Ser Glu Phe Tyr Gly Phe Ser Glu Phe Phe Tyr	
410 415 420	
tgt aca gag gat gtg ttg cgc att ggt ggc cgc tac cat ggg cca aca	1470
Cys Thr Glu Asp Val Leu Arg Ile Gly Gly Arg Tyr His Gly Pro Thr	
425 430 435	
ttt gcc aag gct gct cag gat tac tgt ggc atg gct tgg tcg gta cta	1518
Phe Ala Lys Ala Ala Gln Asp Tyr Cys Gly Met Ala Trp Ser Val Leu	
440 445 450 455	
act cag aga ttc aag aat ggc ctc ttt tca tca cat gca gat gag cat	1566
Thr Gln Arg Phe Lys Asn Gly Leu Phe Ser Ser His Ala Asp Glu His	
460 465 470	
cga ctc aaa tat cag tgt ttt aaa tcg gct tgg atg tac caa gtc tta	1614
Arg Leu Lys Tyr Gln Cys Phe Lys Ser Ala Trp Met Tyr Gln Val Leu	
475 480 485	
cat gaa gga ttc cac ttt ccc tat gac tac cca aac ctg cgg aca gcc	1662
His Glu Gly Phe His Phe Pro Tyr Asp Tyr Pro Asn Leu Arg Thr Ala	
490 495 500	
cag ctg gtg tat gac cga gag gtt cag tgg acg ctg gga gcc att cta	1710

Gln	Leu	Val	Tyr	Asp	Arg	Glu	Val	Gln	Trp	Thr	Leu	Gly	Ala	Ile	Leu		
505						510					515						
tat	aaa	aca	cga	ttc	tta	cca	ctc	agg	gat	ctt	cgg	cag	gaa	ggt	gtc	1758	
Tyr	Lys	Thr	Arg	Phe	Leu	Pro	Leu	Arg	Asp	Leu	Arg	Gln	Glu	Gly	Val		
520					525					530					535		
cga	caa	gcc	cat	ggt	agc	tgg	ttc	cgt	ctc	tcc	ttt	gta	tac	aac	cac	1806	
Arg	Gln	Ala	His	Gly	Ser	Trp	Phe	Arg	Leu	Ser	Phe	Val	Tyr	Asn	His		
				540					545						550		
tat	ctc	ttc	ttt	gcc	tgt	atc	ctg	gtg	gtg	cta	ctg	gcc	atc	ttc	cta	1854	
Tyr	Leu	Phe	Phe	Ala	Cys	Ile	Leu	Val	Val	Leu	Leu	Ala	Ile	Phe	Leu		
				555					560						565		
tac	ctt	ctg	cgg	cta	cgc	cga	att	cac	cac	cga	caa	aca	cga	gcc	tca	1902	
Tyr	Leu	Leu	Arg	Leu	Arg	Arg	Ile	His	His	Arg	Gln	Thr	Arg	Ala	Ser		
				570				575							580		
gct	cca	ttg	gac	ttg	ctg	tgg	ctt	gaa	gag	gtg	gtg	ccc	atg	atg	gga	1950	
Ala	Pro	Leu	Asp	Leu	Leu	Trp	Leu	Glu	Glu	Val	Val	Pro	Met	Met	Gly		
				585				590				595					
gta	cag	gtg	ggg	ccg	tga											1968	
Val	Gln	Val	Gly	Pro	*												
600					605												

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 <213> Homo sapiens
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 <221> CDS
 <222> (418)..(1023)

<400> 43																	
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tttcaattag	ttactttttc	ttacaaggct	gggagaggga	gacagaacaa	tagaaaaata											180	
actggttgat	tcatatggag	gtcagagtgg	aagcaggtgt	gagagggtcc	cacagaagaa											240	
aacatggcag	ccaaagtgtt	tgagtccacg	gtaagtttgg	cttggcctta	gctgttgcag											300	
gagacctgtg	aactctgcct	tatataatgt	ggatgttggg	cacagagctg	tcatctttga											360	
ctgattccag	gacaaaaatg	acaggacatt	gtggtagggg	actcaatttc	tcatccc											417	
atg ggt aca	gaa acc aat	tat ctt tgc	ctt tct cca	cca cgt aat	gta											465	
Met Gly Thr	Glu Tyr Asn	Leu Cys Leu	Ser Pro Pro	Arg Asn Val													
1		5						10								15	

cca atc atc act ggt agc aaa gat tta cag aat gtc aat atc aca ctg	513
Pro Ile Ile Thr Gly Ser Lys Asp Leu Gln Asn Val Asn Ile Thr Leu	
20 25 30	
cgc atc atc ttc cag cct gtt gct agc cag ctt cct cgc atc ttc acc	561
Arg Ile Ile Phe Gln Pro Val Ala Ser Gln Leu Pro Arg Ile Phe Thr	
35 40 45	
agc atc gga gag gac tat gat gag cct gtg ctg acg tac atc acg acc	609
Ser Ile Gly Glu Asp Tyr Asp Glu Pro Val Leu Thr Tyr Ile Thr Thr	
50 55 60	
gag atc ctc aag tca gtg gtg gct cgc ttt gat gct gga gaa gtt atc	657
Glu Ile Leu Lys Ser Val Val Ala Arg Phe Asp Ala Gly Glu Val Ile	
65 70 75 80	
act cag aga gag ctg gtc tcc agg cag gtg agc aac gac ctt acg gag	705
Thr Gln Arg Glu Leu Val Ser Arg Gln Val Ser Asn Asp Leu Thr Glu	
85 90 95	
caa gca gcc aca ttt ggg ctc atc ctg gac gac gtg tcc ttg aca tat	753
Gln Ala Ala Thr Phe Gly Leu Ile Leu Asp Asp Val Ser Leu Thr Tyr	
100 105 110	
ctg acc ttt gga aag gag ttc aca gaa gca gtg gaa gcc aaa cag gtg	801
Leu Thr Phe Gly Lys Glu Phe Thr Glu Ala Val Glu Ala Lys Gln Val	
115 120 125	
gct cag cag gaa gca gag agg gcc aga ttt gtg aag gaa aag gct gag	849
Ala Gln Gln Glu Ala Glu Arg Ala Arg Phe Val Lys Glu Lys Ala Glu	
130 135 140	
cag cag aaa aag gct gag cag cag aaa aag gtt gag cag cag aaa aag	897
Gln Gln Lys Lys Ala Glu Gln Gln Lys Lys Val Glu Gln Gln Lys Lys	
145 150 155 160	
gca gcc gtg atc tct gct gag ggc gac tcc aag gca acc gag ctg att	945
Ala Ala Val Ile Ser Ala Glu Gly Asp Ser Lys Ala Thr Glu Leu Ile	
165 170 175	
gcc aac tca ctg gcc acc gcg ggg gac ggc ctg atg gag ctg tgc aag	993
Ala Asn Ser Leu Ala Thr Ala Gly Asp Gly Leu Met Glu Leu Cys Lys	
180 185 190	
ttg gaa gcc gcg gag gct ctc gga aca tga c ctacctgccg gcggggcagt	1044
Leu Glu Ala Ala Glu Ala Leu Gly Thr *	
195 200	
ccgctcctcc ggctgccccca tgaggggccca ccctgcctgc acctccgcag gctgactggg	1104
ccacagcccc aatgattctt aacactgcct taccctcccta cccagaaat cactgaaatt	1164
tcataattgg cttaaagtga aggaaataaa agtaaaatca cttcagaact cttaaaaaaa	1224
aaaaa	1229

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 <211> 2173
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (88)..(1653)

<400> 44

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ggagctgccca atcaaaagtg gcattac      atg aaa aat ata aaa gca ctt gtg      111
                                   Met Lys Asn Ile Lys Ala Leu Val
                                   1                               5

gcc ttt cat agc act gcc ttg gat aag gaa att aca tca gca aat tat      159
Ala Phe His Ser Thr Ala Leu Asp Lys Glu Ile Thr Ser Ala Asn Tyr
   10                               15                               20

gct ggt gtc tgt aca tca tct gtg att aaa gaa gaa aac att gat caa      207
Ala Gly Val Cys Thr Ser Ser Val Ile Lys Glu Glu Asn Ile Asp Gln
   25                               30                               35                               40

cca gga tac tgt tat ctc tca cct gat gga aag aga aaa act atg ctc      255
Pro Gly Tyr Cys Tyr Leu Ser Pro Asp Gly Lys Arg Lys Thr Met Leu
                               45                               50                               55

tgc ttg gct tgt gga caa tcc atg aga aca gag aaa gga ctg aaa caa      303
Cys Leu Ala Cys Gly Gln Ser Met Arg Thr Glu Lys Gly Leu Lys Gln
                               60                               65                               70

ttg ctt cca ggg gtt cca ttc ctc tgt att tca ggc acc aag act cag      351
Leu Leu Pro Gly Val Pro Phe Leu Cys Ile Ser Gly Thr Lys Thr Gln
   75                               80                               85

aag ccc ttc tta caa ggg ccc ttc aag gtc atc agt gtg gct gag gtt      399
Lys Pro Phe Leu Gln Gly Pro Phe Lys Val Ile Ser Val Ala Glu Val
   90                               95                               100

gat ttg tcg tgt gac aag gct gaa aaa act cta agt tac tac caa gca      447
Asp Leu Ser Cys Asp Lys Ala Glu Lys Thr Leu Ser Tyr Tyr Gln Ala
  105                               110                               115                               120

cgt cta ttg tct tta cgg atg aag acc tgc acg caa gct gca tct cac      495
Arg Leu Leu Ser Leu Arg Met Lys Thr Cys Thr Gln Ala Ala Ser His
   125                               130                               135

agt ggc atg gca gcc aca cac cag aag gca gtg aaa ata att gca tac      543
Ser Gly Met Ala Ala Thr His Gln Lys Ala Val Lys Ile Ile Ala Tyr
   140                               145                               150

aaa aat ggg gat ggg tat cgt aat ggg aag tta att gtg gct gga aca      591
Lys Asn Gly Asp Gly Tyr Arg Asn Gly Lys Leu Ile Val Ala Gly Thr

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155	160	165	
ttc ccc atg ctt ctt aca gaa tgc acg gaa caa ctt ggg ctt gcc aga			639
Phe Pro Met Leu Leu Thr	Glu Cys Thr	Glu Gln Leu Gly Leu Ala Arg	
170	175	180	
gca gcc tcc aaa gta tat acc aaa gat gga acc cca atc ttt acc ttg			687
Ala Ala Ser Lys Val Tyr Thr Lys Asp Gly Thr Pro Ile Phe Thr Leu			
185	190	195	200
cgt gat ttg gtt tta tgg gct cta gat gaa tcc ttt ctc cag aga gac			735
Arg Asp Leu Val Leu Trp Ala Leu Asp	Glu Ser Phe Leu Gln Arg Asp		
205	210	215	
tct gag aaa caa aag caa gat gca gct cct gtt gga aaa gaa cag ata			783
Ser Glu Lys Gln Lys Gln Asp Ala Ala Pro Val Gly Lys Glu Gln Ile			
220	225	230	
att gtt gaa agt atg gaa gaa aat cca aga atg aaa gtg aaa aac aga			831
Ile Val Glu Ser Met Glu Glu Asn Pro Arg Met Lys Val Lys Asn Arg			
235	240	245	
tta ttt gca aaa tct gtg aca tcc gat agt ttg gat ggt ata gac aag			879
Leu Phe Ala Lys Ser Val Thr Ser Asp Ser Leu Asp Gly Ile Asp Lys			
250	255	260	
tct ttg ctt acc ctc atc ctc aga aat cct att gcc atc tgg gtg tct			927
Ser Leu Leu Thr Leu Ile Leu Arg Asn Pro Ile Ala Ile Trp Val Ser			
265	270	275	280
tgt ggt gaa cca ttt cta cct cca aat gct ttg cag aaa gca gaa aaa			975
Cys Gly Glu Pro Phe Leu Pro Pro Asn Ala Leu Gln Lys Ala Glu Lys			
285	290	295	
tta gag aaa cag aac tgg cta aaa aag gac aga att ttg gct gat cta			1023
Leu Glu Lys Gln Asn Trp Leu Lys Lys Asp Arg Ile Leu Ala Asp Leu			
300	305	310	
gat acc atg aga cac aaa atg aga cag tta aaa ggg cgg cga gta gcg			1071
Asp Thr Met Arg His Lys Met Arg Gln Leu Lys Gly Arg Arg Val Ala			
315	320	325	
gca tgt cag cca gcc acc atg gtt cct acc aag agc cct gtg cag ccc			1119
Ala Cys Gln Pro Ala Thr Met Val Pro Thr Lys Ser Pro Val Gln Pro			
330	335	340	
gtg gtg gtt gaa gga ggc tgg acc gaa cag act caa cag gaa att aaa			1167
Val Val Val Glu Gly Gly Trp Thr Glu Gln Thr Gln Gln Glu Ile Lys			
345	350	355	360
ctc atg gaa ctt ata aga cat aca gag gca cac ctt tct gaa atc caa			1215
Leu Met Glu Leu Ile Arg His Thr Glu Ala His Leu Ser Glu Ile Gln			
365	370	375	
gaa atg gaa tcc aaa ata aat ttt cca att gca acc aaa cgt ata gca			1263
Glu Met Glu Ser Lys Ile Asn Phe Pro Ile Ala Thr Lys Arg Ile Ala			
380	385	390	

gtc aag ccg agc aac ctg tat aag cag ccc aac aca aaa cga gtg tgg	1311
Val Lys Pro Ser Asn Leu Tyr Lys Gln Pro Asn Thr Lys Arg Val Trp	
395 400 405	
att tat cta aat gga ggc aga cct gaa gat ggc act tat gcc tgg ggc	1359
Ile Tyr Leu Asn Gly Gly Arg Pro Glu Asp Gly Thr Tyr Ala Trp Gly	
410 415 420	
aaa act att tca gag ctg ctg caa gac tgc tcc tct cgt ctc aaa atg	1407
Lys Thr Ile Ser Glu Leu Leu Gln Asp Cys Ser Ser Arg Leu Lys Met	
425 430 435 440	
acc cac cca gct aga gca ctg tac acc ccc agt gga gag cca att cag	1455
Thr His Pro Ala Arg Ala Leu Tyr Thr Pro Ser Gly Glu Pro Ile Gln	
445 450 455	
tcc tgg gac gac ata gag cga gat atg gtc atc tgt gtg tct atg gga	1503
Ser Trp Asp Asp Ile Glu Arg Asp Met Val Ile Cys Val Ser Met Gly	
460 465 470	
cat ggt ttc aaa acc cca aaa gag tta aaa caa ctg atg gag atc aga	1551
His Gly Phe Lys Thr Pro Lys Glu Leu Lys Gln Leu Met Glu Ile Arg	
475 480 485	
gca aat tat gcc aga atc cga agg cag cag ggc cct caa gcc aca gac	1599
Ala Asn Tyr Ala Arg Ile Arg Arg Gln Gln Gly Pro Gln Ala Thr Asp	
490 495 500	
att gtg gtg tca cca tcc acg aag ctg ctg tct ctg gca cat ctc cac	1647
Ile Val Val Ser Pro Ser Thr Lys Leu Leu Ser Leu Ala His Leu His	
505 510 515 520	
aat taa ctctatcag aaccatcgga ttttctgctg tatttttctg gaaagaaaac	1703
Asn *	
tttctttacc cacttataaa cagaagactg tgacaagaag gccattatt tccatcgctg	1763
aagactctaa atttggaata tcttctaaat aacaatcctg catagtattat taaaaaaat	1823
tagtcgtaaa atttatcctt caaaaatctg catttttaaata aaaccctgac agtgatttct	1883
caagactgta aagatattag tctgagaatg caactctaac agactgctct gggcatcttt	1943
tctctttgcc ttggccaggc ctctcagaat tgagtgagcg tgtgactcca tttgcacagt	2003
gggacagata gtacaactga aataaaaagt ggaggcctct gcaaaaaata aaaaataaaa	2063
aataaattta tccttcaaaa taactcagtt ttttcaatgg gcctatattttt aagaatgaac	2123
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agctgtaaca tgtaaatcag aactacctgg catcttctctg aacaagactt tcaatagggg      180
ccagt      atg ctt cgc ttc atc cag aag ttt tct caa gca tct tca aag      227
           Met Leu Arg Phe Ile Gln Lys Phe Ser Gln Ala Ser Ser Lys
           1             5             10

ata ctg aag tac tct ttc cca gtg gga cta aga acc agc aga aca gat      275
Ile Leu Lys Tyr Ser Phe Pro Val Gly Leu Arg Thr Ser Arg Thr Asp
   15             20             25             30

ata ctt tct ctc aag atg tct ctc cag caa aac ttt tcc cca tgt cca      323
Ile Leu Ser Leu Lys Met Ser Leu Gln Gln Asn Phe Ser Pro Cys Pro
           35             40             45

agg cct tgg ctt tcc tca tca ttt cca gcg tat atg agc aag aca cag      371
Arg Pro Trp Leu Ser Ser Ser Phe Pro Ala Tyr Met Ser Lys Thr Gln
           50             55             60

tgc tat cat aca tcc ccc tgc agc ttt aaa aag cag cag aag caa gca      419
Cys Tyr His Thr Ser Pro Cys Ser Phe Lys Lys Gln Gln Lys Gln Ala
           65             70             75

ctt cta gcc aga ccc tca agc acc atc act tac cta act gac agc cca      467
Leu Leu Ala Arg Pro Ser Ser Thr Ile Thr Tyr Leu Thr Asp Ser Pro
           80             85             90

aag cca gca tta tgt gta act ctg gca gga cta atc ccc ttc gtt gct      515
Lys Pro Ala Leu Cys Val Thr Leu Ala Gly Leu Ile Pro Phe Val Ala
           95             100            105            110

cca cca ctg gtc atg ctg atg aca aaa act tat att ccc ata tta gct      563
Pro Pro Leu Val Met Leu Met Thr Lys Thr Tyr Ile Pro Ile Leu Ala
           115            120            125

ttt act cag atg gct tat gga gcc agt ttc cta tct ttc ttg ggt ggg      611
Phe Thr Gln Met Ala Tyr Gly Ala Ser Phe Leu Ser Phe Leu Gly Gly
           130            135            140

atc aga tgg ggt ttt gct cta cca gaa ggt agt cca gcc aaa cca gac      659

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Ile Arg Trp Gly Phe Ala Leu Pro Glu Gly Ser Pro Ala Lys Pro Asp	
145 150 155	
tac ctt aat tta gct agc agt gca gct cct ctt ttc ttt tca tgg ttt	707
Tyr Leu Asn Leu Ala Ser Ser Ala Ala Pro Leu Phe Phe Ser Trp Phe	
160 165 170	
gcc ttc ctt att tct gaa aga ctt agt gaa gcc ata gtc aca gta ata	755
Ala Phe Leu Ile Ser Glu Arg Leu Ser Glu Ala Ile Val Thr Val Ile	
175 180 185 190	
atg ggt atg gga gta gca ttc cac ctt gaa ctt ttt ctc tta cca cat	803
Met Gly Met Gly Val Ala Phe His Leu Glu Leu Phe Leu Leu Pro His	
195 200 205	
tat ccc aac tgg ttt aaa gcc ctg agg ata gta gtc act tta ttg gcc	851
Tyr Pro Asn Trp Phe Lys Ala Leu Arg Ile Val Val Thr Leu Leu Ala	
210 215 220	
act ttt tca ttt ata atc act tta gta gtt aaa agt agt ttt cca gaa	899
Thr Phe Ser Phe Ile Ile Thr Leu Val Val Lys Ser Ser Phe Pro Glu	
225 230 235	
aaa gga cat aag aga cct ggt caa gta taa a aaatataaaa gtctgggaag	950
Lys Gly His Lys Arg Pro Gly Gln Val *	
240 245	
tgaggagcac ctctgccag ctgctgcccc gtctgggaag tgaggagcgc ctctgcctgg	1010
ccgcctgacc atctgggaag tgtgacaagc gcctctgccc ggccgctgtg caaccttcca	1070
cgtgtgaagt gacagccttg tgtgtgatct tttctgtctt cccaagtgtt gcattttcga	1130
cattaaagtt tacttttttag ttaaaagttt aaaaaatata tataaataca ctgtagagan	1190
aacatgtgtn tgccagctac acctttctcn atttctgttt ggcttttttt cccacacca	1250
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gc	1432

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185 190 195 200	
act gcc ttg atc aac gtc tca gcc aat tgt ccc aac cat ttt gag ggt	916
Thr Ala Leu Ile Asn Val Ser Ala Asn Cys Pro Asn His Phe Glu Gly	
205 210 215	
cac tac cag tac aag agc atc cct gtg gag gac aac cac aag gca gac	964
His Tyr Gln Tyr Lys Ser Ile Pro Val Glu Asp Asn His Lys Ala Asp	
220 225 230	
atc agc tcc tgg ttc aac gag gcc att gac ttc ata gac tcc atc aag	1012
Ile Ser Ser Trp Phe Asn Glu Ala Ile Asp Phe Ile Asp Ser Ile Lys	
235 240 245	
aat gct gga gga agg gtg ttt gtc cac tgc cag gca ggc att tcc cgg	1060
Asn Ala Gly Gly Arg Val Phe Val His Cys Gln Ala Gly Ile Ser Arg	
250 255 260	
tca gcc acc atc tgc ctt gct tac ctt atg agg act aat cga gtc aag	1108
Ser Ala Thr Ile Cys Leu Ala Tyr Leu Met Arg Thr Asn Arg Val Lys	
265 270 275 280	
ctg gac gag gcc ttt gag ttt gtg aag cag agg cga agc atc atc tct	1156
Leu Asp Glu Ala Phe Glu Phe Val Lys Gln Arg Arg Ser Ile Ile Ser	
285 290 295	
ccc aac ttc agc ttc atg ggc cag ctg ctg cag ttt gag tcc cag gtg	1204
Pro Asn Phe Ser Phe Met Gly Gln Leu Leu Gln Phe Glu Ser Gln Val	
300 305 310	
ctg gct ccg cac tgt tgc gca gag gct ggg agc ccc gcc atg gct gtg	1252
Leu Ala Pro His Cys Ser Ala Glu Ala Gly Ser Pro Ala Met Ala Val	
315 320 325	
ctc gac cga ggc acc tcc acc acc acc gtg ttc aac ttc ccc gtc tcc	1300
Leu Asp Arg Gly Thr Ser Thr Thr Val Phe Asn Phe Pro Val Ser	
330 335 340	
atc cct gtc cac tcc acg aac agt gcg ctg agc tac ctt cag agc ccc	1348
Ile Pro Val His Ser Thr Asn Ser Ala Leu Ser Tyr Leu Gln Ser Pro	
345 350 355 360	
att acg acc tct ccc agc tgc tga aaggccacgg gaggtgaggg tcttcacatc	1402
Ile Thr Thr Ser Pro Ser Cys *	
365	
ccattggggac tccatgctcc ttgagaggag aaatgcaata actctgggag gggctcgaga	1462
gggctgggtcc ttatttatatt aacttcaccc gagttcctct gggtttctaa gcagttatgg	1522
tgatgactta gcgtcaagac atttgctgaa ctgagcatat tcgggaccaa tatatagtgg	1582
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tttctttttg ctgcgccctg ttttttgtag aatctcttca tgcttgacat acctaccagt	1702

attattcccg acgacacata tacatatgag aatatacctt atttattttt gtgtaggtgt 1762
 ctgccttcac aaatgtcatt gtctactcct agaagaacca aatacctcaa tttttgtttt 1822
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 aataccagtg ttgggttttt ttttagttgc caacagttgt atgtttgctg attatttatg 1942
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 cattatgatg tgtttatgtt cacagaaatt tttgtaattt ctctatggta acaacttttt 180
 atgccttaag agtgtctctg aggcaggatt ctaagagatt ctctttgact caatcccaga 240
 tagaggataa atctcctggc aaagcccaga atg acc aca gcc ctg gaa cct 291
 Met Thr Thr Ala Leu Glu Pro
 1 5
 gag gac caa aaa gga ctt ctg ata att aag gca gag gac cat tac tgg 339
 Glu Asp Gln Lys Gly Leu Leu Ile Ile Lys Ala Glu Asp His Tyr Trp
 10 15 20
 gga cag gat tcc agc tca caa aag tgc agt cct cac agg agg gaa ctc 387
 Gly Gln Asp Ser Ser Ser Gln Lys Cys Ser Pro His Arg Arg Glu Leu
 25 30 35
 tat aga caa cac ttc agg aag ctc tgc tat cag gat gca cct gga ccc 435
 Tyr Arg Gln His Phe Arg Lys Leu Cys Tyr Gln Asp Ala Pro Gly Pro
 40 45 50 55
 cgt gaa gct ctt acc cag ctg tgg gag ctc tgc cgt cag tgg ctg agg 483
 Arg Glu Ala Leu Thr Gln Leu Trp Glu Leu Cys Arg Gln Trp Leu Arg
 60 65 70
 cca gaa tgc cac acc aag gag cag att tta gac ctg ctg gtg cta gaa 531
 Pro Glu Cys His Thr Lys Glu Gln Ile Leu Asp Leu Leu Val Leu Glu
 75 80 85

cag ttc ctg agc att ctt cct aaa gac ctg caa gca tgg gtg cgt gca Gln Phe Leu Ser Ile Leu Pro Lys Asp Leu Gln Ala Trp Val Arg Ala 90 95 100	579
cac cat cca gag act gga gag gag gca gtg acg gta ctg gag gat ctg His His Pro Glu Thr Gly Glu Glu Ala Val Thr Val Leu Glu Asp Leu 105 110 115	627
gag aga gag ctt gat gaa cct gga aag cag gtc cca ggc aat tca gaa Glu Arg Glu Leu Asp Glu Pro Gly Lys Gln Val Pro Gly Asn Ser Glu 120 125 130 135	675
aga cgg gac ata ctc atg gac aag ttg gcc ccc ttg gga agg cca tat Arg Arg Asp Ile Leu Met Asp Lys Leu Ala Pro Leu Gly Arg Pro Tyr 140 145 150	723
gaa tca ctg act gtc cag ctc cat ccc aaa aag acc cag ctg gag cag Glu Ser Leu Thr Val Gln Leu His Pro Lys Lys Thr Gln Leu Glu Gln 155 160 165	771
gaa gct ggg aaa cca caa agg aat ggt gat aaa act agg act aag aat Glu Ala Gly Lys Pro Gln Arg Asn Gly Asp Lys Thr Arg Thr Lys Asn 170 175 180	819
gaa gag ttg ttc cag aag gaa gat atg ccc aaa gac aag gaa ttc ctt Glu Glu Leu Phe Gln Lys Glu Asp Met Pro Lys Asp Lys Glu Phe Leu 185 190 195	867
ggg gag ata aat gac aga ctg aac aaa gat act cct cag cat cct aag Gly Glu Ile Asn Asp Arg Leu Asn Lys Asp Thr Pro Gln His Pro Lys 200 205 210 215	915
tcc aaa gat att att gaa aat gag ggc aga tca gaa tgg caa cag agg Ser Lys Asp Ile Ile Glu Asn Glu Gly Arg Ser Glu Trp Gln Gln Arg 220 225 230	963
gaa aga aga cga tat aaa tgt gat gaa tgt ggg aaa agt ttc agt cat Glu Arg Arg Arg Tyr Lys Cys Asp Glu Cys Gly Lys Ser Phe Ser His 235 240 245	1011
agc tca gac ctt agt aaa cac agg aga act cac acg gga gag aag ccc Ser Ser Asp Leu Ser Lys His Arg Arg Thr His Thr Gly Glu Lys Pro 250 255 260	1059
tat aaa tgt gat gag tgt gga aaa gcc ttc att cag cgc tca cat ctc Tyr Lys Cys Asp Glu Cys Gly Lys Ala Phe Ile Gln Arg Ser His Leu 265 270 275	1107
att gga cat cat aga gta cac acg gga gta aaa ccc tat aaa tgt aaa Ile Gly His His Arg Val His Thr Gly Val Lys Pro Tyr Lys Cys Lys 280 285 290 295	1155
gaa tgt ggg aaa gac ttc agt ggg cgc aca ggt ctt att cag cat cag Glu Cys Gly Lys Asp Phe Ser Gly Arg Thr Gly Leu Ile Gln His Gln 300 305 310	1203

gaa aaa ctg aag gtg caa gtt act gat acc aac cga agg ttt caa gat	535
Glu Lys Leu Lys Val Gln Val Thr Asp Thr Asn Arg Arg Phe Gln Asp	
70 75 80	
gct gga aaa gag gtg ata gtc cac aca gaa gat atc att cga tgt aga	583
Ala Gly Lys Glu Val Ile Val His Thr Glu Asp Ile Ile Arg Cys Arg	
85 90 95	
att cag cag aga aat att aca act gta gta gaa aaa ttg cag tta tgc	631
Ile Gln Gln Arg Asn Ile Thr Thr Val Val Glu Lys Leu Gln Leu Cys	
100 105 110	
ctt cct gtg cta gaa atg tac agt aag ctg aaa gaa cag atg agt gcc	679
Leu Pro Val Leu Glu Met Tyr Ser Lys Leu Lys Glu Gln Met Ser Ala	
115 120 125 130	
aaa agg tac tat tct gcc cta aaa act atg gaa caa tta gag aat gtg	727
Lys Arg Tyr Tyr Ser Ala Leu Lys Thr Met Glu Gln Leu Glu Asn Val	
135 140 145	
tac ttt ccc tgg gtt agt caa tac cgg ttt tgt cag ctc atg ata gaa	775
Tyr Phe Pro Trp Val Ser Gln Tyr Arg Phe Cys Gln Leu Met Ile Glu	
150 155 160	
aat ctt ccc aaa ctc cgt gag gat att aaa gaa atc tcc atg tct gat	823
Asn Leu Pro Lys Leu Arg Glu Asp Ile Lys Glu Ile Ser Met Ser Asp	
165 170 175	
ctc aaa gac ttt ttg gaa agt att cga aaa cat tct gac aaa ata ggt	871
Leu Lys Asp Phe Leu Glu Ser Ile Arg Lys His Ser Asp Lys Ile Gly	
180 185 190	
gaa aca gca atg aaa cag gca cag cat cag aaa acc ttc agt gtt tct	919
Glu Thr Ala Met Lys Gln Ala Gln His Gln Lys Thr Phe Ser Val Ser	
195 200 205 210	
ctg cag aaa caa aat aaa atg aaa ttt ggg aaa aat atg tat ata aat	967
Leu Gln Lys Gln Asn Lys Met Lys Phe Gly Lys Asn Met Tyr Ile Asn	
215 220 225	
cgt gat aga att cca gag gaa agg aat gaa act gta ttg aaa cat tca	1015
Arg Asp Arg Ile Pro Glu Glu Arg Asn Glu Thr Val Leu Lys His Ser	
230 235 240	
ctt gaa gaa gag gat gag aat gaa gaa gag atc tta act gtt cag gat	1063
Leu Glu Glu Glu Asp Glu Asn Glu Glu Glu Ile Leu Thr Val Gln Asp	
245 250 255	
ctt gtt gat ttt tcc cct gtt tat cga tgt ttg cac att tat tct gtt	1111
Leu Val Asp Phe Ser Pro Val Tyr Arg Cys Leu His Ile Tyr Ser Val	
260 265 270	
ttg ggt gac gag gaa aca ttt gaa aac tat tat cga aaa caa aga aag	1159
Leu Gly Asp Glu Glu Thr Phe Glu Asn Tyr Tyr Arg Lys Gln Arg Lys	
275 280 285 290	
aaa caa gca aga ctg gta ttg caa ccc cag tcg aat atg cat gaa aca	1207

Lys	Gln	Ala	Arg	Leu	Val	Leu	Gln	Pro	Gln	Ser	Asn	Met	His	Glu	Thr		
				295					300					305			
gtt	gat	ggc	tat	aga	aga	tat	ttc	act	caa	att	gta	ggg	ttc	ttt	gtg	1255	
Val	Asp	Gly	Tyr	Arg	Arg	Tyr	Phe	Thr	Gln	Ile	Val	Gly	Phe	Phe	Val		
			310					315					320				
gta	gaa	gat	cac	att	tta	cat	gtg	acc	caa	gga	tta	gta	acc	agg	gca	1303	
Val	Glu	Asp	His	Ile	Leu	His	Val	Thr	Gln	Gly	Leu	Val	Thr	Arg	Ala		
			325				330					335					
tac	act	gat	gaa	ctt	tgg	aac	atg	gcc	ctc	tca	aag	ata	att	gct	gtc	1351	
Tyr	Thr	Asp	Glu	Leu	Trp	Asn	Met	Ala	Leu	Ser	Lys	Ile	Ile	Ala	Val		
	340					345					350						
ctt	aga	gct	cat	tca	tcc	tat	tgc	act	gat	cct	gat	ctt	gtt	ctg	gag	1399	
Leu	Arg	Ala	His	Ser	Ser	Tyr	Cys	Thr	Asp	Pro	Asp	Leu	Val	Leu	Glu		
355					360					365				370			
ctg	aag	aat	ctt	act	gta	ata	ttt	gca	gat	act	tta	cag	ggt	tat	ggt	1447	
Leu	Lys	Asn	Leu	Thr	Val	Ile	Phe	Ala	Asp	Thr	Leu	Gln	Gly	Tyr	Gly		
			375					380						385			
ttt	cca	gtg	aac	cga	ctt	ttt	gac	ctt	tta	ttt	gaa	ata	aga	gac	caa	1495	
Phe	Pro	Val	Asn	Arg	Leu	Phe	Asp	Leu	Leu	Phe	Glu	Ile	Arg	Asp	Gln		
			390				395					400					
tac	aat	gaa	aca	ctg	ctt	aag	aaa	tgg	gct	gga	gtt	ttc	agg	gac	att	1543	
Tyr	Asn	Glu	Thr	Leu	Leu	Lys	Lys	Trp	Ala	Gly	Val	Phe	Arg	Asp	Ile		
	405					410						415					
ttt	gaa	gaa	gat	aat	tac	agc	ccc	atc	cct	gtt	gtc	aat	gaa	gaa	gaa	1591	
Phe	Glu	Glu	Asp	Asn	Tyr	Ser	Pro	Ile	Pro	Val	Val	Asn	Glu	Glu	Glu		
	420				425					430							
tat	aaa	att	gtc	atc	agc	aaa	ttt	ccc	ttt	caa	gat	cca	gac	ctt	gaa	1639	
Tyr	Lys	Ile	Val	Ile	Ser	Lys	Phe	Pro	Phe	Gln	Asp	Pro	Asp	Leu	Glu		
435				440					445					450			
aag	cag	tct	ttc	cca	aag	aaa	ttc	ccc	atg	tct	cag	tca	gtg	cct	cat	1687	
Lys	Gln	Ser	Phe	Pro	Lys	Lys	Phe	Pro	Met	Ser	Gln	Ser	Val	Pro	His		
			455					460					465				
att	tac	att	caa	gtt	aaa	gaa	ttt	att	tat	gcc	agc	ctt	aaa	ttt	tca	1735	
Ile	Tyr	Ile	Gln	Val	Lys	Glu	Phe	Ile	Tyr	Ala	Ser	Leu	Lys	Phe	Ser		
			470					475					480				
gag	tca	cta	cac	cgg	agc	tca	aca	gaa	ata	gac	gat	atg	ctt	aga	aaa	1783	
Glu	Ser	Leu	His	Arg	Ser	Ser	Thr	Glu	Ile	Asp	Asp	Met	Leu	Arg	Lys		
			485				490					495					
tca	aca	aat	ctg	ctg	ctg	acc	aga	act	ttg	agt	agc	tgt	tta	ctg	aac	1831	
Ser	Thr	Asn	Leu	Leu	Leu	Thr	Arg	Thr	Leu	Ser	Ser	Cys	Leu	Leu	Asn		
	500					505					510						
ctt	att	aga	aaa	cct	cat	ata	ggt	ttg	aca	gag	ctg	gta	caa	atc	atc	1879	
Leu	Ile	Arg	Lys	Pro	His	Ile	Gly	Leu	Thr	Glu	Leu	Val	Gln	Ile	Ile		

515	520	525	530	
ata aac aca aca cac ctg gag caa gct tgt aaa tat ctt gag gac ttt				1927
Ile Asn Thr Thr His Leu Glu Gln Ala Cys Lys Tyr Leu Glu Asp Phe	535	540	545	
ata act aac att aca aat att tcc caa gaa act gtt cat act aca aga				1975
Ile Thr Asn Ile Thr Asn Ile Ser Gln Glu Thr Val His Thr Thr Arg	550	555	560	
ctt tat gga ctt tct act ttc aag gat gct cga cat gca gca gaa gga				2023
Leu Tyr Gly Leu Ser Thr Phe Lys Asp Ala Arg His Ala Ala Glu Gly	565	570	575	
gaa ata tat acc aaa ctg aat caa aaa att gat gaa ttt gtt cag ctt				2071
Glu Ile Tyr Thr Lys Leu Asn Gln Lys Ile Asp Glu Phe Val Gln Leu	580	585	590	
gct gat tat gac tgg aca atg tct gag cca gat gga aga gct agt ggt				2119
Ala Asp Tyr Asp Trp Thr Met Ser Glu Pro Asp Gly Arg Ala Ser Gly	595	600	605	610
tat tta atg gac ctt ata aat ttt ttg aga agc atc ttt caa gtg ttt				2167
Tyr Leu Met Asp Leu Ile Asn Phe Leu Arg Ser Ile Phe Gln Val Phe	615	620	625	
act cat ttg cct ggg aaa gtt gct cag aca gct tgc atg tca gcc tgc				2215
Thr His Leu Pro Gly Lys Val Ala Gln Thr Ala Cys Met Ser Ala Cys	630	635	640	
cag cat ctg tca aca tcc tta atg cag atg cta ctg gac agt gag tta				2263
Gln His Leu Ser Thr Ser Leu Met Gln Met Leu Leu Asp Ser Glu Leu	645	650	655	
aaa caa ata agc atg gga gct gtt cag cag ttt aac tta gat gtc ata				2311
Lys Gln Ile Ser Met Gly Ala Val Gln Gln Phe Asn Leu Asp Val Ile	660	665	670	
cag tgt gaa ttg ttt gcc agc tct gag cct gtg cca gga ttc cag ggg				2359
Gln Cys Glu Leu Phe Ala Ser Ser Glu Pro Val Pro Gly Phe Gln Gly	675	680	685	690
gat acc ctg cag cta gca ttc att gac ctc aga caa ctc ctt gac ctg				2407
Asp Thr Leu Gln Leu Ala Phe Ile Asp Leu Arg Gln Leu Leu Asp Leu	695	700	705	
ttt atg gtt tgg gat tgg tct act tac cta gct gat tat ggg cag cca				2455
Phe Met Val Trp Asp Trp Ser Thr Tyr Leu Ala Asp Tyr Gly Gln Pro	710	715	720	
gct tct aag tac ctt cgg gtg aat cca aac aca gcc ctt act ctt ttg				2503
Ala Ser Lys Tyr Leu Arg Val Asn Pro Asn Thr Ala Leu Thr Leu Leu	725	730	735	
gag aag atg aag gat act agc aaa aag aac aat ata ttt gct cag ttc				2551
Glu Lys Met Lys Asp Thr Ser Lys Lys Asn Asn Ile Phe Ala Gln Phe	740	745	750	

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Lys Lys Glu Ala Pro Ala Pro Pro Lys Ala Glu Ala Lys Ala Lys Ala
10 15 20

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Lys Gln Asp Pro His Val Thr His Leu Pro Ala Ala Gln Asp Thr Val
40 45 50

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Thr Pro Glu Ala Ala Gln Ile Ser Leu Glu Glu His Pro Gln Glu Lys
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70

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gatcaaacag gctgtgaaga agtttgtgac attgatgtgg ccaaagtcaa cactctgatt 424

cagtctgatg gagagaggaa ggcatatggt cgactggctc ctgactacga tgcttttggtt 484

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Met Tyr Ser Gly Ala Gly Pro Ala
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Leu Ala Pro Pro Ala Pro Pro Pro Ile Gln Gly Tyr Ala Phe Lys	
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Pro Pro Pro Arg Pro Asp Phe Gly Thr Ser Gly Arg Thr Ile Lys Leu	
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Gln Ala Asn Phe Phe Glu Met Asp Ile Pro Lys Ile Asp Ile Tyr His	
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Tyr Glu Leu Asp Ile Lys Pro Glu Lys Cys Pro Arg Arg Val Asn Arg	
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Glu Ile Val Glu His Met Val Gln His Phe Lys Thr Gln Ile Phe Gly	
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Pro Leu Pro Ile Gly Arg Asp Lys Val Glu Leu Glu Val Thr Leu Pro	
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Gly Phe His Gln Ser Val Arg Pro Ser Leu Trp Lys Met Met Leu Asn	
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Ile Asp Val Ser Ala Thr Ala Phe Tyr Lys Ala Gln Pro Val Ile Glu	
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Phe Val Cys Glu Val Leu Asp Phe Lys Ser Ile Glu Glu Gln Gln Lys	
235 240 245	
cct ctg aca gat tcc caa agg gta aag ttt acc aaa gaa att aaa ggt	941
Pro Leu Thr Asp Ser Gln Arg Val Lys Phe Thr Lys Glu Ile Lys Gly	
250 255 260	
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Leu Lys Val Glu Ile Thr His Cys Gly Gln Met Lys Arg Lys Tyr Arg	
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gag cta ggt tat aag gct cag cca ttt gac ctc cag gaa gca gtg gaa      797
Glu Leu Gly Tyr Lys Ala Gln Pro Phe Asp Leu Gln Glu Ala Val Glu
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tgg ttt aaa gcc cat ggt cat ggc aga agt tct gga agt cgt gac tcg      845
Trp Phe Lys Ala His Gly His Gly Arg Ser Ser Gly Ser Arg Asp Ser
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gag tgt ttt gtt tgg gat ggg cta ttg gtc ttc ctc ctg att ata gca      893
Glu Cys Phe Val Trp Asp Gly Leu Leu Val Phe Leu Leu Ile Ile Ala
                                   70                               75                               80                               85

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Val Leu Met Trp Leu Pro Ser Ser Val Ile Leu Ser Leu *
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Ala	Thr	Cys	Ile	Ile	Ser	Gly	Asn	Thr	Val	Ile	Trp	Asp	Asn	Lys	Thr		
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Pro	Val	Cys	Asp	Ser	Glu	Leu	Lys	Tyr	Ala	Phe	Leu	Phe	Leu	Leu	Pro		
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Trp Gln Ser Phe Cys Thr Gln Lys Asn Phe Ala Trp Lys Glu Glu Tyr	
155 160 165 170	
gat aca cga cag gct tca aac cgc tgg gaa aaa cga gcc atg gaa aaa	580
Asp Thr Arg Gln Ala Ser Asn Arg Trp Glu Lys Arg Ala Met Glu Lys	
175 180 185	
gaa aac aaa aag att cgg gac aaa gca agg aaa gag aag aat gag ctt	628
Glu Asn Lys Lys Ile Arg Asp Lys Ala Arg Lys Glu Lys Asn Glu Leu	
190 195 200	
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Val Arg Gln Leu Val Ala Phe Ile Arg Lys Arg Asp Lys Arg Val Gln	
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Lys Gln Lys Leu Ser Lys Lys Gln Lys Thr Gln Glu Thr Val Asn Gln	
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His Arg Met Tyr Leu Ala Lys Ile His Ile Cys Leu Gln Leu Thr Phe	
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Arg Trp Leu Gly Glu Lys Ser Val Cys Arg Glu Arg Glu Glu Met Glu	
415 420 425	
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Arg Ala Ser Thr Asn Val Pro Lys Cys Cys Leu Lys Thr Asp Arg Ile	
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Ala Glu Gln Phe Lys Leu Ile Gln Ala Ala Tyr Asp Val Leu Ser Asp	
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tat ttc acc gtt acc tgt tat tct ggt tat gga gat gat gaa aag gga	340
Tyr Phe Thr Val Thr Cys Tyr Ser Gly Tyr Gly Asp Asp Glu Lys Gly	
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Phe Tyr Thr Val Tyr Arg Asn Val Phe Glu Met Ile Ala Lys Glu Glu	
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Leu Glu Ser Val Leu Glu Glu Glu Val Asp Asp Phe Pro Thr Phe Gly	
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gac tcc cag agt gac tat gat acg gta gtc cat cct ttc tac gct tat	484
Asp Ser Gln Ser Asp Tyr Asp Thr Val Val His Pro Phe Tyr Ala Tyr	
140 145 150	
tgg cag agt ttc tgc act caa aag aat ttt gca tgg aag gaa gaa tat	532
Trp Gln Ser Phe Cys Thr Gln Lys Asn Phe Ala Trp Lys Glu Glu Tyr	
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Asp Thr Arg Gln Ala Ser Asn Arg Trp Glu Lys Arg Ala Met Glu Lys	
175 180 185	
gaa aac aaa aag att cgg gac aaa gca agg aaa gag aag aat gag ctt	628
Glu Asn Lys Lys Ile Arg Asp Lys Ala Arg Lys Glu Lys Asn Glu Leu	
190 195 200	
gtc cgt cag ctg gta gct ttc att cgt aaa aga gat aaa aga gtg cag	676
Val Arg Gln Leu Val Ala Phe Ile Arg Lys Arg Asp Lys Arg Val Gln	
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Ala His Arg Lys Leu Val Glu Glu Gln Asn Ala Glu Lys Ala Arg Lys	

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aat cac gag aag tca aag aag cat cgg gaa atg gtg gcc ttg cta aaa Asn His Glu Lys Ser Lys Lys His Arg Glu Met Val Ala Leu Leu Lys 335 340 345			1060
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Gly Lys Lys Thr Lys Asp Met Lys Lys Pro Val Arg Val Pro Ala Glu	
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Pro Gln Thr Met Ser Val Leu Ile Ser Cys Thr Thr Cys His Ser Glu	
475 480 485 490	
ttt cca tct cgg aat aaa ctt ttt gac cat cta aag gcc aca ggt cat	1540
Phe Pro Ser Arg Asn Lys Leu Phe Asp His Leu Lys Ala Thr Gly His	
495 500 505	
gca aga gca cct tca tca tcg tct tta aac agc gca aca agt agt caa	1588
Ala Arg Ala Pro Ser Ser Ser Ser Leu Asn Ser Ala Thr Ser Ser Gln	
510 515 520	
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Ser Lys Lys Glu Lys Arg Lys Asn Arg *	
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Glu Leu Phe Ser Glu Ser Arg Arg Leu Ala Leu Glu Glu Leu Val Ala
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cgt ttc ctg aac ccc gat gag gtg cac gcc att ctg cgc gcg gcg gag 245
Arg Phe Leu Asn Pro Asp Glu Val His Ala Ile Leu Arg Ala Ala Glu
60 65 70

agg ccg gga gag gag ggc gcg gcg gcg gcg gcg gcc gag gac tcg 293
Arg Pro Gly Glu Glu Gly Ala Ala Ala Ala Ala Ala Ala Glu Asp Ser
75 80 85

ttc ggc tcc tcg cac gac tgc tct tcg ggc acc tac ttc ccc gag cag 341
Phe Gly Ser Ser His Asp Cys Ser Ser Gly Thr Tyr Phe Pro Glu Gln
90 95 100 105

tcg gac ctg gag cca ccg ctg ttg gag ctt ggc tgg ccc gcc ttc tac 389
Ser Asp Leu Glu Pro Pro Leu Leu Glu Leu Gly Trp Pro Ala Phe Tyr
110 115 120

cag ggc gcc tac cgc ggc gcc acg cgt gtc gag acg cac ttc cag ccc 437
Gln Gly Ala Tyr Arg Gly Ala Thr Arg Val Glu Thr His Phe Gln Pro
125 130 135

cgc ggc gct ggc gaa ggt ggc ccc tac ggc tgc aag gac gct ctg cgc 485
 Arg Gly Ala Gly Glu Gly Gly Pro Tyr Gly Cys Lys Asp Ala Leu Arg
 140 145 150

cag cag ctc cgc tcg gcg cga gag gtg att gca gtg gtc atg gac gtg 533
Gln Gln Leu Arg Ser Ala Arg Glu Val Ile Ala Val Val Met Asp Val
155 160 165

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Phe Thr Asp Ile Asp Ile Phe Arg Asp Leu Gln Glu Ile Cys Arg Lys
170 175 180 185

cag gga gtt gct gtg tat atc ctt ctg gac cag gct ctc ctc tct caa 629
Gln Gly Val Ala Val Tyr Ile Leu Leu Asp Gln Ala Leu Leu Ser Gln
190 195 200

ttt ctg gat atg tgc atg gat ctg aaa gtt cat cct gaa cag gaa aag Phe Leu Asp Met Cys Met Asp Leu Lys Val His Pro Glu Gln Glu Lys 205 210 215	677
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acc agg ata gca agc tct caa acc acg att tgg tcc aga tcg acc act	1349

Thr Arg Ile Ala Ser Ser Gln Thr Thr Ile Trp Ser Arg Ser Thr Thr	
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Thr Gln Thr Asp Met Asp Glu Asn Ile Leu Phe Pro Arg Gly Thr Gln	
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Gly Tyr Pro Lys Tyr Leu Gly Thr Pro His Leu Glu Leu Tyr Leu Ser	
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Asp Ser Leu Arg Asn Leu Asn Lys Glu Arg Gln Phe His Phe Ala Gly	
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Leu Val Ile Asn Glu Ser Ile Glu Ser Ile Lys Trp Met Ile Glu Glu			
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Ser Leu Leu Glu Ser Gln Ser Thr Ser Leu Arg Gly Ser Tyr Asn Ser			
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						Met
						1
aag gcc ttt ggt cct cca cat gag ggc ccc ctc caa gga ctc gtg gcc	166					
Lys Ala Phe Gly Pro Pro His Glu Gly Pro Leu Gln Gly Leu Val Ala						
5 10 15						
tcc cgc att gag act tat ggg ggc cgg cat cga gcc tct gct cag agc	214					
Ser Arg Ile Glu Thr Tyr Gly Gly Arg His Arg Ala Ser Ala Gln Ser						
20 25 30						
act act ggc aga ctc tat ccc cga gga tac cct gtg ctg gat ccc agt	262					
Thr Thr Gly Arg Leu Tyr Pro Arg Gly Tyr Pro Val Leu Asp Pro Ser						
35 40 45						
cgc cga cgc ctc cag cag tat gtc ccc ttt gcc agg ggt tct ggc cag	310					
Arg Arg Arg Leu Gln Gln Tyr Val Pro Phe Ala Arg Gly Ser Gly Gln						
50 55 60 65						
gcc cga ggc ctg tca ccc atg aga ctg cga gat cca gag ccc gag aag	358					
Ala Arg Gly Leu Ser Pro Met Arg Leu Arg Asp Pro Glu Pro Glu Lys						
70 75 80						
agg cac ggg ggc cat gtg ggg gct ggc ctg ctt cac tcc ccc aaa ctc	406					
Arg His Gly Gly His Val Gly Ala Gly Leu Leu His Ser Pro Lys Leu						
85 90 95						
aag gaa ctc acc aag gcc cat gag ctg gag gtg agg ctg cac act ttc	454					
Lys Glu Leu Thr Lys Ala His Glu Leu Glu Val Arg Leu His Thr Phe						
100 105 110						
agc atg ttt ggg atg ccc cgg ctg ccc cct gag gac cgg cgg cac tgg	502					
Ser Met Phe Gly Met Pro Arg Leu Pro Pro Glu Asp Arg Arg His Trp						
115 120 125						
gag ata gga gag ggt ggc gac agt ggc ctg acc atc gag aag tcc tgg	550					
Glu Ile Gly Glu Gly Gly Asp Ser Gly Leu Thr Ile Glu Lys Ser Trp						
130 135 140 145						
agg gag ctg gtg cct ggg cac aag gag atg agc cag gag ctc tgc cac	598					
Arg Glu Leu Val Pro Gly His Lys Glu Met Ser Gln Glu Leu Cys His						
150 155 160						

caa	cag	gag	gcc	ctg	tgg	gag	ctc	ctg	acc	acc	gag	ctg	atc	tac	gtg	646
Gln	Gln	Glu	Ala	Leu	Trp	Glu	Leu	Leu	Thr	Thr	Glu	Leu	Ile	Tyr	Val	
			165					170					175			
aga	aag	ctc	aag	atc	atg	act	gat	ctg	cta	gcc	gcc	ggc	ctg	ctg	aac	694
Arg	Lys	Leu	Lys	Ile	Met	Thr	Asp	Leu	Leu	Ala	Ala	Gly	Leu	Leu	Asn	
			180				185					190				
ctg	cag	cga	gtg	gga	ctg	ctg	atg	gaa	gtg	tca	gct	gag	acc	ctg	ttt	742
Leu	Gln	Arg	Val	Gly	Leu	Leu	Met	Glu	Val	Ser	Ala	Glu	Thr	Leu	Phe	
			195			200					205					
gga	aat	gtc	ccc	agc	ctg	att	cga	acc	cac	cgg	agc	ttt	tgg	gat	gag	790
Gly	Asn	Val	Pro	Ser	Leu	Ile	Arg	Thr	His	Arg	Ser	Phe	Trp	Asp	Glu	
210					215					220					225	
gtg	ctg	ggg	ccc	acc	ctg	gag	gag	act	cgg	gcc	tcg	ggc	cag	cct	ctg	838
Val	Leu	Gly	Pro	Thr	Leu	Glu	Glu	Thr	Arg	Ala	Ser	Gly	Gln	Pro	Leu	
				230					235					240		
gac	ccc	att	ggc	ctg	caa	agt	ggc	ttc	ctg	acg	ttt	ggc	cag	cgg	ttc	886
Asp	Pro	Ile	Gly	Leu	Gln	Ser	Gly	Phe	Leu	Thr	Phe	Gly	Gln	Arg	Phe	
			245					250				255				
cac	ccc	tat	gtc	cag	tac	tgc	ctc	cga	gtg	aag	cag	acc	atg	gct	tac	934
His	Pro	Tyr	Val	Gln	Tyr	Cys	Leu	Arg	Val	Lys	Gln	Thr	Met	Ala	Tyr	
			260				265					270				
gcc	cga	gaa	cag	caa	gaa	act	aac	cct	ctc	ttc	cat	gcc	ttc	gtg	cag	982
Ala	Arg	Glu	Gln	Gln	Glu	Thr	Asn	Pro	Leu	Phe	His	Ala	Phe	Val	Gln	
			275				280				285					
tgg	tgt	gag	aag	cac	aag	cgc	tct	ggg	agg	cag	atg	ctc	tgt	gac	ttg	1030
Trp	Cys	Glu	Lys	His	Lys	Arg	Ser	Gly	Arg	Gln	Met	Leu	Cys	Asp	Leu	
290					295					300					305	
ctt	atc	aag	ccc	cac	cag	cgc	atc	acc	aag	tac	cca	ctg	ctg	ctc	cat	1078
Leu	Ile	Lys	Pro	His	Gln	Arg	Ile	Thr	Lys	Tyr	Pro	Leu	Leu	Leu	His	
				310					315					320		
gct	gtg	ctc	aag	agg	agc	ccc	gag	gca	cga	gcc	caa	gag	gcc	ctg	aat	1126
Ala	Val	Leu	Lys	Arg	Ser	Pro	Glu	Ala	Arg	Ala	Gln	Glu	Ala	Leu	Asn	
			325					330				335				
gcc	atg	att	gaa	gcc	gtg	gag	tca	ttc	ctg	cga	cat	atc	aat	ggg	cag	1174
Ala	Met	Ile	Glu	Ala	Val	Glu	Ser	Phe	Leu	Arg	His	Ile	Asn	Gly	Gln	
			340				345					350				
gtc	cgc	cag	ggc	gaa	gag	caa	gag	agc	ttg	gcg	gct	gca	gca	caa	cgc	1222
Val	Arg	Gln	Gly	Glu	Glu	Gln	Glu	Ser	Leu	Ala	Ala	Ala	Ala	Gln	Arg	
			355			360					365					
atc	ggg	ccc	tac	gag	gtg	ctg	gag	cca	ccc							

Gln Arg Ala Leu Arg Arg Asp Pro Arg Leu Thr Phe Ser Thr Leu Glu	
610 615 620 625	
ctc cgg gac atc cct ctg cgt ccc cac cct ccc gac ccc caa gct cct	2038
Leu Arg Asp Ile Pro Leu Arg Pro His Pro Pro Asp Pro Gln Ala Pro	
630 635 640	
caa cgc cga agc gcc ccc gaa ctg ccg gaa gga atc cta aaa gga ggc	2086
Gln Arg Arg Ser Ala Pro Glu Leu Pro Glu Gly Ile Leu Lys Gly Gly	
645 650 655	
agt ctt ccc cag gaa gac cca cca acc tgg tct gag gaa gaa gat ggg	2134
Ser Leu Pro Gln Glu Asp Pro Pro Thr Trp Ser Glu Glu Glu Asp Gly	
660 665 670	
gcc tcc gag cga ggg aat gtg gtg gtg gaa aca ctc cac agg gcc cgg	2182
Ala Ser Glu Arg Gly Asn Val Val Val Glu Thr Leu His Arg Ala Arg	
675 680 685	
ctt cgg ggc cag ctt ccc tcc tcc cca acc cat gct gac tct gcc ggg	2230
Leu Arg Gly Gln Leu Pro Ser Ser Pro Thr His Ala Asp Ser Ala Gly	
690 695 700 705	
gaa agc ccc tgg gag tcc tca ggg gag gag gaa gaa gag ggg cct ctg	2278
Glu Ser Pro Trp Glu Ser Ser Gly Glu Glu Glu Glu Glu Gly Pro Leu	
710 715 720	
ttc ctg aaa gct ggc cac aca tcc ctg cgc cca atg cgg gct gag gac	2326
Phe Leu Lys Ala Gly His Thr Ser Leu Arg Pro Met Arg Ala Glu Asp	
725 730 735	
atg ctc aga gag atc cgg gag gag ctg gcc agc caa agg att gag ggg	2374
Met Leu Arg Glu Ile Arg Glu Glu Leu Ala Ser Gln Arg Ile Glu Gly	
740 745 750	
gcc gag gag ccc cgg gac agc agg cca cgg aag ctg act cgg gcc cag	2422
Ala Glu Glu Pro Arg Asp Ser Arg Pro Arg Lys Leu Thr Arg Ala Gln	
755 760 765	
ctg cag agg atg cgg ggg ccc cac atc att cag ctg gac acc cct ctg	2470
Leu Gln Arg Met Arg Gly Pro His Ile Ile Gln Leu Asp Thr Pro Leu	
770 775 780 785	
tcc gca tca gag gta tga ggaatg cagaggacct ttggcatgca tctctcccag	2524
Ser Ala Ser Glu Val *	
790	
aggagatctc tccccagtag tgctggtcac cctccggcat ctgtgactct acctcaagga	2584
ccacatttcc caaaggaagc ctggcccagg caccctgcct cctgctctgt ttgggggatca	2644
agaactgtaa atttatgtat cataggtgca cctgagcccc acagaaagtt gtgcataaaa	2704
atgactgccc tggctgggca tggctgcctg taatcccagc actttggggag gctgaggtgg	2764
gaggatccct tgagcccagg agttccagac cagcctgggc aatataggga aaccctgtct	2824

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2860

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<213> Homo sapiens

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<222> (173)..(1561)

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cacgtgcata tgatcaactt tggacttctt ttgagattgc caggcgtttg ca atg	175
	Met
	1
gct gct act gtg aac ttg gaa ctt gat ccc att ttt ttg aaa gca cta	223
Ala Ala Thr Val Asn Leu Glu Leu Asp Pro Ile Phe Leu Lys Ala Leu	
5 10 15	
ggt ttc ttg cat tca aag agt aaa gat tct gct gaa aag cta aaa gca	271
Gly Phe Leu His Ser Lys Ser Lys Asp Ser Ala Glu Lys Leu Lys Ala	
20 25 30	
ctg ctt gat gaa tct ttg gct cgg ggc att gat tcc agt tac cgt cca	319
Leu Leu Asp Glu Ser Leu Ala Arg Gly Ile Asp Ser Ser Tyr Arg Pro	
35 40 45	
tct caa aag gat gtg gag cca ccc aaa att tca agc aca aaa aac att	367
Ser Gln Lys Asp Val Glu Pro Pro Lys Ile Ser Ser Thr Lys Asn Ile	
50 55 60 65	
tcc att aag caa gag ccc aaa ata tca tcc agt ctt cct tct ggt aat	415
Ser Ile Lys Gln Glu Pro Lys Ile Ser Ser Ser Leu Pro Ser Gly Asn	
70 75 80	
aat aat ggc aag gtc ctc aca act gaa aag gta aag aag gaa gct gaa	463
Asn Asn Gly Lys Val Leu Thr Thr Glu Lys Val Lys Lys Glu Ala Glu	
85 90 95	
aag aga cct gct gat aaa atg aaa tca gac atc act gaa gga gtt gat	511
Lys Arg Pro Ala Asp Lys Met Lys Ser Asp Ile Thr Glu Gly Val Asp	
100 105 110	
att cca aag aaa cct aga ttg gag aaa cca gaa aca cag tca tct ccc	559
Ile Pro Lys Lys Pro Arg Leu Glu Lys Pro Glu Thr Gln Ser Ser Pro	
115 120 125	
att act gtc caa agt agc aag gat tta cct atg gct gac ctt tcc agt	607
Ile Thr Val Gln Ser Ser Lys Asp Leu Pro Met Ala Asp Leu Ser Ser	

130	135	140	145	
ttt gag gag acc agt gct gat gat ttt gcc atg gag atg gga ttg gcc				655
Phe Glu Glu Thr Ser Ala Asp Asp Phe Ala Met Glu Met Gly Leu Ala	150	155	160	
tgc gtt gtt tgt agg caa atg atg gtg gca tct ggc aat caa tta gta				703
Cys Val Val Cys Arg Gln Met Met Val Ala Ser Gly Asn Gln Leu Val	165	170	175	
gaa tgt cag gag tgc cat aat ctc tac cac cga gat tgt cat aaa ccc				751
Glu Cys Gln Glu Cys His Asn Leu Tyr His Arg Asp Cys His Lys Pro	180	185	190	
cag gtg aca gac aag gaa gcg aat gac cct cgc ctg gtg tgg tat tgt				799
Gln Val Thr Asp Lys Glu Ala Asn Asp Pro Arg Leu Val Trp Tyr Cys	195	200	205	
gcc cga tgt acc aga caa atg aaa aga atg gct caa aaa act cag aaa				847
Ala Arg Cys Thr Arg Gln Met Lys Arg Met Ala Gln Lys Thr Gln Lys	210	215	220	225
cca ccg cag aaa cca gcc cct gca gtt gtt tct gta act cca gct gtc				895
Pro Pro Gln Lys Pro Ala Pro Ala Val Val Ser Val Thr Pro Ala Val	230	235	240	
aaa gat cca ttg gtt aag aaa cca gaa act aaa ctg aaa caa gag aca				943
Lys Asp Pro Leu Val Lys Lys Pro Glu Thr Lys Leu Lys Gln Glu Thr	245	250	255	
act ttt cta gcg ttt aag aga aca gaa gtc aag aca tcc aca gtt att				991
Thr Phe Leu Ala Phe Lys Arg Thr Glu Val Lys Thr Ser Thr Val Ile	260	265	270	
tca gga aat tct tct agt gcc agc gtt tcc tcg tca gta act agt ggc				1039
Ser Gly Asn Ser Ser Ser Ala Ser Val Ser Ser Ser Val Thr Ser Gly	275	280	285	
tta act gga tgg gca gct ttt gca gcc aaa act tcc tct gct ggt cct				1087
Leu Thr Gly Trp Ala Ala Phe Ala Ala Lys Thr Ser Ser Ala Gly Pro	290	295	300	305
tca aca gca aaa ttg agt tca aca aca caa aac aat act ggg aaa cct				1135
Ser Thr Ala Lys Leu Ser Ser Thr Thr Gln Asn Asn Thr Gly Lys Pro	310	315	320	
gct act tcg tca gct aac cag aaa cct gtg ggt ttg act ggt ctg gca				1183
Ala Thr Ser Ser Ala Asn Gln Lys Pro Val Gly Leu Thr Gly Leu Ala	325	330	335	
aca tca tcc aaa ggt gga ata ggt tcc aaa ata ggt tcc aat aac agc				1231
Thr Ser Ser Lys Gly Gly Ile Gly Ser Lys Ile Gly Ser Asn Asn Ser	340	345	350	
act acg ccc act gta cct tta aaa cca cct cca cct cta acc ttg ggt				1279
Thr Thr Pro Thr Val Pro Leu Lys Pro Pro Pro Pro Leu Thr Leu Gly	355	360	365	

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aaa act ggc ctt agt cgc tca gtt agt tgt gac aat gtc agc aaa gta      1327
Lys Thr Gly Leu Ser Arg Ser Val Ser Cys Asp Asn Val Ser Lys Val
370                               375                               380                               385

ggt ctt cct agt cca agt agt tta gtt cca gga agc agc agc caa cta      1375
Gly Leu Pro Ser Pro Ser Ser Leu Val Pro Gly Ser Ser Ser Gln Leu
                               390                               395                               400

agt ggg aat gga aat agt gga aca tca gga cct agt gga agt act acc      1423
Ser Gly Asn Gly Asn Ser Gly Thr Ser Gly Pro Ser Gly Ser Thr Thr
                               405                               410                               415

agc aaa act act tca gaa tcc agc agc tct ccc tca gca tcc ctt aaa      1471
Ser Lys Thr Thr Ser Glu Ser Ser Ser Ser Pro Ser Ala Ser Leu Lys
                               420                               425                               430

ggc cca act tca caa gaa tca cag ctc aat gct atg aag cga tta cag      1519
Gly Pro Thr Ser Gln Glu Ser Gln Leu Asn Ala Met Lys Arg Leu Gln
                               435                               440                               445

atg gtc aag aag aaa gct gcc caa aag aaa ctc aag aag taa tgtggcc      1568
Met Val Lys Lys Lys Ala Ala Gln Lys Lys Leu Lys Lys *
450                               455                               460

aagtagggttt ttgtatcata ttagcctaaa gatgaaaggc ttattattat gatataatct      1628

gtaatacact gtaatttaaat aaaagtcttc ataatcaaaa aaaaaaaaaa      1676

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<213> Homo sapiens

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<222> (158)..(1051)

<400> 61
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ggggcgaggc gcacctgtgg ggacgggacg acgagttcaa gcctccgtgg gtgcagttgg      120

tcgccagcga gggatgcgga gacgcccctg aacgacc atg gca tcg gcc gac gag      175
                               Met Ala Ser Ala Asp Glu
                               1                               5

ctg acc ttc cat gaa ttc gag gag gcc act aat ctt ctg gct gac acc      223
Leu Thr Phe His Glu Phe Glu Glu Ala Thr Asn Leu Leu Ala Asp Thr
                               10                               15                               20

cca gat gca gcc acc acc agc aga agc gat cag ctg acc cca caa ggg      271
Pro Asp Ala Ala Thr Thr Ser Arg Ser Asp Gln Leu Thr Pro Gln Gly
                               25                               30                               35

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cac gtg gct gtg gcc gtg ggc tca ggt ggc agc tat gga gcc gag gat	319
His Val Ala Val Ala Val Gly Ser Gly Gly Ser Tyr Gly Ala Glu Asp	
40 45 50	
gag gtg gag gag gag agt gac aag gcc gcg ctc ctg cag gag cag cag	367
Glu Val Glu Glu Glu Ser Asp Lys Ala Ala Leu Leu Gln Glu Gln Gln	
55 60 65 70	
cag cag cag cag ccg gga ttc tgg acc ttc agc tac tat cag agc ttc	415
Gln Gln Gln Gln Pro Gly Phe Trp Thr Phe Ser Tyr Tyr Gln Ser Phe	
75 80 85	
ttt gac gtg gac acc tca cag gtc ctg gac cgg atc aaa ggc tca ctg	463
Phe Asp Val Asp Thr Ser Gln Val Leu Asp Arg Ile Lys Gly Ser Leu	
90 95 100	
ctg ccc cgg cct ggc cac aac ttt gtg cgg cac cat ctg cgg aat cgg	511
Leu Pro Arg Pro Gly His Asn Phe Val Arg His His Leu Arg Asn Arg	
105 110 115	
ccg gat ctg tat ggc ccc ttc tgg atc tgt gcc acg ttg gcc ttt gtc	559
Pro Asp Leu Tyr Gly Pro Phe Trp Ile Cys Ala Thr Leu Ala Phe Val	
120 125 130	
ctg gcc gtc act ggc aac ctg acg ctg gtg ctg gcc cag agg agg gac	607
Leu Ala Val Thr Gly Asn Leu Thr Leu Val Leu Ala Gln Arg Arg Asp	
135 140 145 150	
ccc tcc atc cac tac agc ccc cag ttc cac aag gtg acc gtg gca ggc	655
Pro Ser Ile His Tyr Ser Pro Gln Phe His Lys Val Thr Val Ala Gly	
155 160 165	
atc agc atc tac tgc tat gcg tgg ctg gtg ccc ctg gcc ctg tgg ggc	703
Ile Ser Ile Tyr Cys Tyr Ala Trp Leu Val Pro Leu Ala Leu Trp Gly	
170 175 180	
ttc ctg cgg tgg cgc aag ggt gtc cag gag cgc atg ggg ccc tac acc	751
Phe Leu Arg Trp Arg Lys Gly Val Gln Glu Arg Met Gly Pro Tyr Thr	
185 190 195	
ttc ctg gag act gtg tgc atc tac ggc tac tcc ctc ttt gtc ttc atc	799
Phe Leu Glu Thr Val Cys Ile Tyr Gly Tyr Ser Leu Phe Val Phe Ile	
200 205 210	
ccc atg gtg gtc ctg tgg ctc atc cct gtg cct tgg ctg cag tgg ctc	847
Pro Met Val Val Leu Trp Leu Ile Pro Val Pro Trp Leu Gln Trp Leu	
215 220 225 230	
ttt ggg gcg ctg gcc ctg ggc ctg tca gcc gcc ggg ctg gta ttc acc	895
Phe Gly Ala Leu Ala Leu Gly Leu Ser Ala Ala Gly Leu Val Phe Thr	
235 240 245	
ctc tgg ccc gtg gtc cgt gag gac acc agg ctg gtg gcc aca gtg ctg	943
Leu Trp Pro Val Val Arg Glu Asp Thr Arg Leu Val Ala Thr Val Leu	
250 255 260	

ctg tcc gtg gtc gtg ctg ctc cag gcc ctc ctg gcc atg ggc tgt gaa 991
 Leu Ser Val Val Val Leu Leu Gln Ala Leu Leu Ala Met Gly Cys Glu
 265 270 275

gtt gga ctt ctt ccg gtg tgc ctc ggg gac gtg gtc ctc ccc cca ttc 1039
 Val Gly Leu Leu Pro Val Cys Leu Gly Asp Val Val Leu Pro Pro Phe
 280 285 290

att ttg ccc taa att gggggcctac tgtcggggccg ggcccctcag aggcggggccg 1094
 Ile Leu Pro *
 295

gcccttggac ccttgg 1110

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<400> 62
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ggg act ggg ctg ctg gcg ctg cgg acg ctg cca ggg ccc agc tgg gtg 104
 Gly Thr Gly Leu Leu Ala Leu Arg Thr Leu Pro Gly Pro Ser Trp Val
 5 10 15

cga ggc tcg ggc cct tcc gtg ctg agc cgc ctg cag gac gcg gcc gtg 152
 Arg Gly Ser Gly Pro Ser Val Leu Ser Arg Leu Gln Asp Ala Ala Val
 20 25 30

gtg cgg cct ggc ttc ctg agc acg gca gag gag gag acg ctg agc cga 200
 Val Arg Pro Gly Phe Leu Ser Thr Ala Glu Glu Glu Thr Leu Ser Arg
 35 40 45 50

gaa ctg gag ccc gag ctg cgc cgc cgc cgc tac gaa tac gat cac tgg 248
 Glu Leu Glu Pro Glu Leu Arg Arg Arg Arg Tyr Glu Tyr Asp His Trp
 55 60 65

gac gcg gcc atc cac ggc ttc cga gag aca gag aag tcg cgc tgg tca 296
 Asp Ala Ala Ile His Gly Phe Arg Glu Thr Glu Lys Ser Arg Trp Ser
 70 75 80

gaa gcc agc cgg gcc atc ctg cag cgc gtg cag gcg gcc gcc ttt ggc 344
 Glu Ala Ser Arg Ala Ile Leu Gln Arg Val Gln Ala Ala Ala Phe Gly
 85 90 95

ccc ggc cag acc ctg ctc tcc tcc gtg cac gtg ctg gac ctg gaa gcc 392
 Pro Gly Gln Thr Leu Leu Ser Ser Val His Val Leu Asp Leu Glu Ala

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100          105          110
cgc ggc tac atc aag ccc cac gtg gac agc atc aag ttc tgc ggg gcc 440
Arg Gly Tyr Ile Lys Pro His Val Asp Ser Ile Lys Phe Cys Gly Ala
115          120          125          130

acc atc gcc ggc ctg tct ctc ctg tct ccc agc gtt atg cgg ctg gtg 488
Thr Ile Ala Gly Leu Ser Leu Leu Ser Pro Ser Val Met Arg Leu Val
135          140          145

cac acc cag gag ccg ggg gag tgg ctg gaa ctc ttg ctg gag ccg ggc 536
His Thr Gln Glu Pro Gly Glu Trp Leu Glu Leu Leu Leu Glu Pro Gly
150          155          160

tcc ctc tac atc ctt agg ggc tca gcc cgt tat gac ttc tcc cat gag 584
Ser Leu Tyr Ile Leu Arg Gly Ser Ala Arg Tyr Asp Phe Ser His Glu
165          170          175

atc ctt cgg gat gaa gag tcc ttc ttt ggg gaa cgc cag att ccc cgg 632
Ile Leu Arg Asp Glu Glu Ser Phe Phe Gly Glu Arg Gln Ile Pro Arg
180          185          190

ggc cgg cgc atc tcc gtg atc tgc cgc tcc ctc cct gag ggc atg ggg 680
Gly Arg Arg Ile Ser Val Ile Cys Arg Ser Leu Pro Glu Gly Met Gly
195          200          205          210

cca ggg gag tct gga cag ccg ccc cca gcc tgc tga cccc cagctttcta 730
Pro Gly Glu Ser Gly Gln Pro Pro Pro Ala Cys *
215          220

cagacaccag atttgtgaat aaagttgggg aatggacagc ctaactggga cattgcagtg 790

gctgcttgct ggggccggga tttgcagggg aaccaggat ggcaactggcc catagggagc 850

tccaggtgtg gctggctgga cacatgggtca aagtcacaag gccgggagag tgggtgcctt 910

tattgcactc actgctgggc gccccagccc actccctcc tcgttgtctc tgcacccagg 970

tctccaataa ataagtcagc cgagaaaaag aaaaaaaaaa a 1011

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 <212> DNA
 <213> Homo sapiens

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 <222> (194)..(736)

<400> 63

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<210> 64
 <211> 4027
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 <213> Homo sapiens

<220>
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 <222> (1021)..(3825)

<400> 64

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cattcaggct attttttaggg gaaagaaagc tagaagacat ttaaaaatga tgcatatagc      180
cgcaactctc attcagagga gatttagaac tctaattgatg agaagaagat tcctctctct      240
caagaaaact gctattttga ttcagagaaa atatcgggca catctttgta caaagcatca      300
cttacagttc cttcagggtac aaaatgcagt tattaataatc cagtcatcat acagaagatg      360
gatgataagg aaaaggatgc gagagatgca cagggtctgct actttcatcc agtctacttt      420
cagaatgcac agattacata tgagatatca ggctttgaaa caggcctccg ttgtgatcca      480
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Ile Gln Ser Thr Tyr Arg Met Tyr Arg Gln Tyr Cys Phe Tyr Gln Lys
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Leu Gln Trp Ala Thr Lys Ile Ile Gln Glu Lys Tyr Arg Ala Asn Lys
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Tyr Arg Gly Tyr Lys Gly Arg Gln Val Ser Leu Arg Gln Lys Ser Ala			
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Arg Lys Asn Val Gly Ile His Val Pro Thr Val Val Asn Ser Asn Lys
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Asn Arg Tyr Val Cys Cys Asn Ile Phe Lys *
525                      530                      535

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			170					175					180			
att	gaa	tta	atg	cta	agg	aaa	gca	ttg	taa	t	cctt	gtgacc	acacc	gatgg		933
Ile	Glu	Leu	Met	Leu	Arg	Lys	Ala	Leu	*							
		185					190									
agatacagaa	aaagttaacg	actggattct	atcttcattt	tagacttttg	gtctgtgggc											993
catttaacct	ggatgccacc	atcttatggg	gataatgatg	cttaccatgg	ttaatgtttt											1053
ggaagagctt	tttatttata	gcattgttta	ctcagtc	caag	ttcaccatgg	ccgtaatcct										1113
tctaagggaa	acactaaagt	tgttgtagtc	tccatttcag	tcagaaactg	atgtttcagc											1173
taggcacagt	ggtacatgcc	tgt														1196

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 <211> 529
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (209)..(403)

<400> 67

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ttgcaaagtg aataatgtac tagatctctg cccttgaagg tctcactttg tgatttcagt      120
gcaaattact taatctcagt aggcctcagt tctctctttc accaaatcag gagaattatt      180
tttttaatca tcaactgtac attattat   atg caa aac ata ctg gta ggc att      232
                                   Met Gln Asn Ile Leu Val Gly Ile
                                   1               5

atg tgg acc aaa aaa tat gac agc agg tgg tcc ttc cct ttt aag aaa      280
Met Trp Thr Lys Lys Tyr Asp Ser Arg Trp Ser Phe Pro Phe Lys Lys
   10               15               20

cta aga tat aca cac atg aag act gct ggt ggt gca agg tgt gga gtc      328
Leu Arg Tyr Thr His Met Lys Thr Ala Gly Gly Ala Arg Cys Gly Val
   25               30               35               40

att ggt gcc gtg ata gca gtg tgc agg tca gag cta gag agt cca gag      376
Ile Gly Ala Val Ile Ala Val Cys Arg Ser Glu Leu Glu Ser Pro Glu
           45               50               55

aag gga ctt tgc tgt ggg ctg aag tga ccagg aagggctccg tggaggaagt      428
Lys Gly Leu Cys Cys Gly Leu Lys   *
           60               65

ggggcccaag gatggacagg acatggatgt ggcaggaaga gggagagcct taccagatgg      488

gccagacttc cggaaccaag atgttgctgg tgggatgtgt g      529

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<210> 68
 <211> 309
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (16)..(267)

<400> 68

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ctggtcggga ttggg atg tcg aag aac aca gtg tcg tcg gcc cgc ttc cgg      51

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Ser Lys Tyr Arg Lys Asn Ile Trp Ile Lys Arg Gly Asp Phe Leu Ile
55 60 65 70

gtt gac ccc att gaa gag gga gaa aag gtg aag gct gaa atc tcg ttt 352
Val Asp Pro Ile Glu Gly Glu Lys Val Lys Ala Glu Ile Ser Phe
75 80 85

gtg ctc tgc aag gac cac gtg cgc tct ctg cag aag gag ggg ttt tgg 400
Val Leu Cys Lys Asp His Val Arg Ser Leu Gln Lys Glu Gly Phe Trp
90 95 100

cct gag gcc ttc tct gaa gtg gct gag aaa cac aac aac agg aac aga 448
Pro Glu Ala Phe Ser Glu Val Ala Glu Lys His Asn Asn Arg Asn Arg
105 110 115

caa act caa cca gaa ctc cca gct gag cca cag tta tca gga gag gag 496
Gln Thr Gln Pro Glu Leu Pro Ala Glu Pro Gln Leu Ser Gly Glu Glu
120 125 130

tcc agc tca gaa gat gat tct gac ctg ttt gtt aac aca aac cgc aga 544
Ser Ser Ser Glu Asp Ser Asp Leu Phe Val Asn Thr Asn Arg Arg
135 140 145 150

cag tat cat gag agt gag gag gag agt gaa gag gag gag gca gcc tga 592
Gln Tyr His Glu Ser Glu Glu Glu Ser Glu Glu Glu Glu Ala Ala *
155 160 165

gactccagga cccaattctc cacttgctca gggactggcc cctggctctt ctgggcttgg 652

acattcccag ggtgctctgc acatcttcac ccctgcatga ggacaaagca gggctcctct 712

ctgaactgat cttttgattc agagaattaa acccctgggtg gggttggtgaa aaaaaaaaaa 772

<210> 70
<211> 857
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (66)..(725)

<400> 70
cccacgcgtc cgcccacgcg tccgcaggga acgggtcttg tggctttgtc tcccgcgaag 60

aggag atg gcg gag tcg ttg agg tct ccg cgc cgc tcc ctg tac aaa 107
Met Ala Glu Ser Leu Arg Ser Pro Arg Arg Ser Leu Tyr Lys
1 5 10

ctg gtg ggc tcg ccg cct tgg aaa gag gct ttc cgg cag aga tgc ctg 155
Leu Val Gly Ser Pro Trp Lys Glu Ala Phe Arg Gln Arg Cys Leu
15 20 25 30

gag aga atg aga aac agc cgg gac agg ctc cta aac agg tac cgc cag 203

Glu Arg Met Arg Asn Ser Arg Asp Arg Leu Leu Asn Arg Tyr Arg Gln	
35 40 45	
gct gga agc agt ggg cca ggg aat tct cag aac agc ttt cta gtt caa	251
Ala Gly Ser Ser Gly Pro Gly Asn Ser Gln Asn Ser Phe Leu Val Gln	
50 55 60	
gag gtg atg gaa gaa gag tgg aat gct ttg cag tca gtg gag aat tgt	299
Glu Val Met Glu Glu Glu Trp Asn Ala Leu Gln Ser Val Glu Asn Cys	
65 70 75	
cca gaa gac ttg gct cag ctg gag gag ctg ata gac atg gct gtg ctg	347
Pro Glu Asp Leu Ala Gln Leu Glu Glu Leu Ile Asp Met Ala Val Leu	
80 85 90	
gag gaa att caa cag gag ctg atc aac caa gag cag tcc atc atc agc	395
Glu Glu Ile Gln Gln Glu Leu Ile Asn Gln Glu Gln Ser Ile Ile Ser	
95 100 105 110	
gag tat gag aag agc ttg cag ttt gat gaa aag tgt ctc agc atc atg	443
Glu Tyr Glu Lys Ser Leu Gln Phe Asp Glu Lys Cys Leu Ser Ile Met	
115 120 125	
ctg gct gag tgg gag gca aac cca ctc atc tgt cct gta tgt aca aag	491
Leu Ala Glu Trp Glu Ala Asn Pro Leu Ile Cys Pro Val Cys Thr Lys	
130 135 140	
tac aac ctg aga atc aca agc ggt gtg gtg gtg tgt cag tgt ggc ctg	539
Tyr Asn Leu Arg Ile Thr Ser Gly Val Val Val Cys Gln Cys Gly Leu	
145 150 155	
tcc atc cca tct cat tct tct gag ttg aca gag cag aag ctt cgt gcc	587
Ser Ile Pro Ser His Ser Ser Glu Leu Thr Glu Gln Lys Leu Arg Ala	
160 165 170	
tgt tta gag ggt agt ata aat gag cac agt gca cat tgt ccc cac aca	635
Cys Leu Glu Gly Ser Ile Asn Glu His Ser Ala His Cys Pro His Thr	
175 180 185 190	
cct gaa ttt tca gtc act gga gga aca gaa gaa aag tcc agt ctt ctc	683
Pro Glu Phe Ser Val Thr Gly Gly Thr Glu Glu Lys Ser Ser Leu Leu	
195 200 205	
atg agc tgt ctg gcc tgt gat act tgg gct gtg atc ctc tag agccagc	732
Met Ser Cys Leu Ala Cys Asp Thr Trp Ala Val Ile Leu *	
210 215 220	
tgggactcac atcattctat gggcggttgaa gacaactcat tcctctgagg agccttgtag	792
atacaagcct tttattttata acttattttg tattgaaact ttacacccat tctggagaaa	852
aaaaaa	857

<210> 71

<211> 1004
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (207)..(1004)

<400> 71

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ctgcaatcct tccttcttat tccggtttcc agagcacgtc tccaggcttc gacgtcacca      120
cgctgggacg tatgtgccga gggccgcggc gtctgacctc atggcgtaga gcctagcaac      180
agcgcaggct cccagccgag tccggtt atg gcc gct gcc gtc ccg aag agg atg      233
                Met Ala Ala Ala Val Pro Lys Arg Met
                  1                      5

agg ggg cca gca caa gcg aaa ctg ctg ccc ggg tcg gcc atc caa gcc      281
Arg Gly Pro Ala Gln Ala Lys Leu Leu Pro Gly Ser Ala Ile Gln Ala
  10                      15                      20                      25

ctt gtg ggg ttg gcg cgg ccg ctg gtc ttg gcg ctc ctg ctt gtg tcc      329
Leu Val Gly Leu Ala Arg Pro Leu Val Leu Ala Leu Leu Leu Val Ser
                30                      35                      40

gcc gct cta tcc agt gtt gta tca cgg act gat tca ccg agc cca acc      377
Ala Ala Leu Ser Ser Val Val Ser Arg Thr Asp Ser Pro Ser Pro Thr
                45                      50                      55

gta ctc aac tca cat att tct acc cca aat gtg aat gct tta aca cat      425
Val Leu Asn Ser His Ile Ser Thr Pro Asn Val Asn Ala Leu Thr His
                60                      65                      70

gaa aac caa acc aaa cct tct att tcc caa atc agc acc acc ctc cct      473
Glu Asn Gln Thr Lys Pro Ser Ile Ser Gln Ile Ser Thr Thr Leu Pro
  75                      80                      85

ccc acg acg agt acc aag aaa agt gga gga gca tct gtg gtc cct cat      521
Pro Thr Thr Ser Thr Lys Lys Ser Gly Gly Ala Ser Val Val Pro His
  90                      95                      100                      105

ccc tcg cct act cct ctg tct caa gag gaa gct gat aac aat gaa gat      569
Pro Ser Pro Thr Pro Leu Ser Gln Glu Glu Ala Asp Asn Asn Glu Asp
                110                      115                      120

cct agt ata gag gag gag gat ctt ctc atg ctg aac agt tct cca tcc      617
Pro Ser Ile Glu Glu Glu Asp Leu Leu Met Leu Asn Ser Ser Pro Ser
                125                      130                      135

aca gcc aaa gac act cta gac aat ggc gat tat gga gaa cca gac tat      665
Thr Ala Lys Asp Thr Leu Asp Asn Gly Asp Tyr Gly Glu Pro Asp Tyr
                140                      145                      150

gac tgg acc acg ggc ccc agg gac gac gac gag tct gat gac acc ttg      713
Asp Trp Thr Thr Gly Pro Arg Asp Asp Asp Glu Ser Asp Asp Thr Leu

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155	160	165	
gaa gaa aac agg ggt tac atg gaa att gaa cag tca gtg aaa tct ttt			761
Glu Glu Asn Arg Gly Tyr Met Glu Ile Glu Gln Ser Val Lys Ser Phe			
170	175	180	185
aag atg cca tcc tca aat ata gaa gag gaa gac agc cat ttc ttt ttt			809
Lys Met Pro Ser Ser Asn Ile Glu Glu Glu Asp Ser His Phe Phe Phe			
	190	195	200
cat ctt att att ttt gct ttt tgc att gct gtt gtt tac att aca tat			857
His Leu Ile Ile Phe Ala Phe Cys Ile Ala Val Val Tyr Ile Thr Tyr			
	205	210	215
cac aac aaa agg aag att ttt ctt ctg gtt caa agc agg aaa tgg cgt			905
His Asn Lys Arg Lys Ile Phe Leu Leu Val Gln Ser Arg Lys Trp Arg			
	220	225	230
gat ggc ctt tgt tcc aaa aca gtg gaa tac cat cgc cta gat cag aat			953
Asp Gly Leu Cys Ser Lys Thr Val Glu Tyr His Arg Leu Asp Gln Asn			
	235	240	245
gtt aat gag gca atg cct tct ttg aag att acc aat gat tat att ttt			1001
Val Asn Glu Ala Met Pro Ser Leu Lys Ile Thr Asn Asp Tyr Ile Phe			
	250	255	260
taa			1004
*			

<210> 72
 <211> 1562
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (1244)..(1399)

<400> 72	
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aagggaagat aaaccaaatt ctactgtgtg ttttaccac agaaggatac aggacaaagg	120
aatagtaact ggctgttttg gatactaaaa ttgaaaataa cttttagcct cctccttatg	180
atagccgccca gagtaaattgt tgagcattac tacagaaaag ccacaaacca agaattctacc	240
tgtttggaag gatctttttgc atctctgaag gtgcttaaag catacttagt gccttttcctt	300
ttaactggga agataaaaga agtatctgtc caagatatta atatgtaaga taacattgta	360
gacatgttct tctgataata caagggttat tctatttgca ttaggatatt tgtggacatg	420

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tccatctaataataaaggaaa gttttttaat cattgaggca ttaggggctg agttatataa 480
ttagaaaact tctaaagata attggatgag aatatacata ttgacctgta tattatgact 540
aatcatgact cagatcttaa tacagggatg atctcatagc atttagatat cagaaaaggt 600
tttgacctat atgtctttaa tattgtttga atacatgtat aatctttatc attcctcagt 660
gtttcatttc tcaaattctg taaaaggaat ataagaggaa agacaattca tatacaaaga 720
caacgagatt aaaaatatgc agtaggaaaa ataattactt aaggggagat tttttttaca 780
tgaaatctgg gctttggatg tgtgtgtgtg tgtgtgtgtg cacatatgca ctgtggtggg 840
agtggggcaa cttggggaat atgttacatg tgtgactttg ttttgccctg gcgaagttaa 900
tgttgttcag aaagggtaaa tgtttggaca cttgcaattg ctcattgatg aatttatatg 960
ttttagtcataaaaaattg taccctttga tagaagcaca ttttctttcc aaagttgggt 1020
attaaccaca gaattatagc aggtattcat aacttaagtt tgaaaatcaa tagcgtctgc 1080
aatggatta acagattaga gaatcaacag catcgaaaa taggttaatg catattgctt 1140
ctaacaagt catgaagaaa tagaagaagc tatgtagctt tcagttctga cagaaaaggg 1200
tgaaggaggg tatcatttca agaaaaaaaa tagctatcac gca atg gtt atc tct 1255
                                Met Val Ile Ser
                                1
gaa aat att tgt att aag atg tgt ata cat ggc cag gca tgg tgg ctc 1303
Glu Asn Ile Cys Ile Lys Met Cys Ile His Gly Gln Ala Trp Trp Leu
  5              10              15              20
atg cct gta atc cca gca ctt tgg gag gca ggt gga tca cga ggt cag 1351
Met Pro Val Ile Pro Ala Leu Trp Glu Ala Gly Gly Ser Arg Gly Gln
          25              30              35
gag atc aag acc atc ctg gcc aac atg gtg aaa cct cat ctc tac taa 1399
Glu Ile Lys Thr Ile Leu Ala Asn Met Val Lys Pro His Leu Tyr  *
      40              45              50
aaatacaaaaa atgagcgggg tgtggtggcc catgcctgta gtcccagctg ctcgggagac 1459
tgaatctctt gagcctggga agcagagggt gcagtgaact gagatcgct cactgcactc 1519
cagccccgggt gacagagcga gattccatct caaaaaaaaa aaa 1562

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<210> 73
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 <212> DNA
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 <222> (1229)..(1432)

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 <222> (1)...(2100)
 <223> n = a,t,c or g

<400> 73

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aacaagaaac aataattcta agttagccag ccaatcaaac tacttcagta aatgatcata	180
ctacagcctg gaatcactca aacaaaaaat tcttctagtt ctcttttaaag atattttatcg	240
tttatttttt catgaaacca aagtaattga ttcaacaata ctaacagttc tagcatgcaa	300
caaaccatct actatctaata gtttaattctt cttaacatgt atattttcat tcctataaag	360
tttccataag aagcttgcaa tgacaataaa ggtaaataag tacagttgtc ccttggtatc	420
catgggggat tgggttcctgg accgtcccc caaccacag ataccaaaaa tccaagtata	480
ctcaagtccc ttacataaaa tgacatattt gtatataacc aacgcacatc cgctgtata	540
ctttatccct agactaatac ctaatgcaat gtaaatagcta tttaaataac tgttatactg	600
tatttttatt tgtattattt ttattttttc taatattttt gatctgcaat tggtttaatc	660
cacagatgca gagtacatgg atacagaggg ccaactgttt tgttacaggt acttcaaata	720
gcactacagt acatctttga caaaattttt acaatattcc acctttcaat atgaaacagc	780
ttaaaaaggc atgggtcaaa aataaagtat agtagtatca cttacgcaaa taaagtctca	840
gaatcataca agcacaacac tgtaggact ctccctgttt aggctgggaa aaacattata	900
caaaacattt tcttcaaata aaattacata aattgcttag aaaaatgcca aaatcaataa	960
tttcaaacat attaaggaga aaaccttgaa cattattgga aaatataaac tagttattcc	1020
ttgcttttaa cagatgagtt cttgacaagt tttgtgtaaa gcaaattctg taaaccatta	1080
tcttgcttgc actggaggaa catatctcaa ggaaacctaa gagaaagtg tctttaaagc	1140
atgtgattct cctgtttttg ctggatgtct gtatctacat aataaacagg cacacttcta	1200
catcactggg tatttttactc agactgtc atg ttt cat ctc tgt aaa tta aac	1252
Met Phe His Leu Cys Lys Leu Asn	
1 5	
cca agt tac tta aaa atc acc tgt ggt aaa aga agc aag cag atc acc	1300
Pro Ser Tyr Leu Lys Ile Thr Cys Gly Lys Arg Ser Lys Gln Ile Thr	
10 15 20	

ccc atc tac tat ccc tcc cgc ctc ccc cct gtc aaa aga aag ttc tca	1348
Pro Ile Tyr Tyr Pro Ser Arg Leu Pro Pro Val Lys Arg Lys Phe Ser	
25 30 35 40	
ggt tat gat gca aaa ctt aca att gtt cat tta tcc aca ttc tca ata	1396
Val Tyr Asp Ala Lys Leu Thr Ile Val His Leu Ser Thr Phe Ser Ile	
45 50 55	
gag gat ttt cca cta tat tta agt atg gca gga taa ttac ccacctgttc	1446
Glu Asp Phe Pro Leu Tyr Leu Ser Met Ala Gly *	
60 65	
ctctttttcag cttagaaaca taacggttca ttccttttat tgctagagaa tgtcattcct	1506
gaagatttta taaacaaagg caaatatgaa ggaaaatttg taattatgaa ataagtcctt	1566
tgtagtaaag aatatttccc aaatcataac agttctatct ggaatgatac ccacaactct	1626
acaagcatct tatccctcta caggaatgac taccttatta attaaaataa aaatttaaca	1686
aggatcaaaa taaaattctt tagcaataga ctctgcaaa aataaaaact aaaactagac	1746
ctagtcattg ccatttgatc aaacttagaa caggcttaaa taacagaacc actccattaa	1806
agaggcatag aaagaaaagt ttactaaaat aaatgtaaaa gtcttatgga gatgaagatc	1866
tctagaatag tcttaagtct atgactactg ctatcattaa tgagcaaata aatgacttga	1926
aattattccn cctggaaaag gtaaactcat acgtattatg gaaaangcct atgggcactt	1986
agaaaaatat tcttggttaa gtaaaccatg gnaaatatag ggtacatcct aagcctctcc	2046
gccctaactt ttaaaattat tnttgagaa aggatagcac tagccgggga ggaa	2100

<210> 74
 <211> 933
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (267)..(866)

<400> 74	
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agcgaccttg gccgttgcc tgaccatctt agtgctgtct gtctgacta tcatcatctg	180
cttcacctgc tctgctgct gcctttacaa gacgtgccgc cgaccacgtc cggttgtcac	240
caccaccaca tccaccactg tgggtgc atg ccc ctt atc ctc agc ctc caa gtg	293

	Met	Pro	Leu	Ile	Leu	Ser	Leu	Gln	Val	
	1				5					
tgc cgc cca gct acc cgt gga cca agc tac cag gcc tac cac acc atg										341
Cys Arg Pro Ala Thr Arg Gly Pro Ser Tyr Gln Gly Tyr His Thr Met										
10 15 20 25										
ccg cct cag cca ggg atg cca gca gcc acc cta ccc aat gca ggg aag										389
Pro Pro Gln Pro Gly Met Pro Ala Ala Thr Leu Pro Asn Ala Gly Lys										
30 35 40										
atg gcg gac att cag act gag cgt gcc tac caa aag cag ccg acc atc										437
Met Ala Asp Ile Gln Thr Glu Arg Ala Tyr Gln Lys Gln Pro Thr Ile										
45 50 55										
ttt caa aac aag aag agg gtc ctg ctg gga gaa act gcc aag gag aag										485
Phe Gln Asn Lys Lys Arg Val Leu Leu Gly Glu Thr Gly Lys Glu Lys										
60 65 70										
ctc ccg cgg tac tac aag aac atc ggt ctg gcc ttc aag aca ccc aag										533
Leu Pro Arg Tyr Tyr Lys Asn Ile Gly Leu Gly Phe Lys Thr Pro Lys										
75 80 85										
gag gct att gag gcc acc tac att gac aag aaa tgc ccc ttc act ggt										581
Glu Ala Ile Glu Gly Thr Tyr Ile Asp Lys Lys Cys Pro Phe Thr Gly										
90 95 100 105										
aat gtg tcc att cga ggg cgg atc ctc tct gcc gtg gtg acc aag atg										629
Asn Val Ser Ile Arg Gly Arg Ile Leu Ser Gly Val Val Thr Lys Met										
110 115 120										
aag atg cag agg acc att gtc atc cgc cga gac tat ctg cac tac atc										677
Lys Met Gln Arg Thr Ile Val Ile Arg Arg Asp Tyr Leu His Tyr Ile										
125 130 135										
cgc aag tac aac cgc ttc gag aag cgc cac aag aac atg tct gta cac										725
Arg Lys Tyr Asn Arg Phe Glu Lys Arg His Lys Asn Met Ser Val His										
140 145 150										
ctg tcc ccc tgc ttc agg gac gtc cag atc ggt gac atc gtc aca gtg										773
Leu Ser Pro Cys Phe Arg Asp Val Gln Ile Gly Asp Ile Val Thr Val										
155 160 165										
ggc gag tgc cgg cct ctg agc aag aca gtg cgc ttc aac gtg ctc aag										821
Gly Glu Cys Arg Pro Leu Ser Lys Thr Val Arg Phe Asn Val Leu Lys										
170 175 180 185										
gtc acc aag gct gcc ggc acc aag aag cag ttc cag aag ttc tga ggc										869
Val Thr Lys Ala Ala Gly Thr Lys Lys Gln Phe Gln Lys Phe *										
190 195 200										
tggacatcgg cccgctcccc acaatgaaat aaagttatatt tctcattccc aaaaaaaaaa										929
aaaa										933

<210> 75
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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (446)..(2956)

<400> 75

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cgtgctccac ctctggccct tcaccatcca cgacctgcgg gcactcgggtg ctaagaagtt      180
ctacggggcgc ttctgcaccg gcaccctgga ccacatcagc atcaggcagc tccagctgct      240
tctgctgaag gtagcattgc tgctgggggt ggaaattcac tgggggtgtca ctttcactgg      300
cctccagccc cctcctagga aggggagtgg ctggcgtgcc cagctccaac ccaaccccc      360
tgcccagctg gccaaactatg aatttgacgt ctttatctcg gctgcaggag gtaaattcgt      420
ccctgaaggc ttcaaagtgc gagaa  atg cga ggc aaa ctg gcc att ggc atc      472
                               Met Arg Gly Lys Leu Ala Ile Gly Ile
                               1             5

aca gcc aac ttt gtg aat gga cgc acc gtg gag gag aca cag gtg ccg      520
Thr Ala Asn Phe Val Asn Gly Arg Thr Val Glu Glu Thr Gln Val Pro
 10             15             20             25

gag atc agt ggt gta gcc agg atc tac aac cag agc ttc ttc cag agc      568
Glu Ile Ser Gly Val Ala Arg Ile Tyr Asn Gln Ser Phe Phe Gln Ser
             30             35             40

ctt ctc aaa gcc aca ggc att gat ctg gag aac att gtg tac tac aag      616
Leu Leu Lys Ala Thr Gly Ile Asp Leu Glu Asn Ile Val Tyr Tyr Lys
             45             50             55

gac gac acc cac tac ttt gtg atg aca gcc aag aag cag tgc ctg ctg      664
Asp Asp Thr His Tyr Phe Val Met Thr Ala Lys Lys Gln Cys Leu Leu
             60             65             70

cgg ctg ggg gtg ctg cgc cag gac tgg cca gac acc aat cgg ctg ctg      712
Arg Leu Gly Val Leu Arg Gln Asp Trp Pro Asp Thr Asn Arg Leu Leu
             75             80             85

ggc agt gcc aat gtg gtg ccc gag gct ctg cag cgc ttt acc cgg gca      760
Gly Ser Ala Asn Val Val Pro Glu Ala Leu Gln Arg Phe Thr Arg Ala
             90             95             100             105

gct gct gac ttt gcc acc cat ggc aag ctc ggg aaa cta gag ttt gcc      808
Ala Ala Asp Phe Ala Thr His Gly Lys Leu Gly Lys Leu Glu Phe Ala
             110             115             120
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cag gat gcc cat ggg cag cct gat gtc tct gcc ttt gac ttc acg agc	856
Gln Asp Ala His Gly Gln Pro Asp Val Ser Ala Phe Asp Phe Thr Ser	
125 130 135	
atg atg cgg gca gag agt tct gct cgt gtg caa gag aag cat ggc gcc	904
Met Met Arg Ala Glu Ser Ser Ala Arg Val Gln Glu Lys His Gly Ala	
140 145 150	
cgc ctg ctg ctg gga ctg gtg ggg gac tgc ctg gtg gag ccc ttc tgg	952
Arg Leu Leu Leu Gly Leu Val Gly Asp Cys Leu Val Glu Pro Phe Trp	
155 160 165	
ccc ctg ggc act gga gtg gca cgg ggc ttc ctg gca gcc ttt gat gca	1000
Pro Leu Gly Thr Gly Val Ala Arg Gly Phe Leu Ala Ala Phe Asp Ala	
170 175 180 185	
gcc tgg atg gtg aag cgg tgg gca gag ggc gct gag tcc cta gag gtg	1048
Ala Trp Met Val Lys Arg Trp Ala Glu Gly Ala Glu Ser Leu Glu Val	
190 195 200	
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Leu Ala Glu Arg Glu Ser Leu Tyr Gln Leu Leu Ser Gln Thr Ser Pro	
205 210 215	
gaa aac atg cat cgc aat gtg gcc cag tat ggg ctg gac cca gcc acc	1144
Glu Asn Met His Arg Asn Val Ala Gln Tyr Gly Leu Asp Pro Ala Thr	
220 225 230	
cgc tac ccc aac ctg aac ctc cgg gca gtg acc ccc aat cag gta cga	1192
Arg Tyr Pro Asn Leu Asn Leu Arg Ala Val Thr Pro Asn Gln Val Arg	
235 240 245	
gac ctg tat gat gtg cta gcc aag gag cct gtg cag agg aac aac gac	1240
Asp Leu Tyr Asp Val Leu Ala Lys Glu Pro Val Gln Arg Asn Asn Asp	
250 255 260 265	
aag aca gat aca ggg atg cca gcc acc ggg tcg gca ggc acc cag gag	1288
Lys Thr Asp Thr Gly Met Pro Ala Thr Gly Ser Ala Gly Thr Gln Glu	
270 275 280	
gag ctg cta cgc tgg tgc cag gag cag aca gct ggg tac ccg gga gtc	1336
Glu Leu Leu Arg Trp Cys Gln Glu Gln Thr Ala Gly Tyr Pro Gly Val	
285 290 295	
cac gtc tcc gat ttg tct tcc tcc tgg gct gat ggg cta gct ctg tgt	1384
His Val Ser Asp Leu Ser Ser Ser Trp Ala Asp Gly Leu Ala Leu Cys	
300 305 310	
gcc ctg gtg tac cgg ctg cag cct ggc ctg ctg gaa ccc tca gag ctg	1432
Ala Leu Val Tyr Arg Leu Gln Pro Gly Leu Leu Glu Pro Ser Glu Leu	
315 320 325	
cag ggg ctg gga gct ctg gaa gca act gct tgg gca cta aag gtg gca	1480
Gln Gly Leu Gly Ala Leu Glu Ala Thr Ala Trp Ala Leu Lys Val Ala	
330 335 340 345	
gag aat gag ctg ggc atc aca ccg gtg gtg tct gca cag gcc gtg gta	1528

Glu Asn Glu Leu Gly Ile Thr Pro Val Val Ser Ala Gln Ala Val Val	
350 355 360	
gca ggg agt gac cca ctg ggc ctc att gcc tac ctc agc cac ttc cac	1576
Ala Gly Ser Asp Pro Leu Gly Leu Ile Ala Tyr Leu Ser His Phe His	
365 370 375	
agt gcc ttc aag agc atg gcc cac agc cca ggc cct gtc agc cag gcc	1624
Ser Ala Phe Lys Ser Met Ala His Ser Pro Gly Pro Val Ser Gln Ala	
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tcc cca ggg acc tcc agt gct gta tta ttc ctt agt aaa ctt cag agg	1672
Ser Pro Gly Thr Ser Ser Ala Val Leu Phe Leu Ser Lys Leu Gln Arg	
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acc ctg cag cga tcc cgg gcc aag gaa aat gca gag gat gct ggt ggc	1720
Thr Leu Gln Arg Ser Arg Ala Lys Glu Asn Ala Glu Asp Ala Gly Gly	
410 415 420 425	
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Lys Lys Leu Arg Leu Glu Met Glu Ala Glu Thr Pro Ser Thr Glu Val	
430 435 440	
cca cct gac cca gag cct ggt gta ccc ctg aca ccc cca tcc caa cac	1816
Pro Pro Asp Pro Glu Pro Gly Val Pro Leu Thr Pro Pro Ser Gln His	
445 450 455	
cag gag gcc ggt gct ggg gac ctg tgt gca ctt tgt ggg gaa cac ctc	1864
Gln Glu Ala Gly Ala Gly Asp Leu Cys Ala Leu Cys Gly Glu His Leu	
460 465 470	
tat gtc ctg gaa cgc ctc tgt gtc aac ggc cat ttc ttc cac cgg agc	1912
Tyr Val Leu Glu Arg Leu Cys Val Asn Gly His Phe Phe His Arg Ser	
475 480 485	
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Cys Phe Arg Cys His Thr Cys Glu Ala Thr Leu Trp Pro Gly Gly Tyr	
490 495 500 505	
gag cag cac cca gga gat gga cat tcc tac tgc ctc cag cac ctg ccc	2008
Glu Gln His Pro Gly Asp Gly His Ser Tyr Cys Leu Gln His Leu Pro	
510 515 520	
cag aca gac cac aaa gag gaa ggc agc gat aga ggc cct gag agt ccg	2056
Gln Thr Asp His Lys Glu Glu Gly Ser Asp Arg Gly Pro Glu Ser Pro	
525 530 535	
gag ctc ccc aca cca agt gag aat agc atg cca cca ggc ctc tca act	2104
Glu Leu Pro Thr Pro Ser Glu Asn Ser Met Pro Pro Gly Leu Ser Thr	
540 545 550	
ccc aca gcc tcg cag gag ggg gcc ggt cct gtt cca gat ccc agc cag	2152
Pro Thr Ala Ser Gln Glu Gly Ala Gly Pro Val Pro Asp Pro Ser Gln	
555 560 565	
ccc acc cgt cgg cag atc cgc ctc tcc agc ccg gag cgc cag cgg ttg	2200
Pro Thr Arg Arg Gln Ile Arg Leu Ser Ser Pro Glu Arg Gln Arg Leu	

570	575	580	585	
tcc tcc ctt aac ctt acc cct gac ccg gaa atg gag cct cca ccc aag				2248
Ser Ser Leu Asn Leu Thr Pro Asp Pro Glu Met Glu Pro Pro Pro Lys	590	595	600	
cct ccc cgc agc tgc tcc gcc ttg gcc cgc cac gcc ctg gag agc agc				2296
Pro Pro Arg Ser Cys Ser Ala Leu Ala Arg His Ala Leu Glu Ser Ser	605	610	615	
ttt gtg ggc tgg ggc ctg cca gtc cag agc cct caa gct ctt gtg gcc				2344
Phe Val Gly Trp Gly Leu Pro Val Gln Ser Pro Gln Ala Leu Val Ala	620	625	630	
atg gag aag gag gaa aaa gag agt ccc ttc tcc agt gaa gag gaa gaa				2392
Met Glu Lys Glu Glu Lys Glu Ser Pro Phe Ser Ser Glu Glu Glu Glu	635	640	645	
gaa gat gtg cct ttg gac tca gat gtg gaa cag gcc ctg cag acc ttt				2440
Glu Asp Val Pro Leu Asp Ser Asp Val Glu Gln Ala Leu Gln Thr Phe	650	655	660	665
gcc aag acc tca ggc acc atg aat aac tac cca aca tgg cgt cgg act				2488
Ala Lys Thr Ser Gly Thr Met Asn Asn Tyr Pro Thr Trp Arg Arg Thr	670	675	680	
ctg ctg cgc cgt gcg aag gag gag gag atg aag agg ttc tgc aag gcc				2536
Leu Leu Arg Arg Ala Lys Glu Glu Glu Met Lys Arg Phe Cys Lys Ala	685	690	695	
cag acc atc caa cgg cga cta aat gag att gag gct gcc ttg agg gag				2584
Gln Thr Ile Gln Arg Arg Leu Asn Glu Ile Glu Ala Ala Leu Arg Glu	700	705	710	
cta gag gcc gag ggc gtg aag ctg gag ctg gcc ttg agg cgc cag agc				2632
Leu Glu Ala Glu Gly Val Lys Leu Glu Leu Ala Leu Arg Arg Gln Ser	715	720	725	
agt tcc cca gaa cag caa aag aaa cta tgg gta gga cag ctg cta cag				2680
Ser Ser Pro Glu Gln Gln Lys Lys Leu Trp Val Gly Gln Leu Leu Gln	730	735	740	745
ctc gtt gac aag aaa aac agc ctg gtg gct gag gag gcc gag ctc atg				2728
Leu Val Asp Lys Lys Asn Ser Leu Val Ala Glu Glu Ala Glu Leu Met	750	755	760	
atc acg gtg cag gaa ttg aat ctg gag gag aaa cag tgg cag ctg gac				2776
Ile Thr Val Gln Glu Leu Asn Leu Glu Glu Lys Gln Trp Gln Leu Asp	765	770	775	
cag gag cta cga ggc tac atg aac cgg gaa gaa aac cta aag aca gct				2824
Gln Glu Leu Arg Gly Tyr Met Asn Arg Glu Glu Asn Leu Lys Thr Ala	780	785	790	
gct gat cgg cag gct gag gac cag gtc ctg agg aag ctg gtg gat ttg				2872
Ala Asp Arg Gln Ala Glu Asp Gln Val Leu Arg Lys Leu Val Asp Leu	795	800	805	

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Ser Arg Ala Lys Val Leu Ser Asn Met Ile Lys Gln Lys Arg Lys Glu	
100 105 110	
aag gcg gga aaa tgg gaa gtc cct ctg cct aaa gta cgt gcc cag gga	562
Lys Ala Gly Lys Trp Glu Val Pro Leu Pro Lys Val Arg Ala Gln Gly	
115 120 125	
gaa aca gaa gta tta aaa gtt att cga aca gga aag aga aag aag aag	610
Glu Thr Glu Val Leu Lys Val Ile Arg Thr Gly Lys Arg Lys Lys Lys	
130 135 140	
gca tgg aag aga atg gtt act aaa gtg tgc ttt gtt gga gat ggc ttt	658
Ala Trp Lys Arg Met Val Thr Lys Val Cys Phe Val Gly Asp Gly Phe	
145 150 155 160	
aca aga aaa cca cct aaa tat gaa aga ttc atc agg cca atg ggc ttg	706
Thr Arg Lys Pro Pro Lys Tyr Glu Arg Phe Ile Arg Pro Met Gly Leu	
165 170 175	
cgt ttc aag aaa gcc cat gta aca cat cct gaa ctg aaa gcc acc ttt	754
Arg Phe Lys Lys Ala His Val Thr His Pro Glu Leu Lys Ala Thr Phe	
180 185 190	
tgc cta cca ata ctt ggt gta aag aag aat ccc tca tcc cca ctg tat	802
Cys Leu Pro Ile Leu Gly Val Lys Lys Asn Pro Ser Ser Pro Leu Tyr	
195 200 205	
aca act ttg ggt gtt att acc aaa ggt act gtc att gaa gta aat gtg	850
Thr Thr Leu Gly Val Ile Thr Lys Gly Thr Val Ile Glu Val Asn Val	
210 215 220	
agc gaa ttg ggc ctt gtg aca caa gga ggc aaa gtt att tgg gga aaa	898
Ser Glu Leu Gly Leu Val Thr Gln Gly Gly Lys Val Ile Trp Gly Lys	
225 230 235 240	
tat gcc cag gtt acc aac aat cct gaa aat gat gga tgt ata aat gca	946
Tyr Ala Gln Val Thr Asn Asn Pro Glu Asn Asp Gly Cys Ile Asn Ala	
245 250 255	
gtc tta ctg gtt tga cagcaatttc atatataatt attgaggact acacaccaat	1001
Val Leu Leu Val *	
260	
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 <222> (29)..(1714)

<400> 77

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	1 5	
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Ser Ala Ser Leu Ile Asp Arg Thr Ile Lys Met Arg Lys Glu Thr Glu		
10 15 20		
gct agg aaa gtg gtc tta gcc tgg gga ctc cta aat gta tct atg gct	148	
Ala Arg Lys Val Val Leu Ala Trp Gly Leu Leu Asn Val Ser Met Ala		
25 30 35 40		
gga atg ata tat act gaa atg act gga aaa ttg att agt tca tac tac	196	
Gly Met Ile Tyr Thr Glu Met Thr Gly Lys Leu Ile Ser Ser Tyr Tyr		
45 50 55		
aat gtg aca tac tgg ccc ctc tgg tat att gag ctt gcc ctt gca tct	244	
Asn Val Thr Tyr Trp Pro Leu Trp Tyr Ile Glu Leu Ala Leu Ala Ser		
60 65 70		
ctc ttc agc ctt aat gcc tta ttt gat ttt tgg aga tat ttc aaa tat	292	
Leu Phe Ser Leu Asn Ala Leu Phe Asp Phe Trp Arg Tyr Phe Lys Tyr		
75 80 85		
act gtg gca cca aca agt ctg gtt gtt agt cct gga cag caa aca ctt	340	
Thr Val Ala Pro Thr Ser Leu Val Val Ser Pro Gly Gln Gln Thr Leu		
90 95 100		
tta ggg ttg aaa aca gct gtt gta cag act acg cct cca cat gat ctg	388	
Leu Gly Leu Lys Thr Ala Val Val Gln Thr Thr Pro Pro His Asp Leu		
105 110 115 120		
gca gca acc caa atc cct ccc gct cca cct tcc cct tca att cag ggt	436	
Ala Ala Thr Gln Ile Pro Pro Ala Pro Pro Ser Pro Ser Ile Gln Gly		
125 130 135		
cag agt gtg ttg agt tat agc cct tct cgt tcg ccc agt acc agt ccc	484	
Gln Ser Val Leu Ser Tyr Ser Pro Ser Arg Ser Pro Ser Thr Ser Pro		
140 145 150		
aag ttc acc acc agc tgt atg act ggt tac agc cct cag ctg caa ggt	532	
Lys Phe Thr Thr Ser Cys Met Thr Gly Tyr Ser Pro Gln Leu Gln Gly		
155 160 165		
ctg tcc tca ggt ggc agt ggt tct tat agc cct gga gtg acc tac tcg	580	
Leu Ser Ser Gly Gly Ser Gly Ser Tyr Ser Pro Gly Val Thr Tyr Ser		
170 175 180		
ccc gtc agt ggt tat aat aag ttg gcg agc ttt agc ccc tct cct cct	628	
Pro Val Ser Gly Tyr Asn Lys Leu Ala Ser Phe Ser Pro Ser Pro Pro		
185 190 195 200		
tct ccg tac cct acc act gtt gga cca gtg gag agc agt gga ttg aga	676	

Ser	Pro	Tyr	Pro	Thr	Thr	Val	Gly	Pro	Val	Glu	Ser	Ser	Gly	Leu	Arg		
				205					210					215			
tct	cgc	tac	cgt	tct	tca	cct	acc	gtc	tac	aac	tca	cct	act	gac	aaa		724
Ser	Arg	Tyr	Arg	Ser	Ser	Pro	Thr	Val	Tyr	Asn	Ser	Pro	Thr	Asp	Lys		
			220					225					230				
gaa	gac	tac	atg	acc	gac	cta	cga	act	ttg	gat	act	ttt	ctc	aga	agt		772
Glu	Asp	Tyr	Met	Thr	Asp	Leu	Arg	Thr	Leu	Asp	Thr	Phe	Leu	Arg	Ser		
		235					240					245					
gaa	gag	gag	aaa	cag	cat	agg	ggt	aag	ctg	ggg	agc	cca	gat	tct	acc		820
Glu	Glu	Glu	Lys	Gln	His	Arg	Val	Lys	Leu	Gly	Ser	Pro	Asp	Ser	Thr		
	250					255					260						
tct	cct	tcc	agc	agt	cct	act	ttc	tgg	aac	tat	agt	cgt	tct	atg	ggg		868
Ser	Pro	Ser	Ser	Ser	Pro	Thr	Phe	Trp	Asn	Tyr	Ser	Arg	Ser	Met	Gly		
265					270				275						280		
gat	tat	gca	caa	act	tta	aag	aag	ttt	cag	tat	cag	ctt	gcc	tgt	agg		916
Asp	Tyr	Ala	Gln	Thr	Leu	Lys	Lys	Phe	Gln	Tyr	Gln	Leu	Ala	Cys	Arg		
				285				290						295			
tct	cag	gcc	cca	tgt	gct	aac	aaa	gat	gaa	gcc	gat	ctc	agc	tct	aaa		964
Ser	Gln	Ala	Pro	Cys	Ala	Asn	Lys	Asp	Glu	Ala	Asp	Leu	Ser	Ser	Lys		
			300					305					310				
caa	gcc	gca	gaa	gag	gtc	tgg	gca	aga	gtg	gct	atg	aat	aga	caa	ctt		1012
Gln	Ala	Ala	Glu	Glu	Val	Trp	Ala	Arg	Val	Ala	Met	Asn	Arg	Gln	Leu		
		315					320					325					
ctt	gat	cat	atg	gat	tca	tgg	aca	gct	aaa	ttt	aga	aat	tgg	atc	aat		1060
Leu	Asp	His	Met	Asp	Ser	Trp	Thr	Ala	Lys	Phe	Arg	Asn	Trp	Ile	Asn		
	330					335					340						
gag	aca	ata	tta	gtg	cca	ctt	ggt	caa	gag	att	gag	tct	gtc	agc	aca		1108
Glu	Thr	Ile	Leu	Val	Pro	Leu	Val	Gln	Glu	Ile	Glu	Ser	Val	Ser	Thr		
345				350					355						360		
cag	atg	aga	cga	atg	ggt	tgt	cca	gag	cta	cag	ata	gga	gag	gct	agt		1156
Gln	Met	Arg	Arg	Met	Gly	Cys	Pro	Glu	Leu	Gln	Ile	Gly	Glu	Ala	Ser		
				365					370					375			
att	act	agc	ttg	aaa	caa	gct	gcc	ctg	ggt	aaa	gcg	cct	ctc	att	ccg		1204
Ile	Thr	Ser	Leu	Lys	Gln	Ala	Ala	Leu	Val	Lys	Ala	Pro	Leu	Ile	Pro		
			380					385					390				
act	ttg	aac	aca	atc	ggt	cag	tat	cta	gac	ctt	act	cca	aat	cag	gaa		1252
Thr	Leu	Asn	Thr	Ile	Val	Gln	Tyr	Leu	Asp	Leu	Thr	Pro	Asn	Gln	Glu		
		395				400						405					
tac	ttg	ttt	gaa	agg	atc	aaa	gaa	cta	tct	cag	gga	ggt	tgt	atg	agc		1300
Tyr	Leu	Phe	Glu	Arg	Ile	Lys	Glu	Leu	Ser	Gln	Gly	Gly	Cys	Met	Ser		
	410					415					420						
tca	ttt	cga	tgg	aac	aga	ggt	ggc	gac	ttc	aaa	gga	cga	aag	tgg	gat		1348
Ser	Phe	Arg	Trp	Asn	Arg	Gly	Gly	Asp	Phe	Lys	Gly	Arg	Lys	Trp	Asp		

425	430	435	440	
aca gac ctg ccc acc gat tct gct atc atc atg cat gta ttt tgc acc				1396
Thr Asp Leu Pro Thr Asp Ser Ala Ile Ile Met His Val Phe Cys Thr	445	450	455	
tac ctt gat tcc aga tta cct cca cat ccg aag tat ccc gac gga aaa				1444
Tyr Leu Asp Ser Arg Leu Pro Pro His Pro Lys Tyr Pro Asp Gly Lys	460	465	470	
act ttt act tct cag cac ttt gtt cag aca cca aat aaa cca gat gtt				1492
Thr Phe Thr Ser Gln His Phe Val Gln Thr Pro Asn Lys Pro Asp Val	475	480	485	
aca aat gag aat gtt ttt tgc att tat cag agt gct atc aac cct ccc				1540
Thr Asn Glu Asn Val Phe Cys Ile Tyr Gln Ser Ala Ile Asn Pro Pro	490	495	500	
cat tat gag ctc atc tac cag cgt cat gta tac aac ctg cca aag ggc				1588
His Tyr Glu Leu Ile Tyr Gln Arg His Val Tyr Asn Leu Pro Lys Gly	505	510	515	520
aga aat aat atg ttt cat aca ttg ttg atg ttt ctc tac atc ata aag				1636
Arg Asn Asn Met Phe His Thr Leu Leu Met Phe Leu Tyr Ile Ile Lys	525	530	535	
acc aaa gag tca gga atg ctt ggg aga gtt aat ctt ggt cta tct ggt				1684
Thr Lys Glu Ser Gly Met Leu Gly Arg Val Asn Leu Gly Leu Ser Gly	540	545	550	
gtg aat ata ttg tgg atc ttt ggc gag tag c aagtcataata tttaattctg				1735
Val Asn Ile Leu Trp Ile Phe Gly Glu *	555	560		
acatttagac tatttcactg aaccagaagt cgaaactaaa catctctgag ccaactgactc				1795
ttctgaaata aaatacacat ggggtgtaaaa aaaaaaaaaa				1835

<210> 78
 <211> 1029
 <212> DNA
 <213> Homo sapiens

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 <222> (428)..(817)

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aattgaagaa aaaaggccaa gttaaaatag gaaaacaaat ggttttcatt tgggtggcagt	180

tgaaatcaaa gtatacatgt gtatacattc taatccgtca tctatcccat gtggcatttt	240
ccaagggtttt aagagtctac caggccaaac cctttgccac tttcactgct tttgctttgc	300
ttttcccctt tcttttctct cgctttgcct tcagcctttt tctttgcctt tggttcatcc	360
atattgggta ctgtccatgc tggtcggcgt gagcgtgagg tgtgggtggt cgtttctcag	420
gtaaaac atg gct aaa agc tta cgg agt aag tgg aaa aga aag atg cgt Met Ala Lys Ser Leu Arg Ser Lys Trp Lys Arg Lys Met Arg 1 5 10	469
gct gaa aag aga aaa aag aat gcc cca aag gag gcc agc agg ctt aaa Ala Glu Lys Arg Lys Lys Asn Ala Pro Lys Glu Ala Ser Arg Leu Lys 15 20 25 30	517
agt att ctc aaa cta gac ggt gat gtt tta atg aaa gat gtt caa gag Ser Ile Leu Lys Leu Asp Gly Asp Val Leu Met Lys Asp Val Gln Glu 35 40 45	565
ata gca act gtg gtg gta ccc aaa ccc aaa cat tgc caa gag aaa atg Ile Ala Thr Val Val Val Pro Lys Pro Lys His Cys Gln Glu Lys Met 50 55 60	613
caa tgt gag gta aaa gat gaa aaa gat gac atg aaa atg gag act gat Gln Cys Glu Val Lys Asp Glu Lys Asp Asp Met Lys Met Glu Thr Asp 65 70 75	661
att aag aga aac aaa aag act ctt cta gac cag cat gga cag tac cca Ile Lys Arg Asn Lys Lys Thr Leu Leu Asp Gln His Gly Gln Tyr Pro 80 85 90	709
ata tgg atg aac caa agg caa aga aaa agg ctg aag gca aag cga gag Ile Trp Met Asn Gln Arg Gln Arg Lys Arg Leu Lys Ala Lys Arg Glu 95 100 105 110	757
aaa aga aag ggg aaa agc aaa gca aaa gca gtg aaa gtg gca aag ggt Lys Arg Lys Gly Lys Ser Lys Ala Lys Ala Val Lys Val Ala Lys Gly 115 120 125	805
ttg gcc tgg tag act cttaaaacct tggaaaatgc cacatgggat agatgacgga Leu Ala Trp * 130	860
ttagaatgta tacacatgta tacttttgatt tcaactgccca ccaaatgaaa accatttggt	920
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<210> 79

<211> 5476

<212> DNA

<213> Homo sapiens

<220>
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 <222> (188)..(5149)

<400> 79

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tagggcagta gaggtacagg gcccattctt ggagagtggg gatcatggca aaattaaatt	180
tcccacc atg aaa gtg ccg aaa ttt ggt gtc tca aca ggg cgt gag ggc	229
Met Lys Val Pro Lys Phe Gly Val Ser Thr Gly Arg Glu Gly	
1 5 10	
cag aca cca aag gca ggg ctg agg gtt tct gca cct gaa gtc tct gtg	277
Gln Thr Pro Lys Ala Gly Leu Arg Val Ser Ala Pro Glu Val Ser Val	
15 20 25 30	
ggg cac aag ggc ggc aag cca ggc ttg act atc caa gcc cct cag ctg	325
Gly His Lys Gly Gly Lys Pro Gly Leu Thr Ile Gln Ala Pro Gln Leu	
35 40 45	
gaa gtc agt gtg ccc tct gcc aat att gag ggc ctt gag ggg aag ctg	373
Glu Val Ser Val Pro Ser Ala Asn Ile Glu Gly Leu Glu Gly Lys Leu	
50 55 60	
aag ggc ccc caa atc act ggg cca tca ctt gag ggt gac cta ggc ctg	421
Lys Gly Pro Gln Ile Thr Gly Pro Ser Leu Glu Gly Asp Leu Gly Leu	
65 70 75	
aaa ggt gcc aag cca cag ggg cac att ggg gtg gat gcc tct gct ccc	469
Lys Gly Ala Lys Pro Gln Gly His Ile Gly Val Asp Ala Ser Ala Pro	
80 85 90	
caa att ggg ggt agc atc act ggc ccc agt gtg gaa gtt cag gcc cct	517
Gln Ile Gly Gly Ser Ile Thr Gly Pro Ser Val Glu Val Gln Ala Pro	
95 100 105 110	
gac att gat gtt cag ggg cct ggg agc aaa ctg aat gtg ccc aag atg	565
Asp Ile Asp Val Gln Gly Pro Gly Ser Lys Leu Asn Val Pro Lys Met	
115 120 125	
aaa gtc ccc aag ttc tct gta tca ggt gca aag gga gag gaa act ggg	613
Lys Val Pro Lys Phe Ser Val Ser Gly Ala Lys Gly Glu Glu Thr Gly	
130 135 140	
att gat gtg aca ctg cct aca ggt gaa gtg act gtt cct ggg gtc tct	661
Ile Asp Val Thr Leu Pro Thr Gly Glu Val Thr Val Pro Gly Val Ser	
145 150 155	
ggg gat gtc agc ctg cct gag att gct act ggt ggg ctg gaa gga aag	709
Gly Asp Val Ser Leu Pro Glu Ile Ala Thr Gly Leu Glu Gly Lys	
160 165 170	
atg aaa ggt act aaa gtg aag act cct gaa atg att att cag aaa cct	757

400	405	410	
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gat gtt cat ggc cca gac tgg cac ttg aag atg ccc aag atg aaa atg Asp Val His Gly Pro Asp Trp His Leu Lys Met Pro Lys Met Lys Met 435 440 445			1525
ccc aaa ttc agt gtg cca ggg ttc aaa gca gag ggc cca gaa gtg gat Pro Lys Phe Ser Val Pro Gly Phe Lys Ala Glu Gly Pro Glu Val Asp 450 455 460			1573
gtg aac ctg ccc aag gct gat gtg gac att tcc ggg ccc aag ata gat Val Asn Leu Pro Lys Ala Asp Val Asp Ile Ser Gly Pro Lys Ile Asp 465 470 475			1621
gtt act gct cct gat gtg agc att gag gaa cca gaa ggg aaa ttg aaa Val Thr Ala Pro Asp Val Ser Ile Glu Glu Pro Glu Gly Lys Leu Lys 480 485 490			1669
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gaa tat gat gtc aca atg cca aag gtt gaa agt gag att aaa gtt cct Glu Tyr Asp Val Thr Met Pro Lys Val Glu Ser Glu Ile Lys Val Pro 530 535 540			1813
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ccc aag ttc agc atg cct ggc ttc aaa gca gag ggc cca gaa gtg gat Pro Lys Phe Ser Met Pro Gly Phe Lys Ala Glu Gly Pro Glu Val Asp 575 580 585 590			1957
gtg aac ctg ccc aag gct gat gtg gac atc tca gga ccc aag gtg ggt Val Asn Leu Pro Lys Ala Asp Val Asp Ile Ser Gly Pro Lys Val Gly 595 600 605			2005
gtt gaa gtt cca gat gtg aat att gaa gga cct gaa gga aag ctg aag Val Glu Val Pro Asp Val Asn Ile Glu Gly Pro Glu Gly Lys Leu Lys 610 615 620			2053
ggc ccc aag ttc aag atg cca gag atg aat atc aag gcc ccc aag atc Gly Pro Lys Phe Lys Met Pro Glu Met Asn Ile Lys Ala Pro Lys Ile 625 630 635			2101

Phe Lys Gly Glu Gly Pro Glu Val Asp Val Lys Leu Pro Lys Ala Asp	
1090 1095 1100	
gtt gat gtc tca gga ccc aaa atg gat gct gaa gtt cca gat gtg aat	3541
Val Asp Val Ser Gly Pro Lys Met Asp Ala Glu Val Pro Asp Val Asn	
1105 1110 1115	
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Ile Glu Gly Pro Asp Ala Lys Leu Lys Gly Pro Lys Phe Lys Met Pro	
1120 1125 1130	
gaa atg agt ata aag cct cag aag ata tcc ata cca gat gtt ggt ttg	3637
Glu Met Ser Ile Lys Pro Gln Lys Ile Ser Ile Pro Asp Val Gly Leu	
1135 1140 1145 1150	
cat ttg aaa ggt cct aaa atg aaa gga gat tat gat gta aca gtt cca	3685
His Leu Lys Gly Pro Lys Met Lys Gly Asp Tyr Asp Val Thr Val Pro	
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aaa gta gaa gga gag ata aaa gct cct gat gtt gac atc aaa ggc ccc	3733
Lys Val Glu Gly Glu Ile Lys Ala Pro Asp Val Asp Ile Lys Gly Pro	
1170 1175 1180	
aaa gtt gat att aat gca cca gat gtg gag gtt cat ggc cca gac tgg	3781
Lys Val Asp Ile Asn Ala Pro Asp Val Glu Val His Gly Pro Asp Trp	
1185 1190 1195	
cac ctg aag atg ccc aag gta aaa atg ccc aag ttc agc atg cct ggc	3829
His Leu Lys Met Pro Lys Val Lys Met Pro Lys Phe Ser Met Pro Gly	
1200 1205 1210	
ttt aaa gga gag ggc cca gag gtg gat atg aac ctg ccc aag gct gac	3877
Phe Lys Gly Glu Gly Pro Glu Val Asp Met Asn Leu Pro Lys Ala Asp	
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ctt ggt gtt tca gga ccc aag gtg gac att gat gtt cca gat gtg aat	3925
Leu Gly Val Ser Gly Pro Lys Val Asp Ile Asp Val Pro Asp Val Asn	
1235 1240 1245	
ctt gaa gct cca gag ggg aaa cta aaa ggc cct aag ttc aag atg cca	3973
Leu Glu Ala Pro Glu Gly Lys Leu Lys Gly Pro Lys Phe Lys Met Pro	
1250 1255 1260	
agc atg aat ata cag acg cac aaa atc tct atg cct gat gtt gga ctt	4021
Ser Met Asn Ile Gln Thr His Lys Ile Ser Met Pro Asp Val Gly Leu	
1265 1270 1275	
aat ttg aaa gcc cct aaa ctg aaa act gat gta gat gtt tcc ctt ccc	4069
Asn Leu Lys Ala Pro Lys Leu Lys Thr Asp Val Asp Val Ser Leu Pro	
1280 1285 1290	
aaa gtg gaa gga gac ttg aag ggt cct gaa att gat gtg aaa gcc cct	4117
Lys Val Glu Gly Asp Leu Lys Gly Pro Glu Ile Asp Val Lys Ala Pro	
1295 1300 1305 1310	
aag atg gat gtg aat gtt ggt gat att gat att gaa ggt cca gaa ggg	4165
Lys Met Asp Val Asn Val Gly Asp Ile Asp Ile Glu Gly Pro Glu Gly	

1315	1320	1325	
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Lys Leu Lys Gly Pro Lys Phe Lys Met Pro Glu Met His Phe Lys Ala			
1330	1335	1340	
ccc aag atc tcc atg ccc gat gtg gac tta cac ttg aaa ggc ccc aaa			4261
Pro Lys Ile Ser Met Pro Asp Val Asp Leu His Leu Lys Gly Pro Lys			
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gtc aaa ggg gat atg gat gtg tct gtg ccc aag gta gaa ggt gaa atg			4309
Val Lys Gly Asp Met Asp Val Ser Val Pro Lys Val Glu Gly Glu Met			
1360	1365	1370	
aaa gtg cca gat gtt gac att aaa ggg ccc aaa gtg gac att gat gcc			4357
Lys Val Pro Asp Val Asp Ile Lys Gly Pro Lys Val Asp Ile Asp Ala			
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cca gat gtg gag gtt cac gac cca gat tgg cac ctg aaa atg ccc aag			4405
Pro Asp Val Glu Val His Asp Pro Asp Trp His Leu Lys Met Pro Lys			
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atg aaa atg ccc aag ttc agt atg cct ggc ttc aaa gca gag ggc cct			4453
Met Lys Met Pro Lys Phe Ser Met Pro Gly Phe Lys Ala Glu Gly Pro			
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gaa gtg gat gtg aat ctc cga aag gct gac att gat gtg tct gga ccc			4501
Glu Val Asp Val Asn Leu Arg Lys Ala Asp Ile Asp Val Ser Gly Pro			
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agt gtg gac act gat gct cct gat ttg gat att gag gga cca gaa gga			4549
Ser Val Asp Thr Asp Ala Pro Asp Leu Asp Ile Glu Gly Pro Glu Gly			
1440	1445	1450	
aag ttg aaa ggc tcc aaa ttt aag atg ccc aag ttg aat ata aaa gct			4597
Lys Leu Lys Gly Ser Lys Phe Lys Met Pro Lys Leu Asn Ile Lys Ala			
1455	1460	1465	1470
ccc aag gtc tcc atg cca gat gtg gac ttg aat ttg aag gga ccc aaa			4645
Pro Lys Val Ser Met Pro Asp Val Asp Leu Asn Leu Lys Gly Pro Lys			
1475	1480	1485	
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Leu Lys Gly Glu Ile Asp Ala Ser Val Pro Glu Leu Glu Gly Asp Leu			
1490	1495	1500	
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Arg Gly Pro Gln Val Asp Val Lys Gly Pro Leu Val Glu Ala Glu Val			
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ccc gat gtt gat ctg gag tgt cct gat gca aag ctg aag ggc ccc aag			4789
Pro Asp Val Asp Leu Glu Cys Pro Asp Ala Lys Leu Lys Gly Pro Lys			
1520	1525	1530	
ctt aag atg cct gag atg cac ttc aag gcc ccc aag atc tcc atg cct			4837
Leu Lys Met Pro Glu Met His Phe Lys Ala Pro Lys Ile Ser Met Pro			
1535	1540	1545	1550

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Asp Val Asp Leu His Leu Lys Gly Pro Lys Val Lys Gly Asp Val Asp	
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Val Ser Leu Pro Lys Leu Glu Gly Asp Leu Thr Gly Pro Ser Val Asp	
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Val Glu Val Pro Asp Val Glu Leu Glu Cys Pro Asp Ala Lys Leu Lys	
1585 1590 1595	
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Gly Pro Lys Phe Lys Met Pro Glu Met His Phe Lys Thr Pro Lys Ile	
1600 1605 1610	
tcc atg cct gat gtg aac tta aac ttg aaa ggc ccc aaa gtc aaa ggg	5077
Ser Met Pro Asp Val Asn Leu Asn Leu Lys Gly Pro Lys Val Lys Gly	
1615 1620 1625 1630	
gat atg gat gtg tct gtt ccc aaa att gga ggg aga ttt aac agg ccc	5125
Asp Met Asp Val Ser Val Pro Lys Ile Gly Gly Arg Phe Asn Arg Pro	
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cag tgt gga tgt gga ggt gcc tga tggtgagctg gctgtcgttg ttctgagggc	5179
Gln Cys Gly Cys Gly Gly Ala *	
1650	
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gtttaagtgt ttgaaccagc cccgaacca agcaacacca gagtcctcct tacatttctt	5299
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ccgggtaagc gcagggaggt atcgtgccac actgagcatc agttccccaa tccgaatcag	5419
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Met Ala Val Lys Leu Gly	
1 5	

acc ctc ctg ctg gcc ctt gcc ctg ggc ctg gcc cag cca gcc tct gcc	160
Thr Leu Leu Leu Ala Leu Ala Leu Gly Leu Ala Gln Pro Ala Ser Ala	
10 15 20	
cgc cgg aag ctg ctg gtg ttt ctg ctg gat ggt ttt cgc tca gac tac	208
Arg Arg Lys Leu Leu Val Phe Leu Leu Asp Gly Phe Arg Ser Asp Tyr	
25 30 35	
atc agt gat gag gcg ctg gag tca ttg cct ggt ttc aaa gag att gtg	256
Ile Ser Asp Glu Ala Leu Glu Ser Leu Pro Gly Phe Lys Glu Ile Val	
40 45 50	
agc agg gga gta aaa gtg gat tac ttg act cca gac ttc cct agt ctc	304
Ser Arg Gly Val Lys Val Asp Tyr Leu Thr Pro Asp Phe Pro Ser Leu	
55 60 65 70	
tcg tat ccc aat tat tat acc cta atg act ggc cgc cat tgt gaa gtc	352
Ser Tyr Pro Asn Tyr Tyr Thr Leu Met Thr Gly Arg His Cys Glu Val	
75 80 85	
cat cag atg atc ggg aac tac atg tgg gac ccc acc acc aac aag tcc	400
His Gln Met Ile Gly Asn Tyr Met Trp Asp Pro Thr Thr Asn Lys Ser	
90 95 100	
ttt gac att ggc gtc aac aaa gac agc cta atg cct ctc tgg tgg aat	448
Phe Asp Ile Gly Val Asn Lys Asp Ser Leu Met Pro Leu Trp Trp Asn	
105 110 115	
gga tca gaa cct ctg tgg gtc act ctg acc aag gcc aaa agg aag gtc	496
Gly Ser Glu Pro Leu Trp Val Thr Leu Thr Lys Ala Lys Arg Lys Val	
120 125 130	
tac atg tac tac tgg cca ggc tgt gag gtt gag att ctg ggt gtc aga	544
Tyr Met Tyr Tyr Trp Pro Gly Cys Glu Val Glu Ile Leu Gly Val Arg	
135 140 145 150	
ccc acc tac tgc cta gaa tat aaa aat gtc cca acg gat atc aat ttt	592
Pro Thr Tyr Cys Leu Glu Tyr Lys Asn Val Pro Thr Asp Ile Asn Phe	
155 160 165	
gcc aat gca gtc agc gat gct ctt gac tcc ttc aag agt ggc cgg gcc	640
Ala Asn Ala Val Ser Asp Ala Leu Asp Ser Phe Lys Ser Gly Arg Ala	
170 175 180	
gac ctg gca gcc ata tac cat gag cgc att gac gtg gaa ggc cac cac	688
Asp Leu Ala Ala Ile Tyr His Glu Arg Ile Asp Val Glu Gly His His	
185 190 195	
tac ggg cct gca tct ccg cag agg aaa gat gcc ctc aag gct gta gac	736
Tyr Gly Pro Ala Ser Pro Gln Arg Lys Asp Ala Leu Lys Ala Val Asp	
200 205 210	
act gtc ctg aag tac atg acc aag tgg atc cag gag cgg ggc ctg cag	784
Thr Val Leu Lys Tyr Met Thr Lys Trp Ile Gln Glu Arg Gly Leu Gln	
215 220 225 230	

gac cgc ctg aac gtc att att ttc tgc gat cac gga atg acc gac att	832
Asp Arg Leu Asn Val Ile Ile Phe Ser Asp His Gly Met Thr Asp Ile	
235 240 245	
ttc tgg atg gac aaa gtg att gag ctg aat aag tac atc agc ctg aat	880
Phe Trp Met Asp Lys Val Ile Glu Leu Asn Lys Tyr Ile Ser Leu Asn	
250 255 260	
gac ctg cag caa gtg aag gac cgc ggg cct gtt gtg agc ctt tgg ccg	928
Asp Leu Gln Gln Val Lys Asp Arg Gly Pro Val Val Ser Leu Trp Pro	
265 270 275	
gcc cct ggg aaa cac tct gag ata tat aac aaa ctg agc aca gtg gaa	976
Ala Pro Gly Lys His Ser Glu Ile Tyr Asn Lys Leu Ser Thr Val Glu	
280 285 290	
cac atg act gtc tac gag aaa gaa gcc atc cca agc agg ttc tat tac	1024
His Met Thr Val Tyr Glu Lys Glu Ala Ile Pro Ser Arg Phe Tyr Tyr	
295 300 305 310	
aag aaa gga aag ttt gtc tct cct ttg act tta gtg gct gat gaa ggc	1072
Lys Lys Gly Lys Phe Val Ser Pro Leu Thr Leu Val Ala Asp Glu Gly	
315 320 325	
tgg ttc ata act gag aat cga gag atg ctt ccg ttt tgg atg aac agc	1120
Trp Phe Ile Thr Glu Asn Arg Glu Met Leu Pro Phe Trp Met Asn Ser	
330 335 340	
acc ggc agg cgg gaa ggt tgg cag cgt gga tgg cac ggc tac gac aac	1168
Thr Gly Arg Arg Glu Gly Trp Gln Arg Gly Trp His Gly Tyr Asp Asn	
345 350 355	
gag ctg atg gac atg cgg ggc atc ttc ctg gcc ttc gga cct ggt agg	1216
Glu Leu Met Asp Met Arg Gly Ile Phe Leu Ala Phe Gly Pro Gly Arg	
360 365 370	
cga gga aat gac cag atg ctg tca gac ccc att ccc aag gaa gtg tct	1264
Arg Gly Asn Asp Gln Met Leu Ser Asp Pro Ile Pro Lys Glu Val Ser	
375 380 385 390	
gta agg ggg gct acg ggt gcc agg aga ggc tgc agg gat ttc ctt aca	1312
Val Arg Gly Ala Thr Gly Ala Arg Arg Gly Cys Arg Asp Phe Leu Thr	
395 400 405	
gac cct ctt tat gag cca agc aga gca aac cca gcc ggt ctg cat gaa	1360
Asp Pro Leu Tyr Glu Pro Ser Arg Ala Asn Pro Ala Gly Leu His Glu	
410 415 420	
aca tct ttt gct ggc ttc ctt tca aat gct tct tgg gtt tgg caa atg	1408
Thr Ser Phe Ala Gly Phe Leu Ser Asn Ala Ser Trp Val Trp Gln Met	
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caccctcaag	cttcaggtga	gctgagcttc	taacactacc	atcaaagcaa	ctggaacccc	180
ttgaatttga	tttctggaga	cgcgagcata	atccttttgc	aaacatctca	acgctggctc	240
tccaggtgga	gcacc atg	gaa ggc	gac tgt	ctg agc	tgc atg	291
	Met	Glu	Gly	Asp	Cys	
	1		5		10	
atg ttt	gta ttc	aat ttc	ttc ata	ttt ctg	ggc ggc	339
Met Phe	Val Phe	Asn Phe	Phe Ile	Phe Leu	Gly Gly	
	15		20		25	
gcc atc	ggc atc	tgg gtc	atg gtg	gac ccc	acc ggc	387
Ala Ile	Gly Ile	Trp Val	Met Val	Asp Pro	Thr Gly	
	30		35		40	
gtg gct	gcc aat	cct ctg	ctc ctc	acg ggc	gcc tac	435
Val Ala	Ala Asn	Pro Leu	Leu Leu	Thr Gly	Ala Tyr	
	45		50		55	
atg ggg	ggc ctg	ctc ttt	ctg ctc	ggc ttc	ctg ggc	483
Met Gly	Gly Leu	Phe Leu	Leu Gly	Phe Leu	Gly Cys	
	65		70		75	
gtc cgt	gag aac	aag tgt	ctg ctg	cta ttt	ttc ttc	531
Val Arg	Glu Asn	Lys Cys	Leu Leu	Leu Phe	Phe Phe	
	80		85		90	
atc atc	ttc ctg	gca gag	ctc tca	gca gcc	atc ctg	579
Ile Ile	Phe Leu	Ala Glu	Leu Ser	Ala Ala	Ile Leu	
	95		100		105	
agg gaa	aat ctc	acc cga	gaa ttc	ttc acc	aag gag	627
Arg Glu	Asn Leu	Thr Arg	Glu Phe	Phe Thr	Lys Glu	
	110		115		120	
tac cag	ggc aat	aac gac	aca gac	gtc ttc	tct gcc	675
Tyr Gln	Gly Asn	Asn Asp	Thr Asp	Val Phe	Ser Ala	
	125		130		135	
					140	

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Val Met Ile Thr Phe Gly Cys Cys Gly Val Asn Gly Pro Glu Asp Phe
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aag ttt gca tct gtg ttt cga ctc ctg acc ctg gat agt gaa gag gtg      771
Lys Phe Ala Ser Val Phe Arg Leu Leu Thr Leu Asp Ser Glu Glu Val
              160                      165                      170

ccg gag gcc tgc tgc cgg agg gaa ccc caa agt cgg gac ggg gtc ctg      819
Pro Glu Ala Cys Cys Arg Arg Glu Pro Gln Ser Arg Asp Gly Val Leu
              175                      180                      185

ctg agc cgg gag gag tgc ctc ctg gga agg agc cta ttc cta aac aag      867
Leu Ser Arg Glu Glu Cys Leu Leu Gly Arg Ser Leu Phe Leu Asn Lys
              190                      195                      200

cag ggc tgt tac acg gtg atc ctc aac acc ttc gag acc tac gtc tac      915
Gln Gly Cys Tyr Thr Val Ile Leu Asn Thr Phe Glu Thr Tyr Val Tyr
              205                      210                      215                      220

ttg gcc gga gcc ctt gcc atc ggg gta ctg gcc atc gag ctt ttc gcc      963
Leu Ala Gly Ala Leu Ala Ile Gly Val Leu Ala Ile Glu Leu Phe Ala
              225                      230                      235

atg atc ttt gcc atg tgc ctc ttc cgg ggc atc cag tag agggatatggc     1012
Met Ile Phe Ala Met Cys Leu Phe Arg Gly Ile Gln *
              240                      245

ctgaagcctg aagactcgcc ccacccacca ctgcccagca cccaatgtcc tcccgtgccc     1072

ctccccgctg tcctcttggc ccagggggag aagatgaggc catcagagat ggccaggaga     1132

agggccaggg gaatagagct attttttttaa caaaacaaaa tgaagacaaa aatatggact     1192

gatgtatcct cgcttgact cagggcaggt gccgtgggtt ctccagagac ccagcacct     1252

ggcccaggat agcaaggctg ctctagagac aaaggaacac aaggccaggc cactatgggc     1312

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tct tcc cga atg gtg gtg cca aag gca gcc att tac caa aca cag gcc Ser Ser Arg Met Val Val Pro Lys Ala Ala Ile Tyr Gln Thr Gln Ala 220 225 230			962
ttc tat gcc aaa ggg aaa atg aag gaa gta aaa cag ctt gtg gct aac Phe Tyr Ala Lys Gly Lys Met Lys Glu Val Lys Gln Leu Val Ala Asn 235 240 245			1010
ttg cgt ggg gaa tcc tta tca tct gga aag aca gag acg tgg aat ggc Leu Arg Gly Glu Ser Leu Ser Ser Gly Lys Thr Glu Thr Trp Asn Gly 250 255 260 265			1058
aag ttg ctg aaa att cca cca gtt tct ccc tct atc ctc gac tgt agt Lys Leu Leu Lys Ile Pro Pro Val Ser Pro Ser Ile Leu Asp Cys Ser 270 275 280			1106
ata atc cgc gtg gaa tat tca cta atg gta tat gtg gat att cct gga Ile Ile Arg Val Glu Tyr Ser Leu Met Val Tyr Val Asp Ile Pro Gly 285 290 295			1154
gct atg gat tta ttt ctt aat ttg cca ctt gtc atc ggt acc att cct Ala Met Asp Leu Phe Leu Asn Leu Pro Leu Val Ile Gly Thr Ile Pro 300 305 310			1202
cta cat cca ttt ggt agc aga acc tca agt gta agc agt cag tgt agc Leu His Pro Phe Gly Ser Arg Thr Ser Ser Val Ser Ser Gln Cys Ser 315 320 325			1250
atg aat atg aac tgg ctc agt tta tca ctt cct gaa aga cct gaa gca Met Asn Met Asn Trp Leu Ser Leu Ser Leu Pro Glu Arg Pro Glu Ala 330 335 340 345			1298
cca ccc agc tat gca gaa gtg gta aca gag gaa caa agg cgg aac aat Pro Pro Ser Tyr Ala Glu Val Val Thr Glu Glu Gln Arg Arg Asn Asn 350 355 360			1346
ctt gca cca gtg agt gct tgt gat gac ttt gag aga gcc ctt caa gga Leu Ala Pro Val Ser Ala Cys Asp Asp Phe Glu Arg Ala Leu Gln Gly 365 370 375			1394
cca ctg ttt gca tat atc cag gag ttt cga ttc ttg cct cca cct ctt Pro Leu Phe Ala Tyr Ile Gln Glu Phe Arg Phe Leu Pro Pro Pro Leu 380 385 390			1442
tat tca gag att gat cca aat cct gat cag tca gca gat gat aga cca Tyr Ser Glu Ile Asp Pro Asn Pro Asp Gln Ser Ala Asp Asp Arg Pro 395 400 405			1490
tcc tgc ccc tct cgt tga aggaac acttggttga atcaagttga tgtgggttcc Ser Cys Pro Ser Arg * 410 415			1544

Ile Phe *

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ataaggaaat tttctccttg aaatcacgat accaaatagg aaaa atg atc tac aag 596
Met Ile Tyr Lys
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tgc ccc atg tgt agg gaa ttt ttc tct gag aga gca gat ctt ttt atg 644
Cys Pro Met Cys Arg Glu Phe Phe Ser Glu Arg Ala Asp Leu Phe Met
5 10 15 20

cat cag aaa att cac aca gct gag aag ccc cat aaa tgt gac aag tgt 692
His Gln Lys Ile His Thr Ala Glu Lys Pro His Lys Cys Asp Lys Cys
25 30 35

gat aag ggt ttc ttt cat ata tca gaa ctt cat att cat tgg aga gac 740
Asp Lys Gly Phe Phe His Ile Ser Glu Leu His Ile His Trp Arg Asp
40 45 50

cat aca gga gag aag gtc tat aaa tgt gat gat tgt ggt aag gat ttt 788
His Thr Gly Glu Lys Val Tyr Lys Cys Asp Asp Cys Gly Lys Asp Phe
55 60 65

agc act aca aca aaa ctt aat aga cat aag aaa atc cac aca gtg gag	836
Ser Thr Thr Thr Lys Leu Asn Arg His Lys Lys Ile His Thr Val Glu	
70 75 80	
aag ccc tat aaa tgt tac gag tgt ggc aaa gcc ttc aat tgg agc tcc	884
Lys Pro Tyr Lys Cys Tyr Glu Cys Gly Lys Ala Phe Asn Trp Ser Ser	
85 90 95 100	
cat ctt caa att cat atg aga gtt cat aca ggt gag aaa ccg tat gtc	932
His Leu Gln Ile His Met Arg Val His Thr Gly Glu Lys Pro Tyr Val	
105 110 115	
tgt agt gag tgt gga agg ggc ttt agt aat agt tca aac ctt tgc atg	980
Cys Ser Glu Cys Gly Arg Gly Phe Ser Asn Ser Ser Asn Leu Cys Met	
120 125 130	
cat cag aga gtc cac acc gga gag aag ccc ttt aaa tgt gaa gag tgt	1028
His Gln Arg Val His Thr Gly Glu Lys Pro Phe Lys Cys Glu Glu Cys	
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Gly Lys Ala Phe Arg His Thr Ser Ser Leu Cys Met His Gln Arg Val	
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cac aca gga gag aaa ccc tat aaa tgt tat gag tgt ggg aag gcg ttc	1124
His Thr Gly Glu Lys Pro Tyr Lys Cys Tyr Glu Cys Gly Lys Ala Phe	
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agt cag agt tcg agc ctc tgc atc cac cag aga gtc cac act gga gag	1172
Ser Gln Ser Ser Ser Leu Cys Ile His Gln Arg Val His Thr Gly Glu	
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Lys Pro Tyr Arg Cys Cys Gly Cys Gly Lys Ala Phe Ser Gln Ser Ser	
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Ser Leu Cys Ile His Gln Arg Val His Thr Gly Glu Lys Pro Phe Lys	
215 220 225	
tgt gat gag tgc gga aag gcc ttc agt cag agt acg agc ctc tgc atc	1316
Cys Asp Glu Cys Gly Lys Ala Phe Ser Gln Ser Thr Ser Leu Cys Ile	
230 235 240	
cac cag aga gtc cac aca aag gag aga aac cat ctc aaa ata tca gtt	1364
His Gln Arg Val His Thr Lys Glu Arg Asn His Leu Lys Ile Ser Val	
245 250 255 260	
ata taa aacgttttgc taagagttta aaatcttaaa acccataagt gccactagga	1420
Ile *	
aggaaaccct gtatatacct acattgaccc aagaaatatt tacgcaatcc ctagcagaac	1480
attgtttctg aggaggcata tgtgagattg atttgttggt tcatgcccaag tgtgttccac	1540

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           Met Gln Glu Asp Arg Asp Gly Ser Cys Ser Thr Val Gly Gly
            1             5             10

gta ggt tat ggg gac agt aag gat tgt atc ctg gag ccg ctt tcc ctg      155
Val Gly Tyr Gly Asp Ser Lys Asp Cys Ile Leu Glu Pro Leu Ser Leu
 15             20             25             30

cca gaa agt cca ggt ggc acc acc act tta gaa ggt tct cca tct gtg      203
Pro Glu Ser Pro Gly Gly Thr Thr Thr Leu Glu Gly Ser Pro Ser Val
           35             40             45

cct tgt att ttc tgt gaa gaa cat ttt cct gtg gct gaa caa gac aaa      251
Pro Cys Ile Phe Cys Glu Glu His Phe Pro Val Ala Glu Gln Asp Lys
           50             55             60

ctt ctg aag cac atg att att gag cat aag att gtc ata gct gat gtc      299
Leu Leu Lys His Met Ile Ile Glu His Lys Ile Val Ile Ala Asp Val
           65             70             75

aag ttg gtt gct gat ttc caa agg tac att tta tat tgg agg aaa agg      347
Lys Leu Val Ala Asp Phe Gln Arg Tyr Ile Leu Tyr Trp Arg Lys Arg
           80             85             90

ttc act gaa cag ccc atc aca gat ttt tgt agt gta ata aga att aat      395
Phe Thr Glu Gln Pro Ile Thr Asp Phe Cys Ser Val Ile Arg Ile Asn
           95             100             105             110

tcc act gct cca ttt gaa gaa caa gag aat tat ttt ttg tta tgt gac      443
Ser Thr Ala Pro Phe Glu Glu Gln Glu Asn Tyr Phe Leu Leu Cys Asp
           115             120             125

gtt tta cca gaa gat aga att ctt aga gaa gag ctt cag aaa cag aga      491
Val Leu Pro Glu Asp Arg Ile Leu Arg Glu Glu Leu Gln Lys Gln Arg
           130             135             140

ctg aga gaa att ctg gaa caa cag cag caa gaa cga aat gat acc aat      539
Leu Arg Glu Ile Leu Glu Gln Gln Gln Gln Glu Arg Asn Asp Thr Asn
           145             150             155

ttt cat ggc gtt tgt atg ttt tgc aat gaa gaa ttc ctt gga aac aga      587
Phe His Gly Val Cys Met Phe Cys Asn Glu Glu Phe Leu Gly Asn Arg
           160             165             170

tct gtt att ttg aac cac atg gcc aga gaa cat gct ttc aac att gga      635
Ser Val Ile Leu Asn His Met Ala Arg Glu His Ala Phe Asn Ile Gly
           175             180             185             190

ttg cca gac aac att gta aac tgc aat gaa ttt ttg tgt aca tta cag      683
Leu Pro Asp Asn Ile Val Asn Cys Asn Glu Phe Leu Cys Thr Leu Gln
           195             200             205

aaa aag ctt gac aat ttg cag tgc ttg tac tgt gag aag acc ttc agg      731

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taccacagaa gcaatttttc atgtttttct cctatgagac agatatgaaa gaacaattta 1467
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Met Glu Ala Leu Asn Thr Ala Gln Gly Ala Arg Asp Phe Ile Tyr Ser
1 5 10 15
ctg cac tcc acg gag agg agc tgc ctg ctc aaa gag ctg cac cgc ttc 154
Leu His Ser Thr Glu Arg Ser Cys Leu Leu Lys Glu Leu His Arg Phe
20 25 30
gag tct att gcc att gcc caa gaa aaa ttg gaa gct cca cca ccc acc 202
Glu Ser Ile Ala Ile Ala Gln Glu Lys Leu Glu Ala Pro Pro Pro Thr
35 40 45
cca gga cag ctg aga tat gta ttc atc cac aat gcg ata cct ttc ata 250
Pro Gly Gln Leu Arg Tyr Val Phe Ile His Asn Ala Ile Pro Phe Ile
50 55 60
ggg ttt ggc ttt ttg gat aat gca att atg att gtt gct gga acc cat 298
Gly Phe Gly Phe Leu Asp Asn Ala Ile Met Ile Val Ala Gly Thr His
65 70 75 80
att gaa atg tct att gga att att ttg gga att tca act atg gca gct 346
Ile Glu Met Ser Ile Gly Ile Ile Leu Gly Ile Ser Thr Met Ala Ala
85 90 95
gct gct ttg gga aat ctt gtg tca gat cta gct gga ctt gga ctt gca 394
Ala Ala Leu Gly Asn Leu Val Ser Asp Leu Ala Gly Leu Gly Leu Ala
100 105 110
ggc tac gtt gaa gca ttg gct tcc agg tta ggc ctg tca att cct gat 442
Gly Tyr Val Glu Ala Leu Ala Ser Arg Leu Gly Leu Ser Ile Pro Asp
115 120 125

ctc aca cca aag caa gtt gac atg tgg caa aca cgt ctt agt aca cat 490
 Leu Thr Pro Lys Gln Val Asp Met Trp Gln Thr Arg Leu Ser Thr His
 130 135 140

ttg ggc aaa gct gtt ggg gtg act att ggc tgc att cta gga atg ttt 538
 Leu Gly Lys Ala Val Gly Val Thr Ile Gly Cys Ile Leu Gly Met Phe
 145 150 155 160

cct tta att ttc ttt gga gga ggt gaa gaa gat gaa aaa ctg gaa acg 586
 Pro Leu Ile Phe Phe Gly Gly Gly Glu Glu Asp Glu Lys Leu Glu Thr
 165 170 175

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 Lys Ser *

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aataatntag catgtattat ggaaaacact aacttattgt ggcttgatct tcttaggaca 762

tcttttttaa aaagctgttt agtatcattt tgtgtatatt gttgaaatgc tttttcatca 822

atagcagtca acattttatc ctttcttttt atattcataa tgttatttaa gtgtcattga 882

tgtactgtat tgacttgggg tttgcttatt tgttacttaa catgtgtaca tgcattgaaag 942

catttttcgt tgttcctga tagttacatt tcaaccttgg gattttttcca aattacttaa 1002

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tccggggcttt ggtgggatcg gtgtcctcag g atg aga ttt agg gtt tcc tcg 292
 Met Arg Phe Arg Val Ser Ser
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tcg gaa tcc ggg tgc tgc gga ttg agg tcc cgg ttc cta acg gac tgc Ser Glu Ser Gly Cys Cys Gly Leu Arg Ser Arg Phe Leu Thr Asp Cys 40 45 50 55	436
aag atg gag gaa ggc ggg aac cta gga ggc ctg att aag atg gtc cat Lys Met Glu Glu Gly Gly Asn Leu Gly Gly Leu Ile Lys Met Val His 60 65 70	484
cta ctg gtc ttg tca ggt gcc tgg ggc atg caa atg tgg gtg acc ttc Leu Leu Val Leu Ser Gly Ala Trp Gly Met Gln Met Trp Val Thr Phe 75 80 85	532
gtc tca ggc ttc ctg ctt ttc cga agc ctt ccc cga cat acc ttc gga Val Ser Gly Phe Leu Leu Phe Arg Ser Leu Pro Arg His Thr Phe Gly 90 95 100	580
cta gtg cag agc aaa ctc ttc ccc ttc tac ttc cac atc tcc atg ggc Leu Val Gln Ser Lys Leu Phe Pro Phe Tyr Phe His Ile Ser Met Gly 105 110 115	628
tgt gcc ttc atc aac ctc tgc atc ttg gct tca cag cat gct tgg gct Cys Ala Phe Ile Asn Leu Cys Ile Leu Ala Ser Gln His Ala Trp Ala 120 125 130 135	676
cag ctc aca ttc tgg gag gcc agc cag ctt tac ctg ctg ttc ctg agc Gln Leu Thr Phe Trp Glu Ala Ser Gln Leu Tyr Leu Leu Phe Leu Ser 140 145 150	724
ctt acg ctg gcc act gtc aac gcc cgc tgg ctg gaa ccc cgc acc aca Leu Thr Leu Ala Thr Val Asn Ala Arg Trp Leu Glu Pro Arg Thr Thr 155 160 165	772
gct gcc atg tgg gcc ctg caa acc gtg gag aag gag cga ggc ctg ggt Ala Ala Met Trp Ala Leu Gln Thr Val Glu Lys Glu Arg Gly Leu Gly 170 175 180	820
ggg gag gta cca ggc agc cac cag ggt ccc gat ccc tac cgc cag ctg Gly Glu Val Pro Gly Ser His Gln Gly Pro Asp Pro Tyr Arg Gln Leu 185 190 195	868
cga gag aag gac ccc aag tac agt gct ctc cgc aca gaa ttt ctt ccg Arg Glu Lys Asp Pro Lys Tyr Ser Ala Leu Arg Thr Glu Phe Leu Pro 200 205 210 215	916
cta cat ggg ctg tcc tct ctt tgc aat ctg ggc tgc gtc ctg agc aat Leu His Gly Leu Ser Ser Leu Cys Asn Leu Gly Cys Val Leu Ser Asn 220 225 230	964

ggg ctc tgt ctc gct ggc ttg ccc tgg gaa tta gga gct cta gct ggg 1012
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 Ser Ala Ile Phe His Thr Ile Arg Phe Val Leu Ala Ser Arg Leu Gln
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 Ser Asp Trp Met Leu Met Leu Tyr Phe Ala His Thr His Leu Thr Val
 30 35 40

aca gtc acc att ggg ttg ctt ttg att cca aag ttt tca cat tca agc 195
 Thr Val Thr Ile Gly Leu Leu Leu Ile Pro Lys Phe Ser His Ser Ser
 45 50 55

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 Asn Asn Pro Arg Asp Asp Ile Ala Thr Glu Ala Tyr Glu Asp Glu Leu
 60 65 70 75

gac atg ggc cga tct gga tcc tac ctg aac agc agt atc aat tca gcc 291
 Asp Met Gly Arg Ser Gly Ser Tyr Leu Asn Ser Ser Ile Asn Ser Ala
 80 85 90

tgg agt gag cac agc ttg gat cca gag gac att cgg gac gag ctg aaa 339
 Trp Ser Glu His Ser Leu Asp Pro Glu Asp Ile Arg Asp Glu Leu Lys
 95 100 105

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 Lys Leu Tyr Ala Gln Leu Glu Ile Tyr Lys Arg Lys Lys Met Ile Thr
 110 115 120

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 Asn Asn Pro His Leu Gln Lys Lys Arg Cys Ser Lys Lys Gly Leu Gly
 125 130 135

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Arg Ser Ile Met Arg Arg Ile Thr Glu Ile Pro Glu Thr Val Ser Arg	
140 145 150 155	
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Gln Cys Ser Lys Glu Asp Lys Glu Gly Ala Asp His Gly Thr Ala Lys	
160 165 170	
ggc act gcc ctc atc agg aag aac ccc cca gag tct tca ggg aac aca	579
Gly Thr Ala Leu Ile Arg Lys Asn Pro Pro Glu Ser Ser Gly Asn Thr	
175 180 185	
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Gly Lys Ser Lys Glu Glu Thr Leu Lys Asn Arg Val Phe Ser Leu Lys	
190 195 200	
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Lys Ser His Ser Thr Tyr Asp His Val Arg Asp Gln Thr Glu Glu Ser	
205 210 215	
agt agc cta ccc aca gaa agc caa gag gag gag aca aca gaa aat tcc	723
Ser Ser Leu Pro Thr Glu Ser Gln Glu Glu Glu Thr Thr Glu Asn Ser	
220 225 230 235	
aca ctg gaa tcc ctg tcg ggt aaa aaa cta aca caa aaa cta aaa gaa	771
Thr Leu Glu Ser Leu Ser Gly Lys Lys Leu Thr Gln Lys Leu Lys Glu	
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Asp Ser Glu Ala Glu Ser Thr Glu Ser Val Pro Leu Val Cys Lys Ser	
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Ala Ser Ala His Asn Leu Ser Ser Glu Lys Lys Thr Gly His Pro Arg	
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Asn His Ser Asn Ser Asp Asn Thr Glu Thr Lys Asp Pro Ala Pro Gln	
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Pro Trp Glu Val Tyr Asp Leu Thr Pro Gly Pro Val Pro Ser Glu Ser	
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Lys Val Gln Lys His Val Ser Ile Val Ala Ser Glu Met Glu Lys Asn	
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Pro Thr Phe Ser Leu Lys Glu Lys Ser His His Lys Pro Lys Ala Ala	
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Glu Val Cys Gln Gln Ser Asn Gln Lys Arg Ile Asp Lys Ala Glu Val	
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Cys Leu Trp Glu Ser Gln Gly Gln Ser Ile Leu Glu Asp Glu Lys Leu	
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Leu Ile Ser Lys Thr Pro Val Leu Pro Glu Arg Ala Lys Glu Glu Asn	
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495 500 505	
ctg ccc ccc aaa gct gta gca tca aaa aca gag aat gaa aat ctc aac	1587
Leu Pro Pro Lys Ala Val Ala Ser Lys Thr Glu Asn Glu Asn Leu Asn	
510 515 520	
caa ata gga cac cag gaa aaa aag aca tct tct tct gag gag aat gtg	1635
Gln Ile Gly His Gln Glu Lys Lys Thr Ser Ser Ser Glu Glu Asn Val	
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Arg Gly Ser Tyr Asn Ser Ser Asn Asn Phe Gln Gln Pro Leu Thr Ser	
540 545 550 555	
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Arg Ala Glu Val Cys Pro Trp Glu Phe Glu Thr Pro Ala Gln Pro Asn	
560 565 570	
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Ala Gly Arg Ser Val Ala Leu Pro Ala Ser Ser Ala Leu Ser Ala Asn	
575 580 585	
aag ata gca ggg cct agg aaa gaa gag gtc tgg gat agt ttt aaa gtg	1827

Lys Ile Ala Gly Pro Arg Lys Glu Glu Val Trp Asp Ser Phe Lys Val
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Year	Age group	Number of cases	Rate per 100,000
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1980	15-24	20	0.2
1980	25-34	30	0.3
1980	35-44	40	0.4
1980	45-54	50	0.5
1980	55-64	60	0.6
1980	65-74	70	0.7
1980	75-84	80	0.8
1980	85+	90	0.9
1981	0-14	12	0.1
1981	15-24	22	0.2
1981	25-34	32	0.3
1981	35-44	42	0.4
1981	45-54	52	0.5
1981	55-64	62	0.6
1981	65-74	72	0.7
1981	75-84	82	0.8
1981	85+	92	0.9
1982	0-14	14	0.1
1982	15-24	24	0.2
1982	25-34	34	0.3
1982	35-44	44	0.4
1982	45-54	54	0.5
1982	55-64	64	0.6
1982	65-74	74	0.7
1982	75-84	84	0.8
1982	85+	94	0.9
1983	0-14	16	0.1
1983	15-24	26	0.2
1983	25-34	36	0.3
1983	35-44	46	0.4
1983	45-54	56	0.5
1983	55-64	66	0.6
1983	65-74	76	0.7
1983	75-84	86	0.8
1983	85+	96	0.9
1984	0-14	18	0.1
1984	15-24	28	0.2
1984	25-34	38	0.3
1984	35-44	48	0.4
1984	45-54	58	0.5
1984	55-64	68	0.6
1984	65-74	78	0.7
1984	75-84	88	0.8
1984	85+	98	0.9
1985	0-14	20	0.1
1985	15-24	30	0.2
1985	25-34	40	0.3
1985	35-44	50	0.4
1985	45-54	60	0.5
1985	55-64	70	0.6
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1985	75-84	90	0.8
1985	85+	100	0.9

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Ser Lys Asp Lys Ile Ala Ser Tyr Ser Lys Thr Pro Lys Ile Glu Arg

30 35 40 45

Ser Asp Val Ser Lys Glu Met Lys Glu Lys Ser Ser Met Lys Arg Lys

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Leu Pro Phe Thr Ile Ser Pro Ser Arg Asn Glu Glu Arg Asp Ser Asp

65 70 75

Thr Glu Lys Glu Gly Pro Glu Lys Lys Lys Thr Lys Lys Glu Ala Gly

80 85 90

Asn Lys Lys Ser Thr Pro Val Ser Ile Leu Phe Gly Tyr Pro Leu Ser

95 100 105

Glu Arg Lys Gln Met Ala Leu Leu Met Gln Met Thr Ala Arg Asp Asn

110 115 120 125

Ser Pro Asp Ser Thr Pro Asn His Pro Ser Gln Thr Thr Pro Ala Gln

130 135 140

Lys Lys Thr Pro Ser Ser Ser Ser Arg Gln Lys Asp Lys Val Asn Lys

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Arg Asn Glu Arg Gly Glu Thr Pro Leu His Met Ala Ala Ile Arg Gly

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Glu Glu Gly Asn Phe Arg Lys Ser Phe Ser Pro Lys Asp Asp Thr Ser			
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Leu His Leu Phe His Ile Ser Thr Gly Lys Ser Pro Lys His Ser Cys			
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Val Arg Tyr Asp Asn Thr Glu Ser Glu Phe Leu Pro Glu Ser Ser Ser			
560	565	570	
gta aaa tct tgt aag cat aag gaa aaa agc aaa cat cag aaa gat ttc			2016
Val Lys Ser Cys Lys His Lys Glu Lys Ser Lys His Gln Lys Asp Phe			
575	580	585	
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His Leu Glu Phe Gly Glu Lys Ser Asn Ala Lys Ile Lys Asp Glu Asp			
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cat agt cca aca ttt gaa aat tca gat tgc aca ctg aaa aaa atg gat			2112
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Lys Glu Gly Lys Thr Leu Lys Lys His Lys Leu Lys His Lys Glu Arg			
625	630	635	

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 640 645 650

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 655 660 665

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 Arg Glu Phe Trp Lys Glu Asn Phe Phe Lys Ser Asp Glu Thr Glu Asp
 670 675 680 685

ctc ttt tta aat atg gaa cat gaa tcc tta aca tta gaa aaa aaa tca 2352
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 720 725 730

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 Glu Ile Asp Ile Glu Lys Gln Glu Lys His Ile Lys Glu Asn Lys Lys
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Tyr Gln Asn Ile Tyr Asp Val Asn Phe Leu Lys Arg Phe Leu Asn Arg	
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Asn Phe Ile *	
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His Thr Gly Phe Lys Thr Leu Gln Glu Leu Ser Ser Asn Asp Met Leu
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Leu Leu Gln Leu Arg Thr Gly Met Thr Leu Ser Gly Asn Asn Thr Ile
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tgc ttt cat cat gta aaa att tac att gac aga ttt gag gat tta cag      365
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Phe Gly Arg Gln Leu Val Pro Gly Trp Lys Leu Cys Pro Lys Cys Thr
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Pro Leu Ser Gly Met Glu Ser Arg Asn Gly Gln Cys Leu Thr Gly Thr
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aac ctg tac tat gga cac tac cac ggg ttt ggg gac act gct gaa agc Asn Leu Tyr Tyr Gly His Tyr His Gly Phe Gly Asp Thr Ala Glu Ser 110 115 120	1346
atc cca gaa ctg aac agt gtg gtc gag cat tcc aag tcc gtg aag gtg Ile Pro Glu Leu Asn Ser Val Val Glu His Ser Lys Ser Val Lys Val 125 130 135	1394
cag gag cgg tac gac agt gcc gtg ctg ggc acc atg cac ctg cac cac Gln Glu Arg Tyr Asp Ser Ala Val Leu Gly Thr Met His Leu His His 140 145 150 155	1442
ggc tcc tag agacgct gacctggctc tcggaaacgc aggagtcctt cctggtagcc Gly Ser *	1498
agctcagaat acccatgtag cagcaacttg aacgaatgtc acaacttgta ctttttttat	1558
atacttcaac tttctgaaaa agtaaacctc gacaagttcc cagcaactgc ttgtttgtgc	1618
atgagtaggg cttactaagt gcatagatgt ttctacagtg aggtgtcctt ttataaggt	1678
gcacttttgg agtttttctg atgccaatct caacattgtc tttttaatac tgtcaccaga	1738
tattgccatt tttctttttg ttaaaagatt atatgatcaa gataaattgg ggtggtaa	1798
cagggtgcctg gtaatttatc tctttgcaca tgggcatcat tttaaaaagc ttgcttccac	1858
tcttttctgt agaatttgac ggaacacagc tatttcccta tgcaaggtag agccttacia	1918
agatttctgc agtgatttgt gtgaagaaga gaatgtttgt ctttttcaat gaagctttgc	1978
agatcaccat gtgggtgaag gttttagttg tggacacagt ggtccctcct taatgatgaa	2038
gatcactgcc ttgggcttca tggaaaacag gccagcctg gggctgcgtt tggatttatt	2098
gtttttattc cacacttcct acttggctc tggaaagttt accacatgta acagattcct	2158
ttatatgtag tgaaaatcac tatttgtaga aactgtcagg tcaaaatatt taactgactg	2218
ttgacatgta ttttcttttt tccttgtttt tgttttttgg ggttttctgc tttaagatat	2278

ataccactat gtatatccag ttaactgaga gaattttgac tctcttaata aaactgcatt 2338
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<212> DNA
<213> Homo sapiens

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<222> (286)..(759)

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tttactgcag tttcatcatg gggtttgttg atgtgcagtc catttattgc cctgtcttgc 180
ttaaatatctc ttgttgagaa cagctggagg ctttgactgg gttcctagtt ctgttttctg 240
ggaaggcaac gtggattctg tttttagac attaatgagc tttaa atg gga att 294
Met Gly Ile
1
ggg gat gat gta tgt cta caa aaa aaa agt tgg agc ggc cgc caa 342
Gly Asp Asp Val Cys Leu Gln Lys Lys Lys Ser Trp Ser Gly Arg Gln
5 10 15
ctt agg ggc cac gtg agc cac ggc cac ggc cgc ata ggc aag cac cgg 390
Leu Arg Gly His Val Ser His Gly His Gly Arg Ile Gly Lys His Arg
20 25 30 35
aag cac ccc ggc ggc cgc ggt aat gct ggt ggt ctg cat cac cac cgg 438
Lys His Pro Gly Gly Arg Gly Asn Ala Gly Gly Leu His His His Arg
40 45 50
atc aac ttc gac aaa tac cac cca ggc tac ttt ggg aaa gtt ggt atg 486
Ile Asn Phe Asp Lys Tyr His Pro Gly Tyr Phe Gly Lys Val Gly Met
55 60 65
aag cat tac cac tta aag agg aac cag agc ttc tgc cca act gtc aac 534
Lys His Tyr His Leu Lys Arg Asn Gln Ser Phe Cys Pro Thr Val Asn
70 75 80
ctt gac aaa ttg tgg act ttg gtc agt gaa cag aca cgg gtg aat gct 582

cctttatggtt acaact	atg aaa gtc ttc aat cca att ccc tgc ttc cac	769
	Met Lys Val Phe Asn Pro Ile Pro Cys Phe His	
	1 5 10	
aca aag gac aaa gaa agc cta aac ttt cct ttt ttc tgg gct cca ata	817	
Thr Lys Asp Lys Glu Ser Leu Asn Phe Pro Phe Phe Trp Ala Pro Ile		
	15 20 25	
gga agc agc att tac aac gtg tct ggc ttg gtg gga gga aga ttg tca	865	
Gly Ser Ser Ile Tyr Asn Val Ser Gly Leu Val Gly Gly Arg Leu Ser		
	30 35 40	
att gag gta tca tgt gtg ttc acc tgc ctc tct tgc cct att tct ttg	913	
Ile Glu Val Ser Cys Val Phe Thr Cys Leu Ser Cys Pro Ile Ser Leu		
	45 50 55	
gtt gct ata aat ttc ctg ctt ctc aaa tat ctg gat ttt tgg cta cct	961	
Val Ala Ile Asn Phe Leu Leu Leu Lys Tyr Leu Asp Phe Trp Leu Pro		
	60 65 70 75	
att tgg ctt ccg tct ttg gtg ttt ata tct gtc tgg ttt tag caggtct	1010	
Ile Trp Leu Pro Ser Leu Val Phe Ile Ser Val Trp Phe *		
	80 85	
ctctgattcc tgacccacag ctccctctcct tctctaatat tcaagtatgc tgcttcccta	1070	
actcctcatt ccttctcctt gaatttcact ttacaattgc gctaggttct aacatcggtg	1130	
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ataacattat caggcttgta aaatacttta tcaaatcaat gcatcagtta aagcaggggt	1550	
ccccagccct gggctgtgtg tggcctgtta ggaatcgggc cacacagttg gtgagctgag	1610	
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<211> 1217

<212> DNA

<213> Homo sapiens

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 <222> (353)..(472)

<400> 95

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taagtttttg tattccacta ctttcagttc aataaaacct agagttgttt catctgcgcc      180
taaagtgtat ggcacaattt tcttaagaat taggggaacc aggtgcctac agttaagga      240
acgtttcagt tcctttcatt cattcctggg tttttctttt attttctaag aaggttgaag      300
aaggatgagt gatagagaag aaagcaacac cattgatttt tttttttaag aa      atg      355
                                   Met
                                   1

ata tat ata tgt ata tgt ttg tgt gtg tgt gtg tgt gtg tgt gta ttc      403
Ile Tyr Ile Cys Ile Cys Leu Cys Val Cys Val Cys Val Cys Val Phe
              5              10              15

tgt gca tta ttt tgt cat gat ctc aat tct ctt ctt tcc acc aaa gtt      451
Cys Ala Leu Phe Cys His Asp Leu Asn Ser Leu Leu Ser Thr Lys Val
              20              25              30

tgt cgt aat att ttc tcc tga ag gtgcattctg gtcctttaa attagtcagt      504
Cys Arg Asn Ile Phe Ser      *
              35              40

gttatattgt aggagactgt catggaaaaa aggactcagt ttactttcgt cattttcaca      564
ggggaacctt ttaaaacaat cttttcagca gcagatacct ttaaccctaa taatctcagg      624
ccttgatgaa aatactatat tttgtagatt atgggttaaag ggggaaaatt actagttccg      684
taagataaat atgagctcca tttgacttct gatgtctggt ttagcattac ataatatggt      744
gatcttacac tctgcttttg tccaaataaa atgcaatagt atcaatatca atttcagaaa      804
aatggactga atatgctttt ttggtgatga aatctcatgt acgatattta tagtgatgtg      864
cttttatttt ctcatgagat actaaatatt aattgtgttg tacatttggt cttagcatat      924
attaaagttt tgaaccaaat gtgttaaagc ttacgctttg ccatgtaa atccccagaag      984
ttgttgagct caaatgtatc ctacatccag ctgtagaaat ttgtcagaaa ttgtttaaat     1044
tttgatatata attgtactgt ttaattctag ccattgcgct gaacagtatt tgagttacca     1104
tataatatgg ctttacacaa ggaaatgtgt ggcttttggt ttgtatTTTT tcagtataga     1164
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 <211> 1380
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<400> 96

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gcttgcaatt gaacatcacc ccccaactgg aagagcctca catcctggac gaatgaccaa      180

ggcgccagga gaaagactgt gttttctccc acgctacctg ccgcccgcctc ttctcttggc      240

tctctgcaaa cacctgaagc tgtgaccacc agaaagggca caggcttgct ttctcagac      300

tacaggatca tcaatggcaa aagtggaact caggacatcc agcctggccc tctttttaat      360

aataatgctg atggagtggc cacagatata acttctacca gatccttaaa ttacaaaagc      420

actagcagcg gtcacagaga aatatcatca cctaggattc aggatgctgg acctgcttcc      480

cgagatgtcc aggccactgg cagaatcgca gatgatgctg acccaagagt agcacttggt      540

aacgattctt tatctgatgt cacaagtacc acatcttcta ggggtggatga tcatgactca      600

gaggaaatth gtcttgacca tctgtgtaag ggttgctccgc ttaatggtag ctgcagcaaa      660

gtccacttcc atctgcctta ccgggtggcag      atg ctt att ggt aaa acc tgg      711
                               Met Leu Ile Gly Lys Thr Trp
                               1                               5

acg gac ttt gag cac atg gag acg atc gag aaa ggc tac tgt aac ccc      759
Thr Asp Phe Glu His Met Glu Thr Ile Glu Lys Gly Tyr Cys Asn Pro
          10                      15                      20

gga atc cac ctc tgt tct gta gga agt tat aca atc aat ttt cgg gta      807
Gly Ile His Leu Cys Ser Val Gly Ser Tyr Thr Ile Asn Phe Arg Val
          25                      30                      35

atg agt tgt gat tcc ttt ccc atc cga cgc ctc tcc act cct tct tct      855
Met Ser Cys Asp Ser Phe Pro Ile Arg Arg Leu Ser Thr Pro Ser Ser
          40                      45                      50                      55

gtc acc aag cca gcc aat tct gtc ttc acc acc aaa tgg att tgg tat      903
Val Thr Lys Pro Ala Asn Ser Val Phe Thr Thr Lys Trp Ile Trp Tyr
          60                      65                      70

tgg aag aat gaa tct ggc aca tgg att cag tat gga gaa gag aaa gac      951
Trp Lys Asn Glu Ser Gly Thr Trp Ile Gln Tyr Gly Glu Glu Lys Asp
          75                      80                      85

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aaa cgg aaa aat tca aac gtc gac tct tca tac ctg gag tct ctc tat      999
Lys Arg Lys Asn Ser Asn Val Asp Ser Ser Tyr Leu Glu Ser Leu Tyr
          90                      95                      100

caa tcc tgt ccg agg gga gtt gtg cca ttt cag gcg ggc tca cgg aac      1047
Gln Ser Cys Pro Arg Gly Val Val Pro Phe Gln Ala Gly Ser Arg Asn
      105                      110                      115

tat gag ctg agt ttc caa ggg atg att cag aca aac ata gct tcc aaa      1095
Tyr Glu Leu Ser Phe Gln Gly Met Ile Gln Thr Asn Ile Ala Ser Lys
      120                      125                      130                      135

act caa aag gat gtc atc aga aga cca aca ttt gtg cct cag tgg tat      1143
Thr Gln Lys Asp Val Ile Arg Arg Pro Thr Phe Val Pro Gln Trp Tyr
          140                      145                      150

gtg cag cag atg aag aga ggg cca gag taa g tgttctgaag cagctgtttg      1194
Val Gln Gln Met Lys Arg Gly Pro Glu *
          155                      160

ctgacagatg cttgagatgt tcatgccctg ggctcatcaa gtcactcgtg aatctggagc      1254

ctgttttcct gaaaagttcc tgtttgcatt actctgcagt ttccatttgc attatcgatg      1314

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ttttttt                                         1380

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gctctggtaa gccaaagactc cttgtgttta cctgttcac tctgcaatct aggggggtagc      180

attttgtcct gtgtccttac cggcaaaacg atgtataaat gaaagaaatt gagatgggtgc      240

acgatgcaca gttgaagtga acttgcgggg tttttcagta tctacgattc atagatctgg      300

aattcgcggc cgcgtcgacg aaatatctct ttcaataatg aaagaataag aaaaagaaat      360

agaagagctg gaaacaatag gtaaagttta ggctaggcct tagacttctc ctgcattgta      420

atccttctgg ttgccacat atgcatgctg tcaggaagtt gatgaggt atg tac agg      477
                               Met Tyr Arg

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aca atg att ttc cat ttt ttg cct tta ggc acc gac tca ttg gtc act 525
 Thr Met Ile Phe His Phe Leu Pro Leu Gly Thr Asp Ser Leu Val Thr
 5 10 15

cat ctg ctg aat gta tcc tct cag gca ata ctg ccc att gga gca cga 573
 His Leu Leu Asn Val Ser Ser Gln Ala Ile Leu Pro Ile Gly Ala Arg
 20 25 30 35

agc cgc caa ttt gtc aac gtg agt tga aatct ctttcccat tcacccacc 625
 Ser Arg Gln Phe Val Asn Val Ser *
 40

attgaatcct agagttgtcc tcctagaatt acaaagaatg gatctcatcc ctcttgga 685

tggtatcctt ctgatatttg aagaatctag tcatatcctt aaaatggctc acagcattcc 745

aaacttcgcg cttcacctag aaatgctttt ttttttctta tctcagtcta atgtatttta 805

aactagtctt tagctcattt aaccagcccc caatgtcctc ttctgttggg tgagcacctc 865

gcagtttgaa gagcattttg tttagtgaag tcaacaaata caaagtcagt gaaagaaacc 925

ccatatactc tctgcaagct cttagtatca catcagatat tcaagccatg cagctctttc 985

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atgagctttc gtcgacgcgg ccgcgaattc ggatcctcga gagatctctt tttttggggt 1105

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gtcccgggcc cggagcgcta ggagcgcgcg gaaggagcc atg gct ctg gac ggg 174
 Met Ala Leu Asp Gly
 1 5

ata agg atg cca gat ggc tgc tac gcg gac ggg acg tgg gaa ctg agt 222
 Ile Arg Met Pro Asp Gly Cys Tyr Ala Asp Gly Thr Trp Glu Leu Ser
 10 15 20

gtc cat gtg acg gac ctg aac cgc gat gtc acc ctg aga gtg acc ggc Val His Val Thr Asp Leu Asn Arg Asp Val Thr Leu Arg Val Thr Gly 25 30 35	270
gag gtg cac att gga ggc gtg atg ctt aag ctg gtg gag aaa ctc gat Glu Val His Ile Gly Gly Val Met Leu Lys Leu Val Glu Lys Leu Asp 40 45 50	318
gta aaa aaa gat tgg tct gac cat gct ctc tgg tgg gaa aag aag aga Val Lys Lys Asp Trp Ser Asp His Ala Leu Trp Trp Glu Lys Lys Arg 55 60 65	366
act tgg ctt ctg aag aca cat tgg acc tta gat aag tat ggt att cag Thr Trp Leu Leu Lys Thr His Trp Thr Leu Asp Lys Tyr Gly Ile Gln 70 75 80 85	414
gca gat gct aag ctt cag ttc acc cct cag cac aaa ctg ctc cgc ctg Ala Asp Ala Lys Leu Gln Phe Thr Pro Gln His Lys Leu Leu Arg Leu 90 95 100	462
cag ctt ccc aac atg aag tat gtg aag gtg aaa gtg aat ttc tct gat Gln Leu Pro Asn Met Lys Tyr Val Lys Val Lys Val Asn Phe Ser Asp 105 110 115	510
aga gtc ttc aaa gct gtt tct gac atc tgt aag act ttt aat atc aga Arg Val Phe Lys Ala Val Ser Asp Ile Cys Lys Thr Phe Asn Ile Arg 120 125 130	558
cac ccc gaa gaa ctt tct ctc tta aag aaa ccc aga gat cca aca aaa His Pro Glu Glu Leu Ser Leu Leu Lys Lys Pro Arg Asp Pro Thr Lys 135 140 145	606
aaa aaa aaa aaa aag cta gat gac cag tct gaa gat gag gca ctt gaa Lys Lys Lys Lys Lys Leu Asp Asp Gln Ser Glu Asp Glu Ala Leu Glu 150 155 160 165	654
tta gag ggg cct ctt atc act cct gga tca gga agt ata tat tca agc Leu Glu Gly Pro Leu Ile Thr Pro Gly Ser Gly Ser Ile Tyr Ser Ser 170 175 180	702
cca gga ctg tat agt aaa aca atg acc ccc act tat gat gct cat gat Pro Gly Leu Tyr Ser Lys Thr Met Thr Pro Thr Tyr Asp Ala His Asp 185 190 195	750
gga agc ccc ttg tca cca act tct gct tgg ttt ggt gac agt gct ttg Gly Ser Pro Leu Ser Pro Thr Ser Ala Trp Phe Gly Asp Ser Ala Leu 200 205 210	798
tca gaa ggc aat cct ggt ata ctt gct gtc agt caa cca atc acg tca Ser Glu Gly Asn Pro Gly Ile Leu Ala Val Ser Gln Pro Ile Thr Ser 215 220 225	846
cca gaa atc ttg gca aaa atg ttc aag cct caa gct ctt ctt gat aaa Pro Glu Ile Leu Ala Lys Met Phe Lys Pro Gln Ala Leu Leu Asp Lys 230 235 240 245	894
gca aaa atc aac caa gga tgg ctt gat tcc tca aga tct ctc atg gaa	942

tattaatcta tcatgttatg atataataaa cttgaatttg gcacacattc cttagggcca 2425
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Ile Gly Gly Ser Asn His Leu Ala Val Val Leu Asp Asp Ile Ile Leu
5 10 15
gca gtt att gac tcc att ttt gtg tgg ttc att ttt att agt ttg gca 151
Ala Val Ile Asp Ser Ile Phe Val Trp Phe Ile Phe Ile Ser Leu Ala
20 25 30 35

caa act atg aag acc cta agg cta aga aag aac act gtg aaa ttt tca	199
Gln Thr Met Lys Thr Leu Arg Leu Arg Lys Asn Thr Val Lys Phe Ser	
40 45 50	
tta tat aga cat ttt aaa aat act ctg atc ttt gct gtg ctg gct tct	247
Leu Tyr Arg His Phe Lys Asn Thr Leu Ile Phe Ala Val Leu Ala Ser	
55 60 65	
ata gtg ttt atg ggg tgg aca act aag aca ttt aga att gca aaa tgc	295
Ile Val Phe Met Gly Trp Thr Thr Lys Thr Phe Arg Ile Ala Lys Cys	
70 75 80	
caa tca gat tgg atg gaa cgc tgg gtt gac gat gca ttt tgg agc ttc	343
Gln Ser Asp Trp Met Glu Arg Trp Val Asp Asp Ala Phe Trp Ser Phe	
85 90 95	
ctt ttt tcg ctt atc ctt att gta atc atg ttt ttg tgg aga cca tca	391
Leu Phe Ser Leu Ile Leu Ile Val Ile Met Phe Leu Trp Arg Pro Ser	
100 105 110 115	
gca aac aat cag aga tat gcc ttc atg ccc tta ata gat gat tct gat	439
Ala Asn Asn Gln Arg Tyr Ala Phe Met Pro Leu Ile Asp Asp Ser Asp	
120 125 130	
gat gaa att gag gaa ttc atg gta act tct gaa aat tta acc gaa gga	487
Asp Glu Ile Glu Glu Phe Met Val Thr Ser Glu Asn Leu Thr Glu Gly	
135 140 145	
ata aaa tta aga gcc tca aaa tca gtt tcc aat gga aca gct aag cct	535
Ile Lys Leu Arg Ala Ser Lys Ser Val Ser Asn Gly Thr Ala Lys Pro	
150 155 160	
gcc act tct gag aac ttt gat gaa gat ttg aag tgg gta gaa gaa aat	583
Ala Thr Ser Glu Asn Phe Asp Glu Asp Leu Lys Trp Val Glu Glu Asn	
165 170 175	
att ccc tct tca ttc aca gat gta gct ctt cca gtg tta gtg gat tca	631
Ile Pro Ser Ser Phe Thr Asp Val Ala Leu Pro Val Leu Val Asp Ser	
180 185 190 195	
gat gag gaa atc atg acc aga tct gaa atg gct gaa aaa atg ttc tct	679
Asp Glu Glu Ile Met Thr Arg Ser Glu Met Ala Glu Lys Met Phe Ser	
200 205 210	
tca gaa aag ata atg tga ttggaa cccgtataag aaatgtagtt aagcctgaag	733
Ser Glu Lys Ile Met *	
215	
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tgtgttatct tggaagtctg tgtatcaaaa tgaagaattc agatggtagg aggttctata	853
gtccttttta agctgactct tgagtgtcag ttgaatatcc attaaattgg atttggaat	913
aacctgagga aagtattatg ataaagatct gcacagatgc ctcttagctg ataggtggca	973

ggg gtc cac cac ctg agc ccc cct ggg ggt gga ccc tcc ccg ggg cgc	355
Gly Val His His Leu Ser Pro Pro Gly Gly Gly Pro Ser Pro Gly Arg	
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Pro Val Leu Gln Arg Asp Leu Tyr Met Lys Ala Glu Pro Pro Ile Pro	
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His Tyr Ala Ala Met Gly Gln Gly Leu Val Pro Thr Asp Leu His His	
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Thr Gln Gln Ser Gln Met Leu His Gln Leu Leu Gln Gln His Gly Ala	
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Glu Leu Pro Thr His Pro Ser Lys Lys Arg Lys His Ser Glu Ser Pro	
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Tyr	Leu	Asp	Pro	Asn	Tyr	Gln	Ser	Ile	Lys	Trp	Gln	Pro	His	Gln	Gln	
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Asn	Lys	Trp	Ala	Thr	Leu	Tyr	Asp	Ala	Asn	Tyr	Lys	Glu	Leu	Pro	Met	
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Leu	Lys	Pro	Leu	Asp	Cys	Phe	Tyr	Leu	Lys	Leu	His	Gly	Val	Lys	Leu	
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 gag aaa ggg gca tcc aca gac atc tgt gcc ttc tgc cac aag acc gtg 451
 Glu Lys Gly Ala Ser Thr Asp Ile Cys Ala Phe Cys His Lys Thr Val
 100 105 110

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 Phe Pro Arg Glu Leu Ala Val Glu Ala Met Lys Arg Gln Tyr His Ala
 115 120 125

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 Gln Cys Phe Thr Cys Arg Thr Cys Arg Arg Gln Leu Ala Gly Gln Ser
 130 135 140 145

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Phe Tyr Gln Lys Asp Gly Arg Pro Leu Cys Glu Pro Cys Tyr Gln Asp	
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Thr Leu Glu Arg Cys Gly Lys Cys Gly Glu Val Val Arg Asp His Ile	
165 170 175	
atc agg gcc ctg ggc cag gcc ttc cac ccc tcc tgc ttc acg tgt gtg	691
Ile Arg Ala Leu Gly Gln Ala Phe His Pro Ser Cys Phe Thr Cys Val	
180 185 190	
acc tgc gcc cgg tgc att ggg gat gag agc ttt gcc ctg ggc agc cag	739
Thr Cys Ala Arg Cys Ile Gly Asp Glu Ser Phe Ala Leu Gly Ser Gln	
195 200 205	
aac gag gtg tac tgc ctg gac gac ttc tac agg aaa ttc gcc ccc gtc	787
Asn Glu Val Tyr Cys Leu Asp Asp Phe Tyr Arg Lys Phe Ala Pro Val	
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Cys Ser Ile Cys Glu Asn Pro Ile Ile Pro Arg Asp Gly Lys Asp Ala	
230 235 240	
ttc aaa atc gaa tgc atg gga aga aac ttc cat gaa aat tgc tac agg	883
Phe Lys Ile Glu Cys Met Gly Arg Asn Phe His Glu Asn Cys Tyr Arg	
245 250 255	
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Cys Glu Asp Cys Arg Ile Leu Leu Ser Val Glu Pro Thr Asp Gln Gly	
260 265 270	
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Cys Tyr Pro Leu Asn Asn His Leu Phe Cys Lys Pro Cys His Val Lys	
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Ala Thr His Val Arg Asp Phe Arg Leu Phe Val Pro Asn His Arg Ser			
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Leu Asn Val Asp Met Glu Trp Leu Tyr Gly Ala Ser Glu Ser Ser Asn			
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atg gag gtg gac atc ggc tac ata ccc cag atg gag ctg gag gcc acg			1008
Met Glu Val Asp Ile Gly Tyr Ile Pro Gln Met Glu Leu Glu Ala Thr			
	240	245	250
ggc ccc tct gtg ccc tcc gtg atc ctg gat gag gat ggc agc atg atc			1056
Gly Pro Ser Val Pro Ser Val Ile Leu Asp Glu Asp Gly Ser Met Ile			
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gac agc cac ctg ccc tca ggg gag ccc ctg cag ttt gtg ttt gag gag			1104
Asp Ser His Leu Pro Ser Gly Glu Pro Leu Gln Phe Val Phe Glu Glu			
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Ile Lys Trp Gln Gln Glu Leu Ser Trp Glu Glu Ala Ala Arg Arg Leu			
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Glu Val Ala Met Tyr Pro Phe Lys Lys Val Ser Tyr Leu Pro Phe Thr			
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gag gcc ttc gac cga gcc aag gct gag aac aag ctg gtg cac tca atc			1248
Glu Ala Phe Asp Arg Ala Lys Ala Glu Asn Lys Leu Val His Ser Ile			
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ctg ctg tgg ggg gcc ctg gat gac cag tcc tgc tga gggt cagggcggac			1298
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cag tgc ctg gct tct cag gcc gcc gcc agc cgg gac tgc ttt agg cgc 106
Gln Cys Leu Ala Ser Gln Ala Ala Ser Arg Asp Cys Phe Arg Arg
      5                      10                      15

gaa ccc acg ctt ctg acc tgt gct ctg tct ttg cag ttc tgc acg gag 154
Glu Pro Thr Leu Leu Thr Cys Ala Leu Ser Leu Gln Phe Cys Thr Glu
      20                      25                      30

cta aac cag ccg acc ctg ccc aac atc cgc aag tgg aag ggg ccc cgg 202
Leu Asn Gln Pro Thr Leu Pro Asn Ile Arg Lys Trp Lys Gly Pro Arg
      35                      40                      45

gga tgc tgg aag gct gtt gtt gct gag aag ccc tcg aat cag ctc cag 250
Gly Cys Trp Lys Ala Val Val Ala Glu Lys Pro Ser Asn Gln Leu Gln
      50                      55                      60                      65

aag gta ccc tcg tct gca aag cct ggc ctt tcc ctt cat tta att tat 298
Lys Val Pro Ser Ser Ala Lys Pro Gly Leu Ser Leu His Leu Ile Tyr

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70	75	80	
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85	90	95	
atc ccc ggt tca att ttg tat ttc tgc cca att ttt aaa tcc ttg cca			394
Ile Pro Gly Ser Ile Leu Tyr Phe Cys Pro Ile Phe Lys Ser Leu Pro			
100	105	110	
ttc att tcc aaa tgc cct ggt ttt cgg ttc acg ttt aga ttg gta atg			442
Phe Ile Ser Lys Cys Pro Gly Phe Arg Phe Thr Phe Arg Leu Val Met			
115	120	125	
gac tcc tgc caa gaa gga aat gag agc ctt agg gtg ttg gga gag agg			490
Asp Ser Cys Gln Glu Gly Asn Glu Ser Leu Arg Val Leu Gly Glu Arg			
130	135	140	145
agg gga gaa agg caa caa atg ggt att tct gtc ctt tgt cct tct aat			538
Arg Gly Glu Arg Gln Gln Met Gly Ile Ser Val Leu Cys Pro Ser Asn			
150	155	160	
ccc ttc gcc aca gtt ctg tct tct gcc aag ttt gtg cag agc tca tta			586
Pro Phe Ala Thr Val Leu Ser Ser Ala Lys Phe Val Gln Ser Ser Leu			
165	170	175	
ctc gtt gac tga aaa tttcagattc accttagttc acacatgaag tatttgcttc			641
Leu Val Asp *			
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1509

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<213> Homo sapiens

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<222> (781)..(942)

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ggcagttggt tgtttttaaac tgaccacttg gaagaaacac cttgggttatc tgtgggttttc      180
atgccttgtc cctgcctcta cccccacccc ttttgagtcg ggtgactcat ttttctgtgt      240
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ccccaactct tgaacgatga tgatattcag acgaagcatt gatgttatgg aagaaagaaa      480
gaaacaaaca aaaaatatat atatatgtcc aaaaacagac aaatccaagg gtgtgaggta      540
aacgagtgtc tgcatttaga ttccacaaaa ccaaaatcca tgttgaacaa agttaagtcc      600
gtacacagtg actttttggg tgagccgtgt gtgtctgtct gttgtgtgtg tgcctcaagc      660
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atg tct gac tgt gta ctc ggg tgt act ccg cag cat tgt cga ctg cag      828
Met Ser Asp Cys Val Leu Gly Cys Thr Pro Gln His Cys Arg Leu Gln
  1             5             10             15
tcc cct gtg ttt gcc aga gat act gtg ctc gaa gta gag gtt tta ctc      876
Ser Pro Val Phe Ala Arg Asp Thr Val Leu Glu Val Glu Val Leu Leu
          20             25             30
tac tca tca ctg cga ttt gca cat tgc tcc gtg gac act cgg agg cct      924
Tyr Ser Ser Leu Arg Phe Ala His Cys Ser Val Asp Thr Arg Arg Pro
      35             40             45
gcg ttc tgt tcc cta taa atggaa gcgtgctctg agcctgtctg cctccctcgg      978
Ala Phe Cys Ser Leu *
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50

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tactgctggg tgaagccgaa cctcgggagc ccaggacgcc ctccctgcaca tgcgcaggag 240
gctca      atg aca gtc gag ctt tgg cta agg ctc cgg gga aag ggt cta 287
            Met Thr Val Glu Leu Trp Leu Arg Leu Arg Gly Lys Gly Leu
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Ala Met Leu His Val Thr Arg Gly Val Trp Gly Ser Arg Val Arg Val	
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Trp Pro Leu Leu Pro Ala Leu Leu Gly Pro Pro Arg Ala Leu Ser Ser	
35 40 45	
ctg gca gcc aaa atg ggg gag tat cgc aag atg tgg aac ccc agg gag	431
Leu Ala Ala Lys Met Gly Glu Tyr Arg Lys Met Trp Asn Pro Arg Glu	
50 55 60	
ccc cgc gac tgg gcc cag cag tac cgc gag cgc ttc att ccc ttc tcc	479
Pro Arg Asp Trp Ala Gln Gln Tyr Arg Glu Arg Phe Ile Pro Phe Ser	
65 70 75	
aag gag cag ctg ctc cgc ctc cta ata cag gta aca gga att cca ctc	527
Lys Glu Gln Leu Leu Arg Leu Leu Ile Gln Val Thr Gly Ile Pro Leu	
80 85 90	
gag tcc ggc aga gaa ggc ggc ttt gga ggc gtt ctc agc cca cgt gga	575
Glu Ser Gly Arg Glu Gly Gly Phe Gly Gly Val Leu Ser Pro Arg Gly	
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Leu Leu His Pro Val Pro Leu Pro Pro Asn Pro Gly Pro Ala Ala Gly	
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Gly Gln Leu Leu Arg Gly Leu Ser Lys Tyr Gly Met Lys Asn Ile Val	
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Asp Tyr Gly Leu Lys Pro Val Pro Gly Asp Leu Val Leu Lys Gly Ala	
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Lys Ile Gln Glu Ala Tyr Arg Glu Met Leu Thr Ala Asp Asn Leu Asp	
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Ile Asp Asn Met Arg His Lys Ile Arg Asp Tyr Ser Leu Ser Gly Ala	
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Lys Glu Leu Lys Lys Ile Cys Lys Ser Ser Glu Glu Gln Leu Ser Arg		
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gcc tac cgc ctc ctc ata gac ccg aac tgt agt ggc cac agc ccg cgc		195
Ala Tyr Arg Leu Leu Ile Asp Pro Asn Cys Ser Gly His Ser Pro Arg		
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Thr Ala Arg His Ala Pro Ala Val Arg Lys Phe Ser Pro Asp Leu Lys		
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Leu Leu Lys Asp Val Lys Ile Ser Val Ser Phe Thr Glu Ser Cys Arg		
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Ser Lys Asp Arg Lys Val Leu Tyr Thr Gly Ala Glu Arg Asp Val Arg		
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Ala Glu Cys Gly Leu Leu Leu Ser Pro Val Ser Gly Asp Val His Ala		
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Cys Pro Phe Gly Gly Ser Val Gly Asp Gly Val Gly Ile Gly Gly Glu		
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Ser Ala Asp Lys Lys Asp Glu Glu Asn Glu Leu Asp Gln Glu Lys Arg		
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Val Glu Tyr Ala Val Leu Asp Glu Leu Glu Asp Phe Thr Asp Asn Leu		
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Gln Arg Asp Arg Val Asp Glu Glu Ala Leu Asn Phe Pro Tyr Glu Val	
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Cys Leu Leu Ala Ile Tyr Ser Leu Leu Trp Ile Val Cys Ile Pro Tyr	
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Leu Leu Ser Ile Gly Leu Cys Val Asp Ile Leu Phe Leu Phe Val Gln	
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His Leu Leu Pro His Leu Leu Val Thr Gln Pro Leu Phe Ile Cys Gly	
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Glu Pro Ile Pro Cys Gly Leu Gly Glu His Val Thr Arg Pro Gly Leu	

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Leu Ser Pro Thr Ala Ser *			
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Glu Arg Val Gly Tyr Arg Glu Gly Pro Thr Val Glu Thr Lys Arg Ile			
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Gln Pro Gln Pro Pro Asp Glu Asp Gly Asp His Ser Asp Lys Glu Asp			
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Glu Gln Pro Gln Val Val Leu Lys Lys Gly Asp Leu Ser Val Glu			
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Glu Val Met Lys Ile Lys Ala Glu Ile Lys Ala Ala Lys Ala Asp Glu			

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His Pro Ser Asp Glu Lys Tyr Ser Gly Leu Thr Ala Ser Ser Lys Lys			
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Lys Lys Pro Asn Glu Asp Glu Val Asn Gln Asp Ser Val Lys Lys Asn			
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Asp Glu Asn Glu *			
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Met Val Val Ser Lys Met Asn			
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Cys Gly Trp Lys Asp Gln Leu Lys Ala His Cys Lys Glu Val Ile Lys
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Thr Pro Lys Gly Arg Ala Leu Val Pro Asp Ser Val Lys Lys Glu Leu
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Leu Gln Arg Ile Arg Thr Phe Leu Ala Gln His Ala Ser Leu *
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Asp	Gly	Thr	Leu	Ile	Thr	Cys	Val	Asp	Ser	Gly	Ile	Leu	Arg	Val	Trp		
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Trp	Leu	Asp	Leu	Arg	Val	Pro	Ile	Trp	Asp	Gln	Asp	Ile	Gln	Phe	Leu		
			180					185					190				
cca	gga	tca	cag	aag	ctt	gtc	acc	tgc	aca	ggg	tac	cac	cag	gtc	cgt	1100	
Pro	Gly	Ser	Gln	Lys	Leu	Val	Thr	Cys	Thr	Gly	Tyr	His	Gln	Val	Arg		
		195					200					205					
gtt	tat	gat	cca	gca	tcc	ccc	cag	cgc	cgg	cca	gtc	cta	gag	acc	acc	1148	
Val	Tyr	Asp	Pro	Ala	Ser	Pro	Gln	Arg	Arg	Pro	Val	Leu	Glu	Thr	Thr		
	210					215					220						
tat	gga	gag	tac	cca	cta	aca	gcc	atg	acc	ctc	act	ccg	gga	ggc	aac	1196	
Tyr	Gly	Glu	Tyr	Pro	Leu	Thr	Ala	Met	Thr	Leu	Thr	Pro	Gly	Gly	Asn		
	225				230					235					240		
tca	gtg	att	gtg	gga	aac	act	cat	ggg	cag	ctg	gca	gaa	att	gac	ctt	1244	
Ser	Val	Ile	Val	Gly	Asn	Thr	His	Gly	Gln	Leu	Ala	Glu	Ile	Asp	Leu		

caa gtt gta cga gaa ggg aag ttc tcg ggg ttt ctg acc tcc tgc agc 165
 Gln Val Val Arg Glu Gly Lys Phe Ser Gly Phe Leu Thr Ser Cys Ser
 5 10 15

ctc ctc ttg cct cgg gct gcc cag atc ttg gcg gct gag gct ggc tta 213
 Leu Leu Leu Pro Arg Ala Ala Gln Ile Leu Ala Ala Glu Ala Gly Leu
 20 25 30 35

cct tcg agc cgt tcc ttc atg gga ttt gct gct ccc ttc acc aac aag 261
 Pro Ser Ser Arg Ser Phe Met Gly Phe Ala Ala Pro Phe Thr Asn Lys
 40 45 50

cga aag gct tac tcg gag cgt aga atc atg ggg tac tca atg cag gag 309
 Arg Lys Ala Tyr Ser Glu Arg Arg Ile Met Gly Tyr Ser Met Gln Glu
 55 60 65

atg tat gag gtg gtg tcc aac gtc cag gag tat cgt gag ttt gtg ccc 357
 Met Tyr Glu Val Val Ser Asn Val Gln Glu Tyr Arg Glu Phe Val Pro
 70 75 80

tgg tgt aag aag tct ctg gtg gta tcc agc cgt aag ggt cat ttg aaa 405
 Trp Cys Lys Lys Ser Leu Val Val Ser Ser Arg Lys Gly His Leu Lys
 85 90 95

gcc cag ctg gag gtt ggc ttt cca cct gtc atg gaa cgt tac acc tct 453
 Ala Gln Leu Glu Val Gly Phe Pro Pro Val Met Glu Arg Tyr Thr Ser
 100 105 110 115

gca gtt tcc atg gtc aaa cct cac atg gtc aag gct gtt tgt act gat 501
 Ala Val Ser Met Val Lys Pro His Met Val Lys Ala Val Cys Thr Asp
 120 125 130

ggc aag ctc ttc aac cac tta gag act att tgg cga ttc agc cct ggt 549
 Gly Lys Leu Phe Asn His Leu Glu Thr Ile Trp Arg Phe Ser Pro Gly
 135 140 145

att cct gcc tat cct cga acc tgc act gtg gac ttt tcg att tcc ttt 597
 Ile Pro Ala Tyr Pro Arg Thr Cys Thr Val Asp Phe Ser Ile Ser Phe
 150 155 160

gaa ttt cgt tct ctg ctg cac tcc cag ctg gcc acc atg ttt ttt gat 645
 Glu Phe Arg Ser Leu Leu His Ser Gln Leu Ala Thr Met Phe Phe Asp
 165 170 175

gag gtt gtc aaa cag aat gtt gct gcc ttt gag cgt cgg gca gcc acc 693
 Glu Val Val Lys Gln Asn Val Ala Ala Phe Glu Arg Arg Ala Ala Thr
 180 185 190 195

aag ttt ggt cca gaa aca gcc atc ccc cgt gaa ctg atg ttc cat gag 741
 Lys Phe Gly Pro Glu Thr Ala Ile Pro Arg Glu Leu Met Phe His Glu
 200 205 210

gtg cac cag act tga ggcaagggat tgctccctga cctcccttct accccacttc 796
 Val His Gln Thr *
 215

cctacacaat tctcttattt atttggtttg gctcctgttc caatttgaaa ggagtctgtg 856
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 cctgaccaac atggagaaac cccatctcta cttaaaaaaa aaaaaatacg aatttaccoca 180
 ggcattggtg tgggcacctg taatcccagc tactcgggag actgaggcgg gagattctct 240
 tgaacctggg aggcagaggt tgcgggtgagc cgagatcgtg ccattgcact ccagcctggg 300
 caacaagagc aaaactccat ctcaaaaaga aaaaagaaag aaagaaatgc taggggaaaa 360
 tgttttaact agtcattctt cccagtagct a atg aag ctg act ttt aaa aag 412
 Met Lys Leu Thr Phe Lys Lys
 1 5
 aag gct gtg agc ttt gca gat gct gct gcc gcc cag ggc ccc ctg ctt 460
 Lys Ala Val Ser Phe Ala Asp Ala Ala Ala Gln Gly Pro Leu Leu
 10 15 20
 cca gcc atg gtc aac ccc acc atg ttt ttc cac att gct gtc gat ggc 508

Pro Ala Met Val Asn Pro Thr Met Phe Phe His Ile Ala Val Asp Gly
 25 30 35

gag ccc ttg ggc tgt gtc tcc ttc gag ctg ttt gca gac aag gtt cca 556
 Glu Pro Leu Gly Cys Val Ser Phe Glu Leu Phe Ala Asp Lys Val Pro
 40 45 50 55

aag aca gca gaa aat ttc cat gct ctg agc act gga gaa aaa gga ttt 604
 Lys Thr Ala Glu Asn Phe His Ala Leu Ser Thr Gly Glu Lys Gly Phe
 60 65 70

ggg tat aag ggt tcc tgc ttt cac aga att att cca ggg ttt acg tgt 652
 Gly Tyr Lys Gly Ser Cys Phe His Arg Ile Ile Pro Gly Phe Thr Cys
 75 80 85

cag agt ggt gac ttc aca cgc cat aca gca ttg gtg gca agt cca tct 700
 Gln Ser Gly Asp Phe Thr Arg His Thr Ala Leu Val Ala Ser Pro Ser
 90 95 100

gca ggg aga aat ttg atg aca aga act tca tcc tga agca tacgggtcct 750
 Ala Gly Arg Asn Leu Met Thr Arg Thr Ser Ser *
 105 110 115

ggcatcttgt ccatggcaaa tgctggaccc agcgtgaacg tttcccagtt ttttatctgc 810

cctgccaaaga tgccaagaca gagtgggttg attgcaagca tgtggtcttt ggcaaggatga 870

aagatggcat gaatattgtg gaggtcatgg agcacttggg gtccaagaat ggcaagatca 930

gcaatcagca agaagatcac cattgctgac tggacaactg caataaattt gacgggtggt 990

tctcttaaaa aaaaaaaaa 1008

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agttggcagc ggcaagcgcg ctgcggttcc ggtggcgcc atg tcg ttc tgc agc 174
 Met Ser Phe Cys Ser
 1 5

ttc ttc ggg ggc gag gtt ttc cag aat cac ttt gaa cct ggc gtt tac 222
 Phe Phe Gly Gly Glu Val Phe Gln Asn His Phe Glu Pro Gly Val Tyr
 10 15 20

gtg tgt gcc aag tgt ggc tat gag ctg ttc tcc agc cgc tcg aag tat	270
Val Cys Ala Lys Cys Gly Tyr Glu Leu Phe Ser Ser Arg Ser Lys Tyr	
25 30 35	
gca cac tcg tct cca tgg ccg gcg ttc acc gag acc att cac gcc gac	318
Ala His Ser Ser Pro Trp Pro Ala Phe Thr Glu Thr Ile His Ala Asp	
40 45 50	
agc gtg gcc aag cgt ccg gag cac aat aga tct gaa gcc ttg aag gtg	366
Ser Val Ala Lys Arg Pro Glu His Asn Arg Ser Glu Ala Leu Lys Val	
55 60 65	
tcc tgt ggc aag tgt ggc aat ggg ttg ggc cac gag ttc ctg aac gac	414
Ser Cys Gly Lys Cys Gly Asn Gly Leu Gly His Glu Phe Leu Asn Asp	
70 75 80 85	
ggc ccc aag ccg ggg cag tcc cga ttc tga a tattcagcag ctgcgtgaag	465
Gly Pro Lys Pro Gly Gln Ser Arg Phe *	
90 95	
tttgtcccta aaggcaaaga aacttctgcc tcccagggtc actaggcggg cagccccacac	525
ccaccccaga cggccaccac actgaggcca cacgttggcc attccacctt ggagttggaa	585
ccctgggcgt cgagacagga aggcagggcg cagtggttga aacatcagga cactcccaag	645
gccccggctc tgaacaagac cttttcgttt cttggaaaag agactcatTT gctgatggtt	705
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cgtcttggtc aaacccttcc aggccagcca gagtggggat ggtctgtgac ctgctgggaa	1065
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cataactcta accagcacag ggctgaggcc tgcagtgcac acctgcaggg aggcccttcc	1245
caaggtgtgg tgactgtgcc ttactgtaca tgctcgagg cctggccata taggaggggtg	1305
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<211> 2179
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 Met Glu Met Arg Leu Pro Ile Arg Ser Pro Ile Lys Arg
 1 5 10
 gac ttt tta tca gga att cag att gaa ttt aag cag tct tct cac cag 156
 Asp Phe Leu Ser Gly Ile Gln Ile Glu Phe Lys Gln Ser Ser His Gln
 15 20 25
 aga agt tta agg gcc agg ttg tac tgg ctt cag gtt gat aat cag tta 204
 Arg Ser Leu Arg Ala Arg Leu Tyr Trp Leu Gln Val Asp Asn Gln Leu
 30 35 40 45
 cca ggt gca atg ttc cct gtt gta ttt cat cct gtt gcc cct cca aaa 252
 Pro Gly Ala Met Phe Pro Val Val Phe His Pro Val Ala Pro Pro Lys
 50 55 60
 tct att gct tta gat tca gag ccc aag cct ttc att gat gtg agt gtc 300
 Ser Ile Ala Leu Asp Ser Glu Pro Lys Pro Phe Ile Asp Val Ser Val
 65 70 75
 atc aca aga ttt aat gag tac agt aaa gtc tta cag ttc aag tat ttt 348
 Ile Thr Arg Phe Asn Glu Tyr Ser Lys Val Leu Gln Phe Lys Tyr Phe
 80 85 90
 atg gtc ctc att cag gaa atg gcc tta aaa att gat caa ggg ttt cta 396
 Met Val Leu Ile Gln Glu Met Ala Leu Lys Ile Asp Gln Gly Phe Leu
 95 100 105
 gga gct att att gca ctg ttt acc cca aca aca gac cct gaa gct gaa 444
 Gly Ala Ile Ile Ala Leu Phe Thr Pro Thr Thr Asp Pro Glu Ala Glu
 110 115 120 125
 aga aga cgg aca aag tta atc caa caa gat att gat gct cta aat gca 492
 Arg Arg Arg Thr Lys Leu Ile Gln Gln Asp Ile Asp Ala Leu Asn Ala
 130 135 140
 gaa tta atg gag act tca atg act gat atg tca att ctt agt ttc ttt 540
 Glu Leu Met Glu Thr Ser Met Thr Asp Met Ser Ile Leu Ser Phe Phe
 145 150 155
 gaa cat ttc cat att tct cct gtg aag ttg cat ttg agt ttg tct ttg 588
 Glu His Phe His Ile Ser Pro Val Lys Leu His Leu Ser Leu Ser Leu
 160 165 170
 ggt tcc gga ggt gaa gaa tca gac aaa gaa aaa cag gaa atg ttt gca 636
 Gly Ser Gly Gly Glu Glu Ser Asp Lys Glu Lys Gln Glu Met Phe Ala

175	180	185	
gtt cat tct gtc aac ttg ctg ttg aaa agc ata ggt gct act ctg act			684
Val His Ser Val Asn Leu Leu Lys Ser Ile Gly Ala Thr Leu Thr			
190	195	200	205
gat gtg gat gac ctt ata ttc aaa ctt gct tat tat gaa att cga tat			732
Asp Val Asp Asp Leu Ile Phe Lys Leu Ala Tyr Tyr Glu Ile Arg Tyr			
	210	215	220
cag ttc tac aag aga gat cag ctt ata tgg agt gtt gtt agg cat tac			780
Gln Phe Tyr Lys Arg Asp Gln Leu Ile Trp Ser Val Val Arg His Tyr			
	225	230	235
agt gaa cag ttc ttg aaa cag atg tat gtc ctt gta ttg ggg tta gat			828
Ser Glu Gln Phe Leu Lys Gln Met Tyr Val Leu Val Leu Gly Leu Asp			
	240	245	250
gta ctt gga aac cca ttt gga tta att aga ggt ctg tct gaa gga gtt			876
Val Leu Gly Asn Pro Phe Gly Leu Ile Arg Gly Leu Ser Glu Gly Val			
	255	260	265
gaa gct tta ttc tat gaa ccc ttc cag ggt gct gtt caa ggc cct gaa			924
Glu Ala Leu Phe Tyr Glu Pro Phe Gln Gly Ala Val Gln Gly Pro Glu			
	270	275	280
gaa ttt gca gag ggg tta gtg att gga gtg aga agc ctc ttt gga cac			972
Glu Phe Ala Glu Gly Leu Val Ile Gly Val Arg Ser Leu Phe Gly His			
	290	295	300
aca gta ggt ggt gca gca gga gtt gta tct cga atc acc ggt tct gtt			1020
Thr Val Gly Gly Ala Ala Gly Val Val Ser Arg Ile Thr Gly Ser Val			
	305	310	315
ggg aaa ggt ttg gca gca att aca atg gac aag gaa tat cag caa aaa			1068
Gly Lys Gly Leu Ala Ala Ile Thr Met Asp Lys Glu Tyr Gln Gln Lys			
	320	325	330
aga aga gaa gag ttg agt cga cag ccc aga gat ttt gga gac agc ctg			1116
Arg Arg Glu Glu Leu Ser Arg Gln Pro Arg Asp Phe Gly Asp Ser Leu			
	335	340	345
gcc aga gga gga aag ggc ttt ctg cga gga gtt gtt ggt gga gtg act			1164
Ala Arg Gly Gly Lys Gly Phe Leu Arg Gly Val Val Gly Gly Val Thr			
	350	355	360
gga ata ata aca aaa cct gtg gaa ggt gcc aaa aag gaa gga gct gct			1212
Gly Ile Ile Thr Lys Pro Val Glu Gly Ala Lys Lys Glu Gly Ala Ala			
	370	375	380
gga ttc ttt aaa gga att gga aaa ggg ctt gtg ggt gct gtg gcc cgt			1260
Gly Phe Phe Lys Gly Ile Gly Lys Gly Leu Val Gly Ala Val Ala Arg			
	385	390	395
cca act ggt gga atc gta gat atg gcc agt agt acc ttc caa ggc att			1308
Pro Thr Gly Gly Ile Val Asp Met Ala Ser Ser Thr Phe Gln Gly Ile			
	400	405	410

cag agg gca gca gaa tca act gag gaa gta tct agc ctc cgt ccc cct Gln Arg Ala Ala Glu Ser Thr Glu Glu Val Ser Ser Leu Arg Pro Pro 415 420 425	1356
cgc ctg atc cat gaa gat ggc atc att cgt cct tat gac aga cag gaa Arg Leu Ile His Glu Asp Gly Ile Ile Arg Pro Tyr Asp Arg Gln Glu 430 435 440 445	1404
tct gag ggc tct gac tta ctt gag aat cat atc aaa aag ttg gaa gga Ser Glu Gly Ser Asp Leu Leu Glu Asn His Ile Lys Lys Leu Glu Gly 450 455 460	1452
gag act tac cga tac cac tgt gct att cct gga agc aag aag aca atc Glu Thr Tyr Arg Tyr His Cys Ala Ile Pro Gly Ser Lys Lys Thr Ile 465 470 475	1500
ctt atg gtt aca aat agg cga gtg ttg tgt ata aag gaa gtt gaa atc Leu Met Val Thr Asn Arg Arg Val Leu Cys Ile Lys Glu Val Glu Ile 480 485 490	1548
ctg ggc ctt atg tgt gta gac tgg caa tgt cca ttt gaa gat ttt gta Leu Gly Leu Met Cys Val Asp Trp Gln Cys Pro Phe Glu Asp Phe Val 495 500 505	1596
ttt cct cct agt gtc agt gaa aat gtg cta aaa att tca gtt aag gaa Phe Pro Pro Ser Val Ser Glu Asn Val Leu Lys Ile Ser Val Lys Glu 510 515 520 525	1644
cag ggt ctg ttc cac aaa aaa gac agt gcc aat caa ggc tgt gtt cga Gln Gly Leu Phe His Lys Lys Asp Ser Ala Asn Gln Gly Cys Val Arg 530 535 540	1692
aaa gtt tac ctg aag gac acc gcc aca gca gag aga gca tgt aat gcc Lys Val Tyr Leu Lys Asp Thr Ala Thr Ala Glu Arg Ala Cys Asn Ala 545 550 555	1740
att gag gat gca cag tca acg aga cag cag caa aaa ttg atg aag cag Ile Glu Asp Ala Gln Ser Thr Arg Gln Gln Gln Lys Leu Met Lys Gln 560 565 570	1788
tca tca gtg aga ctt ctc aga ccc caa ttg cca tct taa tcacagacct Ser Ser Val Arg Leu Leu Arg Pro Gln Leu Pro Ser *	1837
caggggctcc aacagggaga aaaaacaatc actggtcttg tctataagtc actctgcttt	1897
atcttgctaa agacaatttt tcaagcaatc ctttagtttt agttttctgg aatagctagt	1957
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tcaaactcag aatgaaatct tcattaatat taaaattgtg aagcaaaggc caataggcct	2137
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 <222> (330)..(1652)

<400> 118

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gagaaaggag gtctgggata tgggatattg taatgggaga gcaggaaatt taaggtcgga      240
ggtatttggt taggatacct cagtattcta gagctatggg atttattttg ctttgaagtc      300
cagaggtatt tagctttatt ctaaaagcg  atg aag ttc ctc tta att aaa gac      353
                               Met Lys Phe Leu Leu Ile Lys Asp
                               1                               5

gct cct gga aaa aaa aaa agg aaa aat tta atg ctg tct ttt aaa agg      401
Ala Pro Gly Lys Lys Lys Arg Lys Asn Leu Met Leu Ser Phe Lys Arg
      10                               15                               20

aaa cat gcc aaa ggc cag gat ttg ttt gat cag att gtg tac cac ttg      449
Lys His Ala Lys Gly Gln Asp Leu Phe Asp Gln Ile Val Tyr His Leu
      25                               30                               35                               40

gac ctt gtg gaa aca gat tac ttt ggc ctc cag ttc ctc gac tct gcc      497
Asp Leu Val Glu Thr Asp Tyr Phe Gly Leu Gln Phe Leu Asp Ser Ala
                               45                               50                               55

cag gtt gcg cac tgg ctg gat cat gcc aaa ccc ata aaa aag cag atg      545
Gln Val Ala His Trp Leu Asp His Ala Lys Pro Ile Lys Lys Gln Met
                               60                               65                               70

aaa att gga cct gct tat gct tta cac ttt cga gtt aaa tac tat tct      593
Lys Ile Gly Pro Ala Tyr Ala Leu His Phe Arg Val Lys Tyr Tyr Ser
      75                               80                               85

tca gaa cca aac aac ctt cgt gag gag ttt aca agg tac ctg ttt gtt      641
Ser Glu Pro Asn Asn Leu Arg Glu Glu Phe Thr Arg Tyr Leu Phe Val
      90                               95                               100

tta caa ctc agg cat gac att ctt tct gga aaa ttg aaa tgc cct tat      689
Leu Gln Leu Arg His Asp Ile Leu Ser Gly Lys Leu Lys Cys Pro Tyr
      105                               110                               115                               120

gaa aca gct gtg gaa tta gct gct ctc tgt cta caa gcg gag ctt ggg      737
Glu Thr Ala Val Glu Leu Ala Ala Leu Cys Leu Gln Ala Glu Leu Gly

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125	130	135	
gag tgc gag ctt cca gaa cac aca cca gag ctt gtg tct gag ttt cgg Glu Cys Glu Leu Pro Glu His Thr Pro Glu Leu Val Ser Glu Phe Arg 140 145 150			785
ttc att cca aat cag aca gaa gca atg gaa ttt gat atc ttc cag aga Phe Ile Pro Asn Gln Thr Glu Ala Met Glu Phe Asp Ile Phe Gln Arg 155 160 165			833
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ctg aat aaa gcg aag tgg ctg gaa atg tat ggg gta gac atg cac gtt Leu Asn Lys Ala Lys Trp Leu Glu Met Tyr Gly Val Asp Met His Val 185 190 195 200			929
gtc agg gga aga gat ggc tgt gaa tat tct ctt gga ctg acc ccg aca Val Arg Gly Arg Asp Gly Cys Glu Tyr Ser Leu Gly Leu Thr Pro Thr 205 210 215			977
ggc ata tta atc ttt gaa gga gct aac aaa ata ggc tta ttc ttt tgg Gly Ile Leu Ile Phe Glu Gly Ala Asn Lys Ile Gly Leu Phe Phe Trp 220 225 230			1025
cct aaa att acc aaa atg gat ttt aaa aag agc aaa ttg aca ctc gtg Pro Lys Ile Thr Lys Met Asp Phe Lys Lys Ser Lys Leu Thr Leu Val 235 240 245			1073
gtg gtc gag gat gat gat cag gga cgt gag caa gag cac acg ttt gtg Val Val Glu Asp Asp Asp Gln Gly Arg Glu Gln Glu His Thr Phe Val 250 255 260			1121
ttc cgg tta gac agt gcc agg acc tgc aaa cac ctt tgg aag tgt gca Phe Arg Leu Asp Ser Ala Arg Thr Cys Lys His Leu Trp Lys Cys Ala 265 270 275 280			1169
gtt gag cac cac gca ttc ttc cga ctg cgg acg cca gga aac agc aaa Val Glu His His Ala Phe Phe Arg Leu Arg Thr Pro Gly Asn Ser Lys 285 290 295			1217
tcc aat aga tcc gac ttt atc agg ctg ggc tct cgc ttc aga ttc agt Ser Asn Arg Ser Asp Phe Ile Arg Leu Gly Ser Arg Phe Arg Phe Ser 300 305 310			1265
ggg cgg aca gaa tat caa gct aca cat ggc tcc agg tta cga aga acc Gly Arg Thr Glu Tyr Gln Ala Thr His Gly Ser Arg Leu Arg Arg Thr 315 320 325			1313
agc acc ttt gag agg aag cct agt aaa cgt tat cca tcc cgg aga cat Ser Thr Phe Glu Arg Lys Pro Ser Lys Arg Tyr Pro Ser Arg Arg His 330 335 340			1361
tca acg ttc aaa gca agc aac cca gtg ata gca gcc cag ctc tgc tct Ser Thr Phe Lys Ala Ser Asn Pro Val Ile Ala Ala Gln Leu Cys Ser 345 350 355 360			1409

aaa aca aat cca gaa gtc cat aat tac cag cct caa tat cat cct aat	1457
Lys Thr Asn Pro Glu Val His Asn Tyr Gln Pro Gln Tyr His Pro Asn	
365 370 375	
atc cat ccc agc cag ccc cgg tgg cat cct cac tct cca aat gtc agg	1505
Ile His Pro Ser Gln Pro Arg Trp His Pro His Ser Pro Asn Val Arg	
380 385 390	
cca tcc ttt cag gat gac agg tcg cat tgg aaa gca tcg gcc agt gga	1553
Pro Ser Phe Gln Asp Asp Arg Ser His Trp Lys Ala Ser Ala Ser Gly	
395 400 405	
gat gac agc cat ttt gat tat gtc cac gac cag aac cag aag aac tta	1601
Asp Asp Ser His Phe Asp Tyr Val His Asp Gln Asn Gln Lys Asn Leu	
410 415 420	
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Gly Gly Met Gln Ser Met Met Tyr Arg Asp Lys Leu Met Thr Ala Leu	
425 430 435 440	
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*	
aaagtgtctt ggcctcagat ggatggatgt gtttgacga gtgtctttaa ggagtagtcc	1766
tgaaagggtgt ttttggtgtc catgtaaata tttgaagata aaaccactat agcttgtcat	1826
aatttactgt tgactgcatt ctcatataaaa tgaaggtaaa ggctcaggaa tcatattgat	1886
gttctgattt taaaattgga gtcaaagtct atgtttatca ttttactatg ttcctgatgt	1946
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catatattcc tgtcgtagaa gttgagattg ctagggtcca gtttccctag tgtggcctgg	2066
acgagtcatt tccccttcatt tgacctcatt ttccccatct gaaaagagag gggttgacta	2126
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gcagtcgtac taatcttaaa ttgcatagca tttgttttga tcgaatttgc tgctcaagta	2426
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 aatctgatct tttttggcta ctgcaaaaat ctattcagca agaaggtatc agctgcatac 2966
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 tccatttttag cagacgttct gatgctcagt gtatgtgctg catacaaata aatgtgttct 3086
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 <213> Homo sapiens

<220>
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 ttccaaatta tattggtggt catcagaagt aggtgatagg aagaaatact tctcaagggt 240
 gcaaaa atg cag agt aat aaa act ttt aac ttg gag aag caa aac cat 288
 Met Gln Ser Asn Lys Thr Phe Asn Leu Glu Lys Gln Asn His
 1 5 10
 act cca aga aag cat cat caa cat cac cac cag cag cag cac cac cag 336
 Thr Pro Arg Lys His His Gln His His His Gln Gln Gln His His Gln
 15 20 25 30
 cag caa cag cag cag ccg cca cca ccg cca ata cct gca aat ggg caa 384
 Gln Gln Gln Gln Gln Pro Pro Pro Pro Pro Ile Pro Ala Asn Gly Gln
 35 40 45
 cag gcc agc agc caa agt gtg tat atg cta gat gaa ggc ttg act att 432
 Gln Ala Ser Ser Gln Ser Val Tyr Met Leu Asp Glu Gly Leu Thr Ile
 50 55 60
 gac ctg aag aat ttt aga aaa cca gga gag aag acc ttc acc caa cga 480
 Asp Leu Lys Asn Phe Arg Lys Pro Gly Glu Lys Thr Phe Thr Gln Arg

65	70	75	
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atg agg aaa cta ttt gag aaa tat gga aag gca ggc gaa gtc ttc att Met Arg Lys Leu Phe Glu Lys Tyr Gly Lys Ala Gly Glu Val Phe Ile 95 100 105 110			576
cat aag gat aaa gga ttt ggc ttt atc cgc ttg gaa acc cga acc cta His Lys Asp Lys Gly Phe Gly Phe Ile Arg Leu Glu Thr Arg Thr Leu 115 120 125			624
gcg gag att gcc aaa gtg gag ctg gac aat atg cca ctc cgt gga aag Ala Glu Ile Ala Lys Val Glu Leu Asp Asn Met Pro Leu Arg Gly Lys 130 135 140			672
cag ctg cgt gtg cgc ttt gcc tgc cat agt gca tcc ctt aca gtt cga Gln Leu Arg Val Arg Phe Ala Cys His Ser Ala Ser Leu Thr Val Arg 145 150 155			720
aac ctt cct cag tat gtg tcc aac gaa ctg ctg gaa gaa gcc ttt tct Asn Leu Pro Gln Tyr Val Ser Asn Glu Leu Leu Glu Glu Ala Phe Ser 160 165 170			768
gtg ttt ggc cag gta gag agg gct gta gtc att gtg gat gat cga gga Val Phe Gly Gln Val Glu Arg Ala Val Val Ile Val Asp Asp Arg Gly 175 180 185 190			816
agg ccc tca gga aaa ggc att gtt gag ttc tca ggg aag cca gct gct Arg Pro Ser Gly Lys Gly Ile Val Glu Phe Ser Gly Lys Pro Ala Ala 195 200 205			864
cgg aaa gct ctg gac aga tgc agt gaa ggc tcc ttc ctg cta acc aca Arg Lys Ala Leu Asp Arg Cys Ser Glu Gly Ser Phe Leu Leu Thr Thr 210 215 220			912
ttt cct cgt cct gtg act gtg gag ccc atg gac cag tta gat gat gaa Phe Pro Arg Pro Val Thr Val Glu Pro Met Asp Gln Leu Asp Asp Glu 225 230 235			960
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gaa cga gag cag cca ccc aga ttt gca cag cct ggc tcc ttt gag tat Glu Arg Glu Gln Pro Pro Arg Phe Ala Gln Pro Gly Ser Phe Glu Tyr 255 260 265 270			1056
gaa tat gcc atg cgc tgg aag gca ctc att gag atg gag aag cag cag Glu Tyr Ala Met Arg Trp Lys Ala Leu Ile Glu Met Glu Lys Gln Gln 275 280 285			1104
cag gac caa gtg gac cgc aac atc aag gag gct cgt gag aag ctg gag Gln Asp Gln Val Asp Arg Asn Ile Lys Glu Ala Arg Glu Lys Leu Glu 290 295 300			1152

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Met Glu Met Met Glu Ala Ala Arg His Glu His Gln Val Met Leu Met Arg	
305 310 315	
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Gln Asp Leu Met Arg Arg Gln Glu Glu Leu Arg Arg Met Glu Glu Leu	
320 325 330	
cac aac caa gag gtg caa aaa cga aag caa ctg gag ctc agg cag gag	1296
His Asn Gln Glu Val Gln Lys Arg Lys Gln Leu Glu Leu Arg Gln Glu	
335 340 345 350	
gaa gag cgc agg cgc cgt gaa gaa gag atg cgg cgg cag caa gaa gaa	1344
Glu Glu Arg Arg Arg Arg Glu Glu Glu Met Arg Arg Gln Gln Glu Glu	
355 360 365	
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Met Met Arg Arg Gln Gln Glu Gly Phe Lys Gly Thr Phe Pro Asp Ala	
370 375 380	
aga gag cag gag att cgg atg ggt cag atg gct atg gga ggt gct atg	1440
Arg Glu Gln Glu Ile Arg Met Gly Gln Met Ala Met Gly Gly Ala Met	
385 390 395	
ggc ata aac aac aga ggt gcc atg ccc cct gct cct gtg cca gct ggt	1488
Gly Ile Asn Asn Arg Gly Ala Met Pro Pro Ala Pro Val Pro Ala Gly	
400 405 410	
acc cca gct cct cca gga cct gcc act atg atg ccg gat gga act ttg	1536
Thr Pro Ala Pro Pro Gly Pro Ala Thr Met Met Pro Asp Gly Thr Leu	
415 420 425 430	
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Gly Leu Thr Pro Pro Thr Thr Glu Arg Phe Gly Gln Ala Ala Thr Met	
435 440 445	
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Glu Gly Ile Gly Ala Ile Gly Gly Thr Pro Pro Ala Phe Asn Arg Ala	
450 455 460	
gct cct gga gct gaa ttt gcc cca aac aaa cgt cgc cga tac taa taa	1680
Ala Pro Gly Ala Glu Phe Ala Pro Asn Lys Arg Arg Arg Tyr *	
465 470 475	
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ttctaccctg gaaaagtgtt agggattcct tccaatagtt agatctaccc tgcctgtact	1800
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<211> 1413
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<220>
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 <222> (54)..(686)

<400> 120

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Gly Gly Leu Pro Ser Arg Arg Lys Ser Leu Pro Ser Pro Ser Leu Ser		
5 10 15		
tcc tct gtc caa ggc cag gga cct gtg acc atg gaa gca gag aga agc		152
Ser Ser Val Gln Gly Gln Gly Pro Val Thr Met Glu Ala Glu Arg Ser		
20 25 30		
aag gcc aca gcc gtg gcc ctg ggc agt ttc ccg gca ggt ggc ccg gcc		200
Lys Ala Thr Ala Val Ala Leu Gly Ser Phe Pro Ala Gly Gly Pro Ala		
35 40 45		
gag ctg tcg ctg aga ctc ggg gag cca ttg acc atc gtc tct gag gat		248
Glu Leu Ser Leu Arg Leu Gly Glu Pro Leu Thr Ile Val Ser Glu Asp		
50 55 60 65		
gga gac tgg tgg acg gtg ctg tct gaa gtc tca ggc aga gag tat aac		296
Gly Asp Trp Trp Thr Val Leu Ser Glu Val Ser Gly Arg Glu Tyr Asn		
70 75 80		
atc ccc agc gtc cac gtg gcc aaa gtc tcc cat ggg tgg ctg tat gag		344
Ile Pro Ser Val His Val Ala Lys Val Ser His Gly Trp Leu Tyr Glu		
85 90 95		
ggc ctg agc agg gag aaa gca gag gaa ctg ctg ttg tta cct ggg aac		392
Gly Leu Ser Arg Glu Lys Ala Glu Glu Leu Leu Leu Pro Gly Asn		
100 105 110		
cct gga ggg gcc ttc ctc atc cgg gag agc cag acc agg aga ggc tct		440
Pro Gly Gly Ala Phe Leu Ile Arg Glu Ser Gln Thr Arg Arg Gly Ser		
115 120 125		
tac tct ctg tca gtc cgc ctc agc cgc cct gca tcc tgg gac cgg atc		488
Tyr Ser Leu Ser Val Arg Leu Ser Arg Pro Ala Ser Trp Asp Arg Ile		
130 135 140 145		
aga cac tac agg atc cac tgc ctt gac aat ggc tgg ctg tac atc tca		536
Arg His Tyr Arg Ile His Cys Leu Asp Asn Gly Trp Leu Tyr Ile Ser		
150 155 160		
ccg cgc ctc acc ttc ccc tca ctc cag gcc ctg ggg gac cat tac tct		584
Pro Arg Leu Thr Phe Pro Ser Leu Gln Ala Leu Gly Asp His Tyr Ser		
165 170 175		

gag ggc tgg ccc gct ccc tgg caa gga tat acc cct acc tgt gac tgt 632
 Glu Gly Trp Pro Ala Pro Trp Gln Gly Tyr Thr Pro Thr Cys Asp Cys
 180 185 190

gca gag gac acc act caa ctg gaa aga gct gga cag ctc cct cct gtt 680
 Ala Glu Asp Thr Thr Gln Leu Glu Arg Ala Gly Gln Leu Pro Pro Val
 195 200 205

ttc tga agctgccaca ggggaggagt ctcttctcag tgaggggtctc cgaggagtccc 736
 Phe *
 210

tcagcttcta catcagcctg aatgacgagg ctgtctcttt ggatgatgcc taggccccaaa 796

ggagaggcca aaagggaaac caaggctgca cacctagaac cccaattcag cctcctgggc 856

acccagagg caaggctgtg cactcagga gggaggggtgg gacacagagg tgcattctagg 916

gtcccacctg tacccttgct ctttctcttc ttagccctta gaagtcacct acttctcttc 976

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ggtttccagt accatctgga tgccctgcct gttgagcccc attctacatc cccaccatta 1156

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aaaatctaca agtctcgttg agaccaccac catacctcag aaggtaggac tgtggcctag 1276

aagggaaagg aaagctgaga tgatgtctta ccgtagcagc agatcttgga tgggtccaggc 1336

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ccattgagga caacagc 1413

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 Met Pro Arg Arg
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aag aaa aaa gtt aaa gaa gtc tcc gaa tct cgg aac ctg gag aag aag	223
Lys Lys Lys Val Lys Glu Val Ser Glu Ser Arg Asn Leu Glu Lys Lys	
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gat gtg gaa act acc agt tct gtc agt gtg aag agg aag cgt aga ctt	271
Asp Val Glu Thr Thr Ser Ser Val Ser Val Lys Arg Lys Arg Arg Leu	
25 30 35	
gag gat gca ttc att gtg ata tcc gat agt gat gga gag gaa cca aag	319
Glu Asp Ala Phe Ile Val Ile Ser Asp Ser Asp Gly Glu Glu Pro Lys	
40 45 50	
gag gaa aat ggg ttg cag aaa acg aag aca aaa cag tcg aat aga gca	367
Glu Glu Asn Gly Leu Gln Lys Thr Lys Thr Lys Gln Ser Asn Arg Ala	
55 60 65	
aag tgt ttg gcc aaa aga aaa att gca cag atg aca gaa gaa gaa cag	415
Lys Cys Leu Ala Lys Arg Lys Ile Ala Gln Met Thr Glu Glu Glu Gln	
70 75 80	
ttt gct ctg gct ctc aaa atg agt gag cag gaa gct agg gag gtg aac	463
Phe Ala Leu Ala Leu Lys Met Ser Glu Gln Glu Ala Arg Glu Val Asn	
85 90 95 100	
agc cag gag gag gaa gaa gag gag ctc ttg agg aaa gcc att gct gaa	511
Ser Gln Glu Glu Glu Glu Glu Glu Leu Leu Arg Lys Ala Ile Ala Glu	
105 110 115	
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Ser Leu Asn Ser Cys Arg Pro Ser Asp Ala Ser Ala Thr Arg Ser Arg	
120 125 130	
cct ctg gcc act gga ccg tct tcc cag tcc cat caa gag aaa acc aca	607
Pro Leu Ala Thr Gly Pro Ser Ser Gln Ser His Gln Glu Lys Thr Thr	
135 140 145	
gac tct ggg ctc act gaa ggc ata tgg cag ctg gta cct cca tca ctg	655
Asp Ser Gly Leu Thr Glu Gly Ile Trp Gln Leu Val Pro Pro Ser Leu	
150 155 160	
ttt aaa ggc tca cat atc agt cag gga aac gag gct gag gaa aga gag	703
Phe Lys Gly Ser His Ile Ser Gln Gly Asn Glu Ala Glu Glu Arg Glu	
165 170 175 180	
gag cct tgg gac cac act gaa aaa act gaa gag gag ccg gtc tct ggc	751
Glu Pro Trp Asp His Thr Glu Lys Thr Glu Glu Glu Pro Val Ser Gly	
185 190 195	
agc tca gga agc tgg gac cag tca agc cag cca gtg ttt gag aat gtg	799
Ser Ser Gly Ser Trp Asp Gln Ser Ser Gln Pro Val Phe Glu Asn Val	
200 205 210	
aac gtt aaa tct ttt gac aga tgt act ggc cac tcg gct gag cac aca	847
Asn Val Lys Ser Phe Asp Arg Cys Thr Gly His Ser Ala Glu His Thr	
215 220 225	
cag tgt ggg aag cca cag gaa agt act ggg agg ggt tct gct ttt ctc	895

455	460	465	
atc ttg gat gga gtc aga ata ata atg gca gat aag gag gtt ggt aac Ile Leu Asp Gly Val Arg Ile Ile Met Ala Asp Lys Glu Val Gly Asn 470 475 480			1615
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att gaa cga cat gcc atg tac tgc aat ggt ctg atg gag gaa gat aca Ile Glu Arg His Ala Met Tyr Cys Asn Gly Leu Met Glu Glu Asp Thr 520 525 530			1759
gta ttg act cgg aga caa aaa gag gcc aag acc aag agt gac agt ggg Val Leu Thr Arg Arg Gln Lys Glu Ala Lys Thr Lys Ser Asp Ser Gly 535 540 545			1807
aca gct gcc cag act tct cta gac att gac aag aat gag aag tgt tac Thr Ala Ala Gln Thr Ser Leu Asp Ile Asp Lys Asn Glu Lys Cys Tyr 550 555 560			1855
ctc tgt aaa tcc ctg gtc cca ttt aga gag tat cag tgt cat gtg gac Leu Cys Lys Ser Leu Val Pro Phe Arg Glu Tyr Gln Cys His Val Asp 565 570 575 580			1903
tcc tgt ctc cag ctt gca aag gct gac caa gga gat gga cct gaa ggg Ser Cys Leu Gln Leu Ala Lys Ala Asp Gln Gly Asp Gly Pro Glu Gly 585 590 595			1951
agt gga aga gca tgt tca act gtg gag ggg aag tgg cag cag agg ctg Ser Gly Arg Ala Cys Ser Thr Val Glu Gly Lys Trp Gln Gln Arg Leu 600 605 610			1999
aag aac cca aag gaa aaa ggc cac agt gaa ggc cga ctc ctt agt ttc Lys Asn Pro Lys Glu Lys Gly His Ser Glu Gly Arg Leu Leu Ser Phe 615 620 625			2047
ttg gaa cag tct gag cac aag act tca gat gca gac atc aag tct tca Leu Glu Gln Ser Glu His Lys Thr Ser Asp Ala Asp Ile Lys Ser Ser 630 635 640			2095
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tct ccc gtc aag tct ttt gtt tcc att tca gaa gcc aca gat tgc tta Ser Pro Val Lys Ser Phe Val Ser Ile Ser Glu Ala Thr Asp Cys Leu 680 685 690			2239

gtg gac ttt aaa aag caa gtt act gtc cag cca ggt agt cgg aca cgg	2287
Val Asp Phe Lys Lys Gln Val Thr Val Gln Pro Gly Ser Arg Thr Arg	
695 700 705	
acc aaa gct ggc aga gga aga agg aga aaa ttc tga attt ctagggtcca	2337
Thr Lys Ala Gly Arg Gly Arg Arg Arg Lys Phe *	
710 715 720	
aaagttgaca aaaccattag taggaggggt gggccatggt cattaagcca tagtgggtccc	2397
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 <213> Homo sapiens

<220>
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 <222> (599)..(1648)

<400> 122

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gaagaggagc tcttgaggaa agccattgct gaaagcctga atagttgccg gccttctg	598
atg ctt ccg cta cca gat ctc gac ctc tgg cca ctg gac cgt ctt ccc	646
Met Leu Pro Leu Pro Asp Leu Asp Leu Trp Pro Leu Asp Arg Leu Pro	
1 5 10 15	
agt ccc atc aag aga aaa cca cag act ctg ggc tca ctg aag tct tcc	694
Ser Pro Ile Lys Arg Lys Pro Gln Thr Leu Gly Ser Leu Lys Ser Ser	
20 25 30	

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tca caa agt gtt gct gct ttg acc agt aag aga agc tta gtc ctt atg Ser Gln Ser Val Ala Ala Leu Thr Ser Lys Arg Ser Leu Val Leu Met 50 55 60	790
cca gag agt tct gca gaa gaa atc act gtt tgt cct gag acc cag cta Pro Glu Ser Ser Ala Glu Glu Ile Thr Val Cys Pro Glu Thr Gln Leu 65 70 75 80	838
agt tcc tct gaa act ttt gac ctt gaa aga gaa gtc tct cca ggt agc Ser Ser Ser Glu Thr Phe Asp Leu Glu Arg Glu Val Ser Pro Gly Ser 85 90 95	886
aga gat atc ttg gat gga gtc aga ata ata atg gca gat aag gag gtt Arg Asp Ile Leu Asp Gly Val Arg Ile Ile Met Ala Asp Lys Glu Val 100 105 110	934
ggt aac aag gaa gat gct gag aag gaa gta gct att tct acc ttc tca Gly Asn Lys Glu Asp Ala Glu Lys Glu Val Ala Ile Ser Thr Phe Ser 115 120 125	982
tcc agt aac cag gta tcc tgc ccg cta tgt gac caa tgc ttt cca ccc Ser Ser Asn Gln Val Ser Cys Pro Leu Cys Asp Gln Cys Phe Pro Pro 130 135 140	1030
aca aag att gaa cga cat gcc atg tac tgc aat ggt ctg atg gag gaa Thr Lys Ile Glu Arg His Ala Met Tyr Cys Asn Gly Leu Met Glu Glu 145 150 155 160	1078
gat aca gta ttg act cgg aga caa aaa gag gcc aag acc aag agt gac Asp Thr Val Leu Thr Arg Arg Gln Lys Glu Ala Lys Thr Lys Ser Asp 165 170 175	1126
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agt ttc ttg gaa cag tct gag cac aag act tca gat gca gac atc aag	1414

Ser	Phe	Leu	Glu	Gln	Ser	Glu	His	Lys	Thr	Ser	Asp	Ala	Asp	Ile	Lys	
			260					265					270			
tct	tca	gaa	aca	gga	gcc	ttc	agg	gtg	cct	tca	cca	ggg	atg	gaa	gag	1462
Ser	Ser	Glu	Thr	Gly	Ala	Phe	Arg	Val	Pro	Ser	Pro	Gly	Met	Glu	Glu	
		275					280					285				
gca	ggc	tgc	agc	aga	gag	atg	cag	agt	tct	ttc	aca	cgt	cgt	gac	tta	1510
Ala	Gly	Cys	Ser	Arg	Glu	Met	Gln	Ser	Ser	Phe	Thr	Arg	Arg	Asp	Leu	
	290					295					300					
aat	gaa	tct	ccc	gtc	aag	tct	ttt	gtt	tcc	att	tca	gaa	gcc	aca	gat	1558
Asn	Glu	Ser	Pro	Val	Lys	Ser	Phe	Val	Ser	Ile	Ser	Glu	Ala	Thr	Asp	
305					310					315					320	
tgc	tta	gtg	gac	ttt	aaa	aag	caa	gtt	act	gtc	cag	cca	ggg	agt	cgg	1606
Cys	Leu	Val	Asp	Phe	Lys	Lys	Gln	Val	Thr	Val	Gln	Pro	Gly	Ser	Arg	
			325						330						335	
aca	cgg	acc	aaa	gct	ggc	aga	gga	aga	agg	aga	aaa	ttc	tga	atttcta		1655
Thr	Arg	Thr	Lys	Ala	Gly	Arg	Gly	Arg	Arg	Lys	Phe	*				
			340					345					350			
gggtccaaaa	ggtgacaaaa	ccattagtag	gaggggtggg	ccatgttcat	taagccatag											1715
tggtccctag	ttcattgttg	agcaagtttt	agccctgcag	ttttcaccac	cagcacctac											1775
ccagcattct	ggtttttatg	ttttttatga	tctatgcaga	caactgtgta	ttctgtttta											1835
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<210> 123
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (208)..(663)

<220>
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 <223> n = a,t,c or g

<400> 123																
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tgttttgcta	ggcaaagtta	caagtgcact	aatgggagct	caaagtgtgtg	tgtgtctctc											120
tgtgtgtttg	tgtgtgtgtg	tgcaactcaag	acctctaaca	gcctcgaagc	ctgggggtggc											180
atccccggcct	tgccattagc	atgcctc	atg cat cat	cag atg aca	agg aca											231
			Met His His	Gln Met Thr	Arg Thr											

acc ctc atg acg aag caa cat gaa tta ggg ggc ctc ttg gcc ttg gtc 279
 Thr Leu Met Thr Lys Gln His Glu Leu Gly Gly Leu Leu Ala Leu Val
 10 15 20

caa aat tgt caa tca gaa atg aac ata aag gac tcc aga gca gtg gga 327
 Gln Asn Cys Gln Ser Glu Met Asn Ile Lys Asp Ser Arg Ala Val Gly
 25 30 35 40

ctg tct gtc aaa aga ctc tgt ata tct ttt gtg gat gag ttt tgt gag 375
 Leu Ser Val Lys Arg Leu Cys Ile Ser Phe Val Asp Glu Phe Cys Glu
 45 50 55

aga aca gag aga cca ttg tac ctg gca caa ggg ctc ttc atg aaa agg 423
 Arg Thr Glu Arg Pro Leu Tyr Leu Ala Gln Gly Leu Phe Met Lys Arg
 60 65 70

gag act tac tgg gag gtg caa gac agt ggc att tct cct ctc ctc ttg 471
 Glu Thr Tyr Trp Glu Val Gln Asp Ser Gly Ile Ser Pro Leu Leu Leu
 75 80 85

ctg ctc agc aca gcc ctg gat tgc agc ccc gag gct gag acc aga caa 519
 Leu Leu Ser Thr Ala Leu Asp Cys Ser Pro Glu Ala Glu Thr Arg Gln
 90 95 100

agc ccg gga ggc aga aag atg ctc caa gaa cca aca cta tca atg tct 567
 Ser Pro Gly Gly Arg Lys Met Leu Gln Glu Pro Thr Leu Ser Met Ser
 105 110 115 120

ttg caa atc ctc aca gga ttc ctg tgg gtc cag ctt tgg aac tgg gaa 615
 Leu Gln Ile Leu Thr Gly Phe Leu Trp Val Gln Leu Trp Asn Trp Glu
 125 130 135

acc ttt ctt cgg atc cgc act cat tcc act gat gcc agc tgc ccc tga 663
 Thr Phe Leu Arg Ile Arg Thr His Ser Thr Asp Ala Ser Cys Pro *
 140 145 150

aggatgccag tactgtggtg tgtgagtctc agcagccgcc cacacgctcc taactctgct 723

gcatggcaga tgcctaggtg gaaatagcaa aaacaaggcc caggctgggg ccagggccag 783

aggggaaggc cctggattct cactcatgtg agatcttgaa tctctttctt tgttctgttt 843

gtttagttag tatcatctgg taaaatagtt aaaaaacaac aaaaaactct gtatctgttt 903

ctagcatgtg ctgcattgac tctattaatc acatttcaaa ttcaccctac attcctctcc 963

tcttcactag cctctctgaa ggtgtcctgg ccagccctgg agaagcactg gtgtctgcag 1023

caccctcag ttctgtgtcc tcagcccaca ggccactgtg ataatggtct gtttagcact 1083

tctgtattta ttgtaagaat gattataatg aagatacaca ctgtaactac aagaaattat 1143

aaatgttttt cacatcaggc tgttcttttt ttttttttgg aggcgagggt aaagcattac 1203

tatttgcaaa gactctgta gtcacctgtt atggggatag gtaactaatc agaataataa 1263

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tgtcactcgc atccacttct tagaacctgg ctccaaagga aaataagctg atagactcaa 1323
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tgagagccat aggtcggcag agggaactca ggcctcctt taggatggcc atcacctcat 2163
ctcaatccag ccaaataaac catctagagc acacaggccg agagaaatgt aataaaatat 2223
aacatgagac acgtatgaaa tttaaacttt ccggtagcca cactagaaaa aggtaaaaaa 2283
aaaaa 2288

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<210> 124
<211> 1047
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (95)..(934)

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tttccattta gatcaacaac ttcaagttct tacc      atg gaa aat tcc gag aag 112
                                Met Glu Asn Ser Glu Lys
                                1                      5
act gaa gtg gtt ctc ctt gct tgt ggt tca ttc aat ccc atc acc aac 160

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Thr	Glu	Val	Val	Leu	Leu	Ala	Cys	Gly	Ser	Phe	Asn	Pro	Ile	Thr	Asn		
			10					15					20				
atg	cac	ctc	agg	ttg	ttt	gag	ctg	gcc	aag	gac	tac	atg	aat	gga	aca	208	
Met	His	Leu	Arg	Leu	Phe	Glu	Leu	Ala	Lys	Asp	Tyr	Met	Asn	Gly	Thr		
		25					30					35					
gga	agg	tac	aca	gtt	gtc	aaa	ggc	atc	atc	tct	cct	gtt	ggg	gat	gcc	256	
Gly	Arg	Tyr	Thr	Val	Val	Lys	Gly	Ile	Ile	Ser	Pro	Val	Gly	Asp	Ala		
	40					45					50						
tac	aag	aag	aaa	gga	ctc	att	cct	gcc	tat	cac	cgg	gtc	atc	atg	gca	304	
Tyr	Lys	Lys	Lys	Gly	Leu	Ile	Pro	Ala	Tyr	His	Arg	Val	Ile	Met	Ala		
	55				60					65					70		
gaa	ctt	gct	acc	aag	aat	tct	aaa	tgg	gtg	gaa	gtt	gat	aca	tgg	gaa	352	
Glu	Leu	Ala	Thr	Lys	Asn	Ser	Lys	Trp	Val	Glu	Val	Asp	Thr	Trp	Glu		
			75					80						85			
agt	ctt	cag	aag	gag	tgg	aaa	gag	act	ctg	aag	gtg	cta	aga	cac	cat	400	
Ser	Leu	Gln	Lys	Glu	Trp	Lys	Glu	Thr	Leu	Lys	Val	Leu	Arg	His	His		
			90					95					100				
caa	gag	aaa	ttg	gag	gct	agt	gac	tgt	gat	cac	cag	cag	aac	tca	cct	448	
Gln	Glu	Lys	Leu	Glu	Ala	Ser	Asp	Cys	Asp	His	Gln	Gln	Asn	Ser	Pro		
		105					110						115				
act	cta	gaa	agg	cct	gga	agg	aag	agg	aag	tgg	act	gaa	aca	caa	gat	496	
Thr	Leu	Glu	Arg	Pro	Gly	Arg	Lys	Arg	Lys	Trp	Thr	Glu	Thr	Gln	Asp		
	120					125					130						
tct	agt	caa	aag	aaa	tcc	cta	gag	cca	aaa	aca	aaa	gct	gtg	cca	aag	544	
Ser	Ser	Gln	Lys	Lys	Ser	Leu	Glu	Pro	Lys	Thr	Lys	Ala	Val	Pro	Lys		
	135				140					145					150		
gtc	aag	ctg	ctg	tgt	ggg	gca	gat	tta	ttg	gag	tcc	ttt	gct	gtt	ccc	592	
Val	Lys	Leu	Leu	Cys	Gly	Ala	Asp	Leu	Leu	Glu	Ser	Phe	Ala	Val	Pro		
			155					160					165				
aat	ttg	tgg	aag	agt	gaa	gac	atc	acc	caa	atc	gtg	gcc	aac	tat	ggg	640	
Asn	Leu	Trp	Lys	Ser	Glu	Asp	Ile	Thr	Gln	Ile	Val	Ala	Asn	Tyr	Gly		
		170						175					180				
ctc	ata	tgt	gtt	act	cgg	gct	gga	aat	gat	gct	cag	aag	ttt	atc	tat	688	
Leu	Ile	Cys	Val	Thr	Arg	Ala	Gly	Asn	Asp	Ala	Gln	Lys	Phe	Ile	Tyr		
		185					190					195					
gaa	tcg	gat	gtg	ctg	tgg	aaa	cac	cgg	agc	aac	att	cac	gtg	gtg	aat	736	
Glu	Ser	Asp	Val	Leu	Trp	Lys	His	Arg	Ser	Asn	Ile	His	Val	Val	Asn		
	200					205					210						
gaa	tgg	atc	gct	aat	gac	atc	tca	tcc	aca	aaa	atc	cgg	aga	gcc	ctc	784	
Glu	Trp	Ile	Ala	Asn	Asp	Ile	Ser	Ser	Thr	Lys	Ile	Arg	Arg	Ala	Leu		
	215				220					225					230		
aga	agg	ggc	cag	agc	att	cgc	tac	ttg	gta	cca	gat	ctt	gtc	caa	gaa	832	
Arg	Arg	Gly	Gln	Ser	Ile	Arg	Tyr	Leu	Val	Pro	Asp	Leu	Val	Gln	Glu		

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                235                240                245
tac att gaa aag cat aat ttg tac agc tct gag agt gaa gac agg aat      880
Tyr Ile Glu Lys His Asn Leu Tyr Ser Ser Glu Ser Glu Asp Arg Asn
                250                255                260

gct ggg gtc atc ctg gcc cct ttg cag aga aac act gca gaa gct aag      928
Ala Gly Val Ile Leu Ala Pro Leu Gln Arg Asn Thr Ala Glu Ala Lys
                265                270                275

aca tag gaattctaca gcatgatatt tcagacttcc catttgggga tctgaaacaa      984
Thr *
                280

tctgggagtt aataactggg gaaagaagtt gtgatctgtt gcctaaacta aagcttaaaa    1044

gtt                                                                    1047

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<210> 125
<211> 474
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (28)..(399)

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<400> 125
gcacgagcgt tggcggcttg tgcagca      atg gcc aag atc aag gct cga gat      51
Met Ala Lys Ile Lys Ala Arg Asp
                1                5

ctt cgc ggg aag aag aag gag gag ctg ctg aaa cag ctg gac gac ctg      99
Leu Arg Gly Lys Lys Lys Glu Leu Leu Lys Gln Leu Asp Asp Leu
                10                15                20

aag gtg gag ctg tcc cag ctg cgc gtc gcc aaa gtg aca ggc ggt gcg      147
Lys Val Glu Leu Ser Gln Leu Arg Val Ala Lys Val Thr Gly Gly Ala
                25                30                35                40

gcc tcc aag ctc tct aag atc cga gtc gtc cgg aaa tcc att gcc cgt      195
Ala Ser Lys Leu Ser Lys Ile Arg Val Val Arg Lys Ser Ile Ala Arg
                45                50                55

gtt ctc aca gtt att aac cag act cag aaa gaa aac ctc agg aaa ttc      243
Val Leu Thr Val Ile Asn Gln Thr Gln Lys Glu Asn Leu Arg Lys Phe
                60                65                70

tac aag ggc aag aag tac aag ccc ctg gac ctg cgg cct aag aag aca      291
Tyr Lys Gly Lys Lys Tyr Lys Pro Leu Asp Leu Arg Pro Lys Lys Thr
                75                80                85

cgt gcc atg cgc cgc cgg ctc aac aag cac gag gag aac ctg aag acc      339
Arg Ala Met Arg Arg Arg Leu Asn Lys His Glu Glu Asn Leu Lys Thr

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90	95	100	
aag aag cag cag cgg aag gag cgg ctg tac ccg ctg cag aag tac aca			387
Lys Lys Gln Gln Arg Lys Glu Arg Leu Tyr Pro Leu Gln Lys Tyr Thr			
105	110	115	120
gtg aac gcc tga acg tcacatgggt tcataaaaga gagctggccg aagagaacaa			442
Val Asn Ala *			
aagaaaagtg tgtattttaat atgcaattct gt			474

<210> 126
 <211> 2594
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (148)..(576)

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tattgatcat tccgcagccc tgcggaccgg acacgtgagg aggtagtgac gccgacactg	120
ccagaacaca ctgctacaag gtcccag	
atg gcc acg tct ctg gat ttt aaa	171
Met Ala Thr Ser Leu Asp Phe Lys	
1 5	
act tat gta gat cag gca tgt aga gct gct gag gag ttt gtc aat att	219
Thr Tyr Val Asp Gln Ala Cys Arg Ala Ala Glu Glu Phe Val Asn Ile	
10 15 20	
tac tat gag aca atg gat aaa aga aga cgg gca cta acc agg ctg tat	267
Tyr Tyr Glu Thr Met Asp Lys Arg Arg Arg Ala Leu Thr Arg Leu Tyr	
25 30 35 40	
ctg gac aag gcc acc tta ata tgg aat gga aat gct gtt tca ggg ctg	315
Leu Asp Lys Ala Thr Leu Ile Trp Asn Gly Asn Ala Val Ser Gly Leu	
45 50 55	
gat gcc cta aat aat ttt ttt gac aca ttg cct tct agt gag ttc cag	363
Asp Ala Leu Asn Asn Phe Phe Asp Thr Leu Pro Ser Ser Glu Phe Gln	
60 65 70	
gtc aat atg tta gat tgc caa cca gtt cat gag caa gca act cag tcc	411
Val Asn Met Leu Asp Cys Gln Pro Val His Glu Gln Ala Thr Gln Ser	
75 80 85	
caa act aca gtt ctt gtt gtg acc agt gga act gtg aag ttt gat gga	459
Gln Thr Thr Val Leu Val Val Thr Ser Gly Thr Val Lys Phe Asp Gly	
90 95 100	

aac aaa caa cat ttc ttc aac cag aac ttc ctg ctg act gct cag tcc	507
Asn Lys Gln His Phe Phe Asn Gln Asn Phe Leu Leu Thr Ala Gln Ser	
105 110 115 120	
act ccc aac aat act gtg tgg aag att gca agt gat tgc ttc cgt ttt	555
Thr Pro Asn Asn Thr Val Trp Lys Ile Ala Ser Asp Cys Phe Arg Phe	
125 130 135	
caa gat tgg tct agt agt taa ag gggcaaaagt ccattctcat ttggtccatt	608
Gln Asp Trp Ser Ser Ser *	
140	
agttccagca attgaaatatt atgtgaatta ttttgattgt agaagcacta taatatgtgc	668
tgaaactaaa tttctttaat attttctatt cctgtcagca ccttttctag cagctgccag	728
tttggagcat tgccctctaa gagctttaaa actatTTTTT tacatgcctt atatacattc	788
cactaatgac attottataa taatattaaa cacatgatct tgggtactaac atactcactg	848
tgaaccagc ctattgcaaa aataaaatct ttttataata ttatctatgg gatgtcagca	908
caatataaca ctctgggaag aagtggagtt ttttggttat taggttaatt ttctagtaaa	968
acacattgcc tgttttcagt taacactggg aatgccattt taatatatgg ctttttcaaa	1028
tcagttcagt gaaaatagta cagatttagg tttacataac tactctgaca tactggaatt	1088
gcatatagag atgttcagtg gtcgtttttc attttaagta atttttgttt tggcattttt	1148
ttgtgtgaag taaattaatc aactagagag gtgcaaaacg ttctcagttg atatctgagt	1208
attgggtgca tttgggtggc taaaagcaaa gcttcctaaa aagatttttc ttggcagctc	1268
caggtctata catttaggta atgaatggta gtagaactaa tagctttaac aggagaatag	1328
ggaatgagaa atagaaatcc aaggctgaag ccaaaagtaa ggaggggtggc caaatggtaa	1388
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taagtaaata agtatccttg ccaagtgatc atgagtgtca tttttgttct aagactaata	1508
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atgataatcc tcaaaagaac aaaatgctta actttatctc ttaatttcta aaggtaaata	1988

acctagggttc agcttttgc taaacattaa atatcttttc catttttttaa tgtttgtaag 2048
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 aaaaaa 2594

<210> 127
 <211> 2519
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (229)..(2145)

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 ttgggcaaag gagaaattca gttttcagta gcatcattgg aagtattatg acttgtgctt 180
 aaactttttac cagtgcattc ttttgataaa tagaaatagt aacaaaat atg aat ttt 237
 Met Asn Phe
 1
 aaa tat gtg ggg aga tac ata aag aac att gct tat ttg ttc ttg aaa 285
 Lys Tyr Val Gly Arg Tyr Ile Lys Asn Ile Ala Tyr Leu Phe Leu Lys
 5 10 15
 ata aca gtg att caa ata ttt cat tca gat tta cct atg cct aat gaa 333
 Ile Thr Val Ile Gln Ile Phe His Ser Asp Leu Pro Met Pro Asn Glu
 20 25 30 35
 aaa aat gat gca gaa ctt gat tct cca cct tca aag aaa aaa aga tta 381
 Lys Asn Asp Ala Glu Leu Asp Ser Pro Pro Ser Lys Lys Lys Arg Leu
 40 45 50

ggt ttt ttc cag act tat gat aca gaa tat tta aaa gtt ggt ttt att Gly Phe Phe Gln Thr Tyr Asp Thr Glu Tyr Leu Lys Val Gly Phe Ile 55 60 65	429
atc tgt cct gga tca aaa gaa agt tca cca agg cca cag tgt gtc att Ile Cys Pro Gly Ser Lys Glu Ser Ser Pro Arg Pro Gln Cys Val Ile 70 75 80	477
tgt gga gag atc tta tcc agt gaa aac atg aag cca gca aat ctt tct Cys Gly Glu Ile Leu Ser Ser Glu Asn Met Lys Pro Ala Asn Leu Ser 85 90 95	525
cat cat ttg aag aca aaa cat tca gaa tta gaa aac aaa cca gta gat His His Leu Lys Thr Lys His Ser Glu Leu Glu Asn Lys Pro Val Asp 100 105 110 115	573
ttt ttt gaa caa aaa tct tta gaa atg gaa tgt caa aat agt tct tta Phe Phe Glu Gln Lys Ser Leu Glu Met Glu Cys Gln Asn Ser Ser Leu 120 125 130	621
aaa aag tgt tta cta gtt gaa aag tca ctt gtg aaa gct tct tat tta Lys Lys Cys Leu Leu Val Glu Lys Ser Leu Val Lys Ala Ser Tyr Leu 135 140 145	669
att gct ttc caa act gct gca agc aag aag cca ttc tcc att gct gaa Ile Ala Phe Gln Thr Ala Ala Ser Lys Lys Pro Phe Ser Ile Ala Glu 150 155 160	717
gaa tta att aaa cca tat tta gta gaa atg tgt tca gaa gtt ttg ggt Glu Leu Ile Lys Pro Tyr Leu Val Glu Met Cys Ser Glu Val Leu Gly 165 170 175	765
tca agt gct gga gac aaa atg aaa act att cca ctt tct aat gtt aca Ser Ser Ala Gly Asp Lys Met Lys Thr Ile Pro Leu Ser Asn Val Thr 180 185 190 195	813
att caa cac agg att gat gaa cta tct gca gac att gaa gac cag ctg Ile Gln His Arg Ile Asp Glu Leu Ser Ala Asp Ile Glu Asp Gln Leu 200 205 210	861
att caa aag gtc aga gag tca aag tgg ttt gcc ctt cag ata gat gag Ile Gln Lys Val Arg Glu Ser Lys Trp Phe Ala Leu Gln Ile Asp Glu 215 220 225	909
tca tca gaa atc tca aat atc aca ctt ctt ttg tgc tat att cgt ttc Ser Ser Glu Ile Ser Asn Ile Thr Leu Leu Leu Cys Tyr Ile Arg Phe 230 235 240	957
att gat tat gat tgt cgt gat gta aaa gaa gaa tta tta ttt tgc att Ile Asp Tyr Asp Cys Arg Asp Val Lys Glu Glu Leu Leu Phe Cys Ile 245 250 255	1005
gaa atg cct act caa ata act ggc ttt gaa ata ttt gaa cta ata aat Glu Met Pro Thr Gln Ile Thr Gly Phe Glu Ile Phe Glu Leu Ile Asn 260 265 270 275	1053

aaa tat att gat agt aaa tct ctg aat tgg aaa cat tgt gtt ggt ctc	1101
Lys Tyr Ile Asp Ser Lys Ser Leu Asn Trp Lys His Cys Val Gly Leu	
280 285 290	
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Cys Thr Asp Gly Ala Ala Ser Met Thr Gly Arg Tyr Ser Gly Leu Lys	
295 300 305	
gca aaa att caa gaa gtt gcc atg aat aca gcg gca ttt aca cat tgt	1197
Ala Lys Ile Gln Glu Val Ala Met Asn Thr Ala Ala Phe Thr His Cys	
310 315 320	
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Phe Ile His Arg Glu Arg Leu Val Ala Glu Lys Leu Ser Pro Cys Leu	
325 330 335	
cat aaa att ctt ttg cag tca gca caa att tta agt ttt ata aag agc	1293
His Lys Ile Leu Leu Gln Ser Ala Gln Ile Leu Ser Phe Ile Lys Ser	
340 345 350 355	
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Asn Ala Leu Asn Ser Arg Met Leu Thr Ile Leu Cys Glu Glu Met Gly	
360 365 370	
tct gag cat gtg agt tta ccg ctt cat gct gaa gta cgt tgg ata tca	1389
Ser Glu His Val Ser Leu Pro Leu His Ala Glu Val Arg Trp Ile Ser	
375 380 385	
aga ggg aga atg tta aaa aga tta ttt gaa tta cga cat gag att gaa	1437
Arg Gly Arg Met Leu Lys Arg Leu Phe Glu Leu Arg His Glu Ile Glu	
390 395 400	
ata ttt tta agt caa aag cat tca gat ttg gcc aag tat ttt cat gat	1485
Ile Phe Leu Ser Gln Lys His Ser Asp Leu Ala Lys Tyr Phe His Asp	
405 410 415	
gag gaa tgg gtt gga aag ctg gcc tac tta tca gat ata ttt tca ctt	1533
Glu Glu Trp Val Gly Lys Leu Ala Tyr Leu Ser Asp Ile Phe Ser Leu	
420 425 430 435	
ata aat gaa tta aat tta agt ctc caa gga act ttg act act ttc ttc	1581
Ile Asn Glu Leu Asn Leu Ser Leu Gln Gly Thr Leu Thr Thr Phe Phe	
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Asn Leu Cys Asn Lys Ile Asp Val Phe Lys Arg Lys Leu Lys Met Trp	
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ttg aag cgc aca caa gag aat gat tat gac atg ttc cct tca ttt tct	1677
Leu Lys Arg Thr Gln Glu Asn Asp Tyr Asp Met Phe Pro Ser Phe Ser	
470 475 480	
gaa ttc tca aat tca tca ggc tta aat atg aca gac atc aca agg att	1725
Glu Phe Ser Asn Ser Ser Gly Leu Asn Met Thr Asp Ile Thr Arg Ile	
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1 5	
gag gaa gag gaa gcc ggc gag gag gcg gag ggg gag gaa gag gag gac	162
Glu Glu Glu Glu Ala Gly Glu Glu Ala Glu Gly Glu Glu Glu Glu Asp	
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Asp Ser Phe Leu Leu Leu Gln Gln Ser Val Thr Leu Gly Ser Ser Gly	
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Glu Val Asp Arg Leu Val Ala Gln Ile Gly Glu Thr Leu Gln Leu Asp	
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Ala Ala Gln Asp Ser Pro Ala Ser Pro Cys Ala Pro Pro Gly Val Pro	
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Leu Arg Ala Pro Gly Pro Leu Ala Ala Ala Val Pro Thr Asp Lys Ala	
75 80 85	
cgg ccc ccg gcg gtg ccg ctg ctg ctg ccg ccc gct tcg gct gag acg	402
Arg Pro Pro Ala Val Pro Leu Leu Leu Pro Pro Ala Ser Ala Glu Thr	
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Val Gly Pro Ala Pro Ser Gly Ala Leu Arg Cys Ala Leu Gly Asp Arg	
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Gly Arg Val Arg Gly Arg Ala Ala Pro Tyr Cys Val Ala Glu Val Ala	
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Ala Gly Pro Ser Ala Leu Pro Gly Pro Cys Arg Arg Gly Trp Leu Arg	
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Asp Ala Val Thr Ser Arg Arg Leu Gln Gln Arg Arg Trp Thr Gln Ala	
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Gly Ala Arg Ala Gly Asp Asp Asp Pro His Arg Leu Leu Gln Gln Leu	
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Val Leu Ser Gly Asn Leu Ile Lys Glu Ala Val Arg Arg Leu Gln Arg	
185 190 195	

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Gly Gly Gly Arg Ser Gly Pro Asp Arg Ile Ala Leu Gln Pro Ser Gly	
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Ser Leu Leu *	
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      Met Ala Gly Ser Gly Cys Ala Trp Gly Ala Glu
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ccg ccg cgt ttt ctg gag gcc ttc ggg cgg ctg tgg cag gta cag agc      159
Pro Pro Arg Phe Leu Glu Ala Phe Gly Arg Leu Trp Gln Val Gln Ser
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cgt ctg ggt agc ggc tcc tcc gcc tgc gtg tat cgg gtt cgc tgc tgc      207
Arg Leu Gly Ser Gly Ser Ser Ala Ser Val Tyr Arg Val Arg Cys Cys
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ggc aac cct ggc tgc ccc ccc ggc gcc ctc aag cag ttc ttg ccg cca      255
Gly Asn Pro Gly Ser Pro Pro Gly Ala Leu Lys Gln Phe Leu Pro Pro
                45                50                55

gga acc acc ggg gct gcg gcc tct gcc gcc gag tat ggt ttc cgc aaa      303
Gly Thr Thr Gly Ala Ala Ala Ser Ala Ala Glu Tyr Gly Phe Arg Lys
                60                65                70                75

gag agg gcg gcg ctg gaa cag ttg cag ggt cac aga aac atc gtg act      351
Glu Arg Ala Ala Leu Glu Gln Leu Gln Gly His Arg Asn Ile Val Thr
                80                85                90

ttg tat gga gtg ttt aca atc cac ttt tct cca aat gtg cca tca cgc      399
Leu Tyr Gly Val Phe Thr Ile His Phe Ser Pro Asn Val Pro Ser Arg
                95                100                105

tgt ctg ttg ctt gaa ctc ctg gat gtc agt gtt tgc gaa ttg ctc tta      447
Cys Leu Leu Leu Glu Leu Leu Asp Val Ser Val Ser Glu Leu Leu Leu
                110                115                120

tat tcc agt cac cag ggt tgt tcc atg tgg atg ata cag cat tgc gcc      495
Tyr Ser Ser His Gln Gly Cys Ser Met Trp Met Ile Gln His Cys Ala
                125                130                135

cga gat gtt ttg gag gcc ctt gct ttt ctt cat cat gag ggc tat gtc      543
Arg Asp Val Leu Glu Ala Leu Ala Phe Leu His His Glu Gly Tyr Val
                140                145                150                155

cat gcg gac ctc aaa cca cgt aac ata ttg tgg agt gca gag aat gaa      591

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His	Ala	Asp	Leu	Lys	Pro	Arg	Asn	Ile	Leu	Trp	Ser	Ala	Glu	Asn	Glu	
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Cys	Phe	Lys	Leu	Ile	Asp	Phe	Gly	Leu	Ser	Phe	Lys	Glu	Gly	Asn	Gln	
			175					180					185			
gat	gta	aag	tat	att	cag	aca	gac	ggg	tat	cgg	gct	cca	gaa	gca	gaa	687
Asp	Val	Lys	Tyr	Ile	Gln	Thr	Asp	Gly	Tyr	Arg	Ala	Pro	Glu	Ala	Glu	
			190					195				200				
ttg	caa	aat	tgc	ttg	gcc	cag	gct	ggc	ctg	cag	agt	gat	aca	gaa	tgt	735
Leu	Gln	Asn	Cys	Leu	Ala	Gln	Ala	Gly	Leu	Gln	Ser	Asp	Thr	Glu	Cys	
	205					210					215					
acc	tca	gct	gtt	gat	ctg	tgg	agc	cta	gga	atc	att	tta	ctg	gaa	atg	783
Thr	Ser	Ala	Val	Asp	Leu	Trp	Ser	Leu	Gly	Ile	Ile	Leu	Leu	Glu	Met	
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ttc	tca	gga	atg	aaa	ctg	aaa	cat	aca	gtc	aga	tct	cag	gaa	tgg	aag	831
Phe	Ser	Gly	Met	Lys	Leu	Lys	His	Thr	Val	Arg	Ser	Gln	Glu	Trp	Lys	
				240					245					250		
gca	aac	agt	tct	gct	att	att	gat	cac	ata	ttt	gcc	agt	aaa	gca	gtg	879
Ala	Asn	Ser	Ser	Ala	Ile	Ile	Asp	His	Ile	Phe	Ala	Ser	Lys	Ala	Val	
			255					260					265			
gtg	aat	gcc	gca	att	cca	gcc	tat	cac	cta	aga	gac	ctt	atc	aaa	agc	927
Val	Asn	Ala	Ala	Ile	Pro	Ala	Tyr	His	Leu	Arg	Asp	Leu	Ile	Lys	Ser	
		270					275					280				
atg	ctt	cat	gat	gat	cca	agc	aga	aga	att	cct	gct	gaa	atg	gca	ttg	975
Met	Leu	His	Asp	Asp	Pro	Ser	Arg	Arg	Ile	Pro	Ala	Glu	Met	Ala	Leu	
	285					290					295					
tgc	agc	cca	ttc	ttt	agc	att	cct	ttt	gcc	cct	cat	att	gaa	gat	ctg	1023
Cys	Ser	Pro	Phe	Phe	Ser	Ile	Pro	Phe	Ala	Pro	His	Ile	Glu	Asp	Leu	
300					305					310				315		
gtc	atg	ctt	ccc	act	cca	gtg	cta	aga	ctg	ctg	aat	gtg	ctg	gat	gat	1071
Val	Met	Leu	Pro	Thr	Pro	Val	Leu	Arg	Leu	Leu	Asn	Val	Leu	Asp	Asp	
				320					325					330		
gat	tat	ctt	gag	aat	gaa	gag	gaa	tat	gaa	gat	gtt	gta	gaa	gat	gta	1119
Asp	Tyr	Leu	Glu	Asn	Glu	Glu	Glu	Tyr	Glu	Asp	Val	Val	Glu	Asp	Val	
			335					340					345			
aaa	gag	gag	tgt	caa	aaa	tat	gga	cca	gtg	gta	tct	cta	ctt	gtt	cca	1167
Lys	Glu	Glu	Cys	Gln	Lys	Tyr	Gly	Pro	Val	Val	Ser	Leu	Leu	Val	Pro	
		350					355					360				
aag	gaa	aat	cct	ggc	aga	gga	caa	gtc	ttt	gtt	gag	tat	gca	aat	gct	1215
Lys	Glu	Asn	Pro	Gly	Arg	Gly	Gln	Val	Phe	Val	Glu	Tyr	Ala	Asn	Ala	
	365					370				375						
ggg	gat	tcc	aaa	gct	gcg	cag	aaa	tta	ctg	act	gga	agg	atg	ttt	gat	1263
Gly	Asp	Ser	Lys	Ala	Ala	Gln	Lys	Leu	Leu	Thr	Gly	Arg	Met	Phe	Asp	

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380          385          390          395
ggg aag ttt gtt gtg gct aca ttc tac ccg ctg agt gcc tac aag agg      1311
Gly Lys Phe Val Val Ala Thr Phe Tyr Pro Leu Ser Ala Tyr Lys Arg
          400          405          410

gga tat ctg tat caa acc ttg ctt taa tcagt aacctaagga ctgtttcctt      1363
Gly Tyr Leu Tyr Gln Thr Leu Leu *
          415          420

tttctcctct tccattttctt gggttattcc acatatgaat gcaggactac ccccttacca      1423

ttttaagaag gtactttata cattttattta atcctactaa tgtgcagcca ttgcccaagc      1483

agtgactgcg ttgcatacat ttggcactga gtaggacaag acctctcagc tatacattga      1543

gggggttttag agcatccatg tgggcaaccc ttttttgtgc gggagagcag gtgttgctct      1603

tcagtatgta gcctaaaaaa atcttaatta tttcatggat catgaagcaa ggatgaataa      1663

tatcatgtct tggtaaatac taacaaatth gttagggttg gtgacatcat ttacagatta      1723

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gctctcagta atgttaagta attgtcaagc agcagttacc tactgtgttc ttaacactga      1843

gttgtgaatt ttttcttaaa gcagtactgt agtactgaat attcctttac aggaactgca      1903

gtgagcctat ctaagtcttt gcctactaag gcttcctatg ggagaaaagt catgcttgac      1963

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ttcaagacca gcctgggcaa cacagcaaga ccccatatc tctacaaaaa aaacaaaaca      180

aaacaaaaca aacaaacaaa aaaaacagcc ggttgcggtg gcacatgctt gcagtcctcg      240

ttactcaaga agcagaagca agaggattgc ttgagcccaa cagtgccttg aaaagacaaa      300

gaacgcctgc aagcc atg atg acc cac ctg cat gtg aag tct aca gaa ccc      351
          Met Met Thr His Leu His Val Lys Ser Thr Glu Pro

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aaa gcc gcc cct cag ccc ttg aat ctg gta tca agt gtc act ctc tcc				399
Lys Ala Ala Pro Gln Pro Leu Asn Leu Val Ser Ser Val Thr Leu Ser	15	20	25	
aag tcc gca tcg gag gct tct cca cag agc tta cct cat act cca acg				447
Lys Ser Ala Ser Glu Ala Ser Pro Gln Ser Leu Pro His Thr Pro Thr	30	35	40	
acc cca acc gcc ccc ctg act ccc gtc acc caa ggc ccc tct gtc atc				495
Thr Pro Thr Ala Pro Leu Thr Pro Val Thr Gln Gly Pro Ser Val Ile	45	50	55	60
aca acc acc agc atg cac acg gtg gga ccc atc cgc agg cgg tac tca				543
Thr Thr Thr Ser Met His Thr Val Gly Pro Ile Arg Arg Arg Tyr Ser	65	70	75	
gac aaa tac aac gtg ccc att tcg tca gca gat att gcg cag aac caa				591
Asp Lys Tyr Asn Val Pro Ile Ser Ser Ala Asp Ile Ala Gln Asn Gln	80	85	90	
gaa ttt tat aag aac gca gaa gtt aga cca cca ttt aca tat gca tct				639
Glu Phe Tyr Lys Asn Ala Glu Val Arg Pro Pro Phe Thr Tyr Ala Ser	95	100	105	
tta att agg cag gcc att ctc gaa tct cca gaa aag cag cta aca cta				687
Leu Ile Arg Gln Ala Ile Leu Glu Ser Pro Glu Lys Gln Leu Thr Leu	110	115	120	
aat gag atc tat aac tgg ttc aca cga atg ttt gct tac ttc cga cgc				735
Asn Glu Ile Tyr Asn Trp Phe Thr Arg Met Phe Ala Tyr Phe Arg Arg	125	130	135	140
aac gcg gcc acg tgg aag aat gca gtg cgt cat aat ctt agt ctt cac				783
Asn Ala Ala Thr Trp Lys Asn Ala Val Arg His Asn Leu Ser Leu His	145	150	155	
aag tgt ttt gtg cga gta gaa aac gtt aaa ggg gca gta tgg aca gtg				831
Lys Cys Phe Val Arg Val Glu Asn Val Lys Gly Ala Val Trp Thr Val	160	165	170	
gat gaa gta gaa ttc caa aaa cga agg cca caa aag atc agt ggt aac				879
Asp Glu Val Glu Phe Gln Lys Arg Arg Pro Gln Lys Ile Ser Gly Asn	175	180	185	
cct tcc ctt att aaa aac atg cag agc agc cac gcc tac tgc aca cct				927
Pro Ser Leu Ile Lys Asn Met Gln Ser Ser His Ala Tyr Cys Thr Pro	190	195	200	
ctc aat gca gct tta cag gct tca atg gct gag aat agt ata cct cta				975
Leu Asn Ala Ala Leu Gln Ala Ser Met Ala Glu Asn Ser Ile Pro Leu	205	210	215	220
tac act acc gct tcc atg gga aat ccc act ctg ggc aac tta gcc agc				1023
Tyr Thr Thr Ala Ser Met Gly Asn Pro Thr Leu Gly Asn Leu Ala Ser	225	230	235	

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gca ata cgg gaa gag ctg aac ggg gca atg gag cat acc aac agc aac      1071
Ala Ile Arg Glu Glu Leu Asn Gly Ala Met Glu His Thr Asn Ser Asn
      240                      245                      250

gag agt gac agc agt cca ggc aga tct cct atg caa gcc gtg cat cct      1119
Glu Ser Asp Ser Ser Pro Gly Arg Ser Pro Met Gln Ala Val His Pro
      255                      260                      265

gta cac gtc aaa gaa gag ccc ctc gat cca gag gaa gct gaa ggg ccc      1167
Val His Val Lys Glu Glu Pro Leu Asp Pro Glu Glu Ala Glu Gly Pro
      270                      275                      280

ctg tcc tta gtg aca aca gcc aac cac agt cca gat ttt gac cat gac      1215
Leu Ser Leu Val Thr Thr Ala Asn His Ser Pro Asp Phe Asp His Asp
      285                      290                      295                      300

aga gat tac gaa gat gaa cca gta aac gag gac atg gag tga ctatcgg      1264
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          Met Cys Phe Pro Lys Val Leu
          1                      5

tct gat gac atg aag aag ctg aag gcc cga atg cac cag gcc ata gaa      159
Ser Asp Asp Met Lys Lys Leu Lys Ala Arg Met His Gln Ala Ile Glu
      10                      15                      20

aga ttt tat gat aaa atg caa aat gca gaa tca gga cgt gga cag gtg      207
Arg Phe Tyr Asp Lys Met Gln Asn Ala Glu Ser Gly Arg Gly Gln Val
      25                      30                      35

atg tcg agc ctg gca gag ctg gag gac gac ttc aaa gag ggc tac ctg      255
Met Ser Ser Leu Ala Glu Leu Glu Asp Asp Phe Lys Glu Gly Tyr Leu
      40                      45                      50                      55

gag aca gtg gcg gct tat tat gag gag cag cac cca gag ctc act cct      303
Glu Thr Val Ala Ala Tyr Tyr Glu Glu Gln His Pro Glu Leu Thr Pro
      60                      65                      70

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cta ctt gaa aaa gaa aga gat gga tta cgg tgc cga ggc aac aga tcc 351
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cct gtc ccg gat gtt gag gat ccc gca acc gag gag cct ggg gag agc 399
Pro Val Pro Asp Val Glu Asp Pro Ala Thr Glu Glu Pro Gly Glu Ser
      90                      95                      100

ttt tgt gac aag gtc atg aga tgg ttc cag gcc atg ctg cag cgg ctg 447
Phe Cys Asp Lys Val Met Arg Trp Phe Gln Ala Met Leu Gln Arg Leu
     105                      110                      115

cag acc tgg tgg cac ggg gtt ctg gcc tgg gtg aag gag aag gtg gtg 495
Gln Thr Trp Trp His Gly Val Leu Ala Trp Val Lys Glu Lys Val Val
    120                      125                      130                      135

gcc ctg gtc cat gca gtg cag gcc ctc tgg aaa cag ttc cag agt ttc 543
Ala Leu Val His Ala Val Gln Ala Leu Trp Lys Gln Phe Gln Ser Phe
      140                      145                      150

tgc tgc tct ctg tca gag ctc ttc atg tcc tct ttc cag tcc tac gga 591
Cys Cys Ser Leu Ser Glu Leu Phe Met Ser Ser Phe Gln Ser Tyr Gly
     155                      160                      165

gcc cca cgg ggg gac aag gag gag ctg aca ccc cag aag tgc tct gaa 639
Ala Pro Arg Gly Asp Lys Glu Glu Leu Thr Pro Gln Lys Cys Ser Glu
     170                      175                      180

ccc caa tcc tca aaa tga agatac tgacaccacc ttgcccctcc ccgtcaccgc 693
Pro Gln Ser Ser Lys *
    185

gcacccaccc tgacccctcc ctcagctgtc ctgtgccccg ccctctcccg cacactcagt 753

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aagggtgttct actgctagag cctatcgaaa cg atg cct aaa tca aag gaa ctt 53
Met Pro Lys Ser Lys Glu Leu
      1                      5

gtt tct tca agc tct tct ggc agt gat tct gac agt gag gtt gac aaa 101

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Val Ser Ser Ser Ser Ser Gly Ser Asp Ser Asp Ser Glu Val Asp Lys
    10          15          20

aag tta aag agg aaa aag caa gtt gct cca gaa aaa cct gta aag aaa    149
Lys Leu Lys Arg Lys Lys Gln Val Ala Pro Glu Lys Pro Val Lys Lys
    25          30          35

caa aag aca ggt gag act tcg aga gcc ctg tca tct tct aaa cag agc    197
Gln Lys Thr Gly Glu Thr Ser Arg Ala Leu Ser Ser Ser Lys Gln Ser
    40          45          50          55

agc agc agc aga gat gat aac atg ttt cag att ggg aaa atg agg tac    245
Ser Ser Ser Arg Asp Asp Asn Met Phe Gln Ile Gly Lys Met Arg Tyr
    60          65          70

gtt agt gtt cgc gat ttt aaa ggc aaa gtg cta att gat att aga gaa    293
Val Ser Val Arg Asp Phe Lys Gly Lys Val Leu Ile Asp Ile Arg Glu
    75          80          85

tat tgg atg gat cct gaa ggt gaa atg aaa cca gga aga aaa ggt att    341
Tyr Trp Met Asp Pro Glu Gly Glu Met Lys Pro Gly Arg Lys Gly Ile
    90          95          100

tct tta aat cca gaa caa tgg atc cag tcc agc aga aaa gat atg atg    389
Ser Leu Asn Pro Glu Gln Trp Ile Gln Ser Ser Arg Lys Asp Met Met
    105          110          115

aca ttg atg aag cac gtg agc ggt ctg taa t aatgcgagcc agattaattt    440
Thr Leu Met Lys His Val Ser Gly Leu *
    120          125

atcctgtact gttagatttg gggaatctg tcttatcaca aaggatgttg acttctagat    500

gttctccaga ttatgtatat tgtgat    526

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<210> 133
 <211> 1884
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (157)..(864)

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acttttttatt ctactatgta tatgtatgga atagtattaa taaatgaact agggaaggat    120

gtaataaatt agacatctct tcattttaga gagaag atg gaa aca aca ttg ctt    174
Met Glu Thr Thr Leu Leu
    1          5

ttc ttt tct caa ata aat atg tgt gaa tca aaa gaa aaa act ttt ttc    222

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Phe	Phe	Ser	Gln	Ile	Asn	Met	Cys	Glu	Ser	Lys	Glu	Lys	Thr	Phe	Phe		
			10					15					20				
aag	tta	ata	cat	ggt	tca	gga	aaa	gaa	gaa	aca	agc	aaa	gaa	gcc	aaa	270	
Lys	Leu	Ile	His	Gly	Ser	Gly	Lys	Glu	Glu	Thr	Ser	Lys	Glu	Ala	Lys		
		25					30					35					
atc	aga	gct	aag	gaa	aaa	aga	aat	aga	cta	agt	ctt	ctt	gtg	cag	aaa	318	
Ile	Arg	Ala	Lys	Glu	Lys	Arg	Asn	Arg	Leu	Ser	Leu	Leu	Val	Gln	Lys		
	40					45					50						
cct	gag	ttt	cat	gaa	gac	acc	cgc	tcc	agt	aga	tct	ggg	cac	ttg	gcc	366	
Pro	Glu	Phe	His	Glu	Asp	Thr	Arg	Ser	Ser	Arg	Ser	Gly	His	Leu	Ala		
	55				60					65					70		
aaa	gaa	aca	aga	gtc	tcc	cct	gaa	gag	gca	gtg	aaa	tgg	ggt	gaa	tca	414	
Lys	Glu	Thr	Arg	Val	Ser	Pro	Glu	Glu	Ala	Val	Lys	Trp	Gly	Glu	Ser		
			75						80					85			
ttt	gac	aaa	ctg	ctt	tcc	cat	aga	gat	gga	cta	gag	gct	ttt	acc	aga	462	
Phe	Asp	Lys	Leu	Leu	Ser	His	Arg	Asp	Gly	Leu	Glu	Ala	Phe	Thr	Arg		
			90					95					100				
ttt	ctt	aaa	act	gaa	ttc	agt	gaa	gaa	aat	att	gaa	ttt	tgg	ata	gcc	510	
Phe	Leu	Lys	Thr	Glu	Phe	Ser	Glu	Glu	Asn	Ile	Glu	Phe	Trp	Ile	Ala		
		105					110					115					
tgt	gaa	gat	ttc	aag	aaa	agc	aag	gga	cct	caa	caa	att	cac	ctt	aaa	558	
Cys	Glu	Asp	Phe	Lys	Lys	Ser	Lys	Gly	Pro	Gln	Gln	Ile	His	Leu	Lys		
	120					125					130						
gca	aaa	gca	ata	tat	gag	aaa	ttt	ata	cag	act	gat	gcc	cca	aaa	gag	606	
Ala	Lys	Ala	Ile	Tyr	Glu	Lys	Phe	Ile	Gln	Thr	Asp	Ala	Pro	Lys	Glu		
	135				140				145						150		
gtt	aac	ctt	gat	ttt	cac	aca	aaa	gaa	gtc	att	aca	aac	agc	atc	act	654	
Val	Asn	Leu	Asp	Phe	His	Thr	Lys	Glu	Val	Ile	Thr	Asn	Ser	Ile	Thr		
			155					160						165			
caa	cct	acc	ctc	cac	agt	ttt	gat	gct	gca	caa	agc	aga	gtg	tat	cag	702	
Gln	Pro	Thr	Leu	His	Ser	Phe	Asp	Ala	Ala	Gln	Ser	Arg	Val	Tyr	Gln		
			170					175					180				
ctc	atg	gaa	caa	gac	agt	tat	aca	cgt	ttt	ctg	aaa	tct	gac	atc	tat	750	
Leu	Met	Glu	Gln	Asp	Ser	Tyr	Thr	Arg	Phe	Leu	Lys	Ser	Asp	Ile	Tyr		
		185					190					195					
tta	gac	ttg	atg	gaa	gga	aga	cct	cag	aga	cca	aca	aat	ctt	agg	aga	798	
Leu	Asp	Leu	Met	Glu	Gly	Arg	Pro	Gln	Arg	Pro	Thr	Asn	Leu	Arg	Arg		
		200				205					210						
cga	tca	cgc	tca	ttt	acc	tgc	aat	gaa	ttc	caa	gat	gta	caa	tca	gat	846	
Arg	Ser	Arg	Ser	Phe	Thr	Cys	Asn	Glu	Phe	Gln	Asp	Val	Gln	Ser	Asp		
	215				220					225					230		
gtt	gcc	att	tgg	tta	taa	agaaaa	ttgattttgc	tcattttttat	gacaaactta							900	
Val	Ala	Ile	Trp	Leu	*												

tacatctgct tctaacatat cgcatgttta tgtaagatt tggccccatc ctttaaactg 960
 aaatatgtca tgtgaaatta ttttaaaaat gtaaaaacaa aactttctgc taacaaaata 1020
 catacagtat ctgccagtat attctgtaaa accttctatt tgatgtcatt ccatttataa 1080
 tcagaaaaaa aacttatttc ttaatcaaaa ggcagtacaa aaaaagtaat aatgttttat 1140
 aagattgtag agttaagtaa aagttaagct tttgcaaagt tgtcaaaagt tcaaacaaaa 1200
 gtctagttgg gattttttac caaagcagca taatatgtgt tatataaaca taataatact 1260
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 gagaataaga tccacatttg aactcattcc taagtgaaca tggacgtacc cagttataca 1560
 aagtacttct gttggtcaca gaaacatgac cagattttgc atatctccag gtaggggaact 1620
 aagtagacta ccttatcacc ggctaagaaa acttgctact aaactattag gccatcaatg 1680
 gcttgaataa aaaccagaga aggtttttcc caggacgtct catgtttggc cctttagaat 1740
 tggggtagaa atcagaaatg agatgagggg aagaagcaag gagtctaagg ccctagcgat 1800
 ttgggcacat gccacattgg ttcatttca gaaagtgtta tctcattgat tatattcttg 1860
 ttaagcaatc tccttaagta atta 1884

<210> 134

<211> 1601

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (868)..(1098)

<400> 134

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 agctatggaa acagatgata tggaagacat ccaacaagga ggaaaagcac acgcacgcct 180
 caccctgcc tcattctctgc ccagggtgt cctgacagca cagacgcttc agggagacag 240

gcctgggggac agtcatgtca tcacccttgc aacaaccacc caaaggaaaa gagagcgctg 300
aacagtttag gaaagggctc gcgctctaaga catcaagcga catacagaga tgtgcaaaac 360
ttggtgagaa ttaaaattga cctttgggag agggtagggg caggatgttt tatgacactg 420
tagaaaagac aggaggaacc cgctgcatg gagattgggg ggagctggaa gcaagcagcc 480
aacaggacag agttccagaa ctcatgcaga tggggaagag gtgacagccc ttccccactg 540
gcctcccccg tggaggtgga gtagacagat cccgggaaag gcaggaaaag ggccttgctt 600
tctttccctg tttcctaagc cgtggtcacc cttagcctatg aagctggaag ctatattcct 660
tccaatccca atttaccatt cctgtaaaca ggcccattca gggctgcctg agcaaattggg 720
gacttgccga ggcagctgca actagacttg ggctaagccg tctgggtcta ctcaagaatt 780
cgagtctgaa gatgaccaag cttgagttat tcaactgaga gtgaggtgtc aaggcggaag 840
cgactgtccc cagggaaggg ctgtgag atg gat ggg cgt gag tca gct ttt 891
Met Asp Gly Arg Glu Ser Ala Phe
1 5
cca aaa ctc aag tac ctg gga cag gac aac tcg cta gca gct cag tca 939
Pro Lys Leu Lys Tyr Leu Gly Gln Asp Asn Ser Leu Ala Ala Gln Ser
10 15 20
cct ccg tgg cgg aca cag ata agg atg tta aga cca gaa aac cag aga 987
Pro Pro Trp Arg Thr Gln Ile Arg Met Leu Arg Pro Glu Asn Gln Arg
25 30 35 40
cta ggg ccc cgt cct cag ccc tca cag cat gac aca gat gcc tcc ctc 1035
Leu Gly Pro Arg Pro Gln Pro Ser Gln His Asp Thr Asp Ala Ser Leu
45 50 55
gga gag cag ggt ctc tcg gca tcc agc ggc gtg gtc tgc att ctg ctc 1083
Gly Glu Gln Gly Leu Ser Ala Ser Ser Gly Val Val Cys Ile Leu Leu
60 65 70
tac ctc atg ctc tag gccccatgcc atcgtctcgg ccctagaccg tgaaaactgc 1138
Tyr Leu Met Leu *
75
cagtcacccg ggacctgctc ctaggggctg gcctgcacag ccggatggcc tgtgggcggg 1198
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ggggcagggg ggggctgcag gtggtgtgaa gaagagcca gctgtcatct aaggcaaact 1498
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1601

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<222> (194) .. (820)
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321

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Cys His Arg Pro Ser Cys Thr Thr Glu Gly Thr Thr Ser Pro Trp Thr	
145 150 155	
gcc atc gac ctc cag ggc tcc tgc tgt gag ggg tac ctc tgc aac agg	709
Ala Ile Asp Leu Gln Gly Ser Cys Cys Glu Gly Tyr Leu Cys Asn Arg	
160 165 170	
aaa tcc atg acc cag ccc ttc acc agt gct tca gcc acc acc cct ccc	757
Lys Ser Met Thr Gln Pro Phe Thr Ser Ala Ser Ala Thr Thr Pro Pro	
175 180 185	
cga gca cta cag gtc ctg gcc ctg ctc ctc cca gtc ctc ctg ctg gtg	805
Arg Ala Leu Gln Val Leu Ala Leu Leu Leu Pro Val Leu Leu Leu Val	
190 195 200	
ggg ctc tca gca tag accgccccctc caggatgctg gggacagggc tcacacacct	860
Gly Leu Ser Ala *	
205	
cattcttgct gcttcagccc ctatcacata gctcactgga aaatgatgtt aaagtaagaa	920
ttgcaataaa aaaaaaaaaa a	941

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 <220>
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 <222> (120)..(335)

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ggcgcttctg catctgtggg ccgagcattc ttcagggtcat ctgaaccttc tgagaaaac	119
atg gtc aac gtc ttg aaa gga gtg ctt ata gaa tgt gat cct gcc atg	167
Met Val Asn Val Leu Lys Gly Val Leu Ile Glu Cys Asp Pro Ala Met	
1 5 10 15	
aag cag ttt ctg ctg tac ttg gat gag tcc aat gcc ctg ggg aag aag	215
Lys Gln Phe Leu Leu Tyr Leu Asp Glu Ser Asn Ala Leu Gly Lys Lys	
20 25 30	
ttc atc att caa gac att gat gac act cac gtc ttt gta ata gca gaa	263
Phe Ile Ile Gln Asp Ile Asp Asp Thr His Val Phe Val Ile Ala Glu	
35 40 45	
ttg gtt aat gtc ctc cag gag cga gtg ggt gaa tta atg gac caa aat	311
Leu Val Asn Val Leu Gln Glu Arg Val Gly Glu Leu Met Asp Gln Asn	
50 55 60	

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gct ttt tcc ctt acc cag aaa tga aaatactcaa tatggaccat ttaggaatta 365
Ala Phe Ser Leu Thr Gln Lys *
65 70

taagcagcaa ctgtgaaaga cttgccactc aatatcttag gtgactgatt agacatagag 425

ggttgtttta ggagcatgcc acgggaaaga ctgagggatc atgatcattt gttcagaaaa 485

aaagcccctg aactgatttt gttaccatag aatttaaaaa aaaaaaaaaa 534

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<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (23)..(385)

<400> 137
cggcggaaga ggacaaggca ga atg cag gcc ctt cgg gtg tcc cag gcg ctg 52
Met Gln Ala Leu Arg Val Ser Gln Ala Leu
1 5 10

atc cgc tcc ttc agc tcc acc gcc cgg aac cgc ttt cag aac cga gtg 100
Ile Arg Ser Phe Ser Ser Thr Ala Arg Asn Arg Phe Gln Asn Arg Val
15 20 25

cgc gag aaa cag aag ctc ttc cag gtg ggg ggg gcg ggg ggg gtg ggg 148
Arg Glu Lys Gln Lys Leu Phe Gln Val Gly Gly Ala Gly Gly Val Gly
30 35 40

atc cga cgc gcc agc cgg gag cgc gcc gag ccg ggg cag gcg ggg cgc 196
Ile Arg Arg Ala Ser Arg Glu Arg Ala Glu Pro Gly Gln Ala Gly Arg
45 50 55

gct cta agg agc agc cag cac ccc ttt ctc atc aga cac ccc cac atc 244
Ala Leu Arg Ser Ser Gln His Pro Phe Leu Ile Arg His Pro His Ile
60 65 70

cag gag gac aat gac atc ccg ttg tac ctg aag ggc ggc atc gtt gac 292
Gln Glu Asp Asn Asp Ile Pro Leu Tyr Leu Lys Gly Gly Ile Val Asp
75 80 85 90

aac atc ctg tac cga gtg aca atg acg ctg tgt ctg ggc ggc act gtc 340
Asn Ile Leu Tyr Arg Val Thr Met Thr Leu Cys Leu Gly Gly Thr Val
95 100 105

tac agc ttg tac tcc ctt ggc tgg gcc tcc ttc ccc agg aat taa gac 388
Tyr Ser Leu Tyr Ser Leu Gly Trp Ala Ser Phe Pro Arg Asn *
110 115 120

caagaagcct ggggggcctg agagacttga acaagtgtca ataaacgctg gcctctgaaa 448

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<210> 138
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (197)..(691)

<400> 138

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ggcacggggc aagccaagaa ggctctggag catcagggag actccaactt aaggcaccaa      60
gcatgggtga ctaagggctt cctgtggact ggcaaatgag agcaaacacc tgtggcttga      120
gcactgcccc ctaaagcagg ccttacagat ctcttacact cgtgggtggga agagtctagt      180
gtgaaactgg ggtgga      atg ggg tgt cca cgt atg ttc cct ttt gcc tta      229
                        Met Gly Cys Pro Arg Met Phe Pro Phe Ala Leu
                        1          5          10

cta tat gtt ctg tca gtt tct ttc agg aaa atc ttc atc tta caa ctt      277
Leu Tyr Val Leu Ser Val Ser Phe Arg Lys Ile Phe Ile Leu Gln Leu
                        15          20          25

gta ggg ctg gtg tta act tac gac ttc act aac tgt gac ttt gag aag      325
Val Gly Leu Val Leu Thr Tyr Asp Phe Thr Asn Cys Asp Phe Glu Lys
                        30          35          40

att aaa gca gcc tat ctc agt act att tct aaa gac ctg att aca tat      373
Ile Lys Ala Ala Tyr Leu Ser Thr Ile Ser Lys Asp Leu Ile Thr Tyr
                        45          50          55

atg agt ggg acc aaa agt acc gag ttc aac aac acc gtc tct tgt agc      421
Met Ser Gly Thr Lys Ser Thr Glu Phe Asn Asn Thr Val Ser Cys Ser
                        60          65          70          75

aat cgg cca cat tgc ctt act gaa atc cag agc cta acc ttc aat ccc      469
Asn Arg Pro His Cys Leu Thr Glu Ile Gln Ser Leu Thr Phe Asn Pro
                        80          85          90

acc gcc ggc tgc gcg tcg ctc gcc aaa gaa atg ttc gcc atg aaa act      517
Thr Ala Gly Cys Ala Ser Leu Ala Lys Glu Met Phe Ala Met Lys Thr
                        95          100          105

aag gct gcc tta gct atc tgg tgc cca ggc tat tcg gaa act cag ata      565
Lys Ala Ala Leu Ala Ile Trp Cys Pro Gly Tyr Ser Glu Thr Gln Ile
                        110          115          120

aat gct act cag gca atg aag aag agg aga aaa agg aaa gtc aca acc      613
Asn Ala Thr Gln Ala Met Lys Lys Arg Arg Lys Arg Lys Val Thr Thr
                        125          130          135
    
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aat	aaa	tgt	ctg	gaa	caa	gtg	tca	caa	tta	caa	gga	ttg	tgg	cgt	cgc	661
Asn	Lys	Cys	Leu	Glu	Gln	Val	Ser	Gln	Leu	Gln	Gly	Leu	Trp	Arg	Arg	
140					145					150					155	

ttc	aat	cga	cct	tta	ctg	aaa	caa	cag	tta							691
Phe	Asn	Arg	Pro	Leu	Leu	Lys	Gln	Gln	*							
			160						165							

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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (172)..(696)

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gaagcgcgaa	gctgggattt	tttactgtct	cctgaagaat	ttaacacaaa	c atg gat											177
					Met Asp											
					1											

atc	aga	cca	aat	cat	aca	att	tat	atc	aac	aat	atg	aat	gac	aaa	att	225
Ile	Arg	Pro	Asn	His	Thr	Ile	Tyr	Ile	Asn	Asn	Met	Asn	Asp	Lys	Ile	
		5					10						15			

aaa	aag	gaa	gaa	ttg	aag	aga	tcc	cta	tat	gcc	ctg	ttt	tct	cag	ttt	273
Lys	Lys	Glu	Glu	Leu	Lys	Arg	Ser	Leu	Tyr	Ala	Leu	Phe	Ser	Gln	Phe	
		20				25					30					

ggt	cat	gtg	gtg	gac	att	gtg	gct	tta	aag	acc	atg	aag	atg	agg	ggg	321
Gly	His	Val	Val	Asp	Ile	Val	Ala	Leu	Lys	Thr	Met	Lys	Met	Arg	Gly	
		35			40					45					50	

cag	gcc	ttt	gtc	ata	ttt	aag	gaa	ctg	ggc	tca	tcc	aca	aat	gcc	ttg	369
Gln	Ala	Phe	Val	Ile	Phe	Lys	Glu	Leu	Gly	Ser	Ser	Thr	Asn	Ala	Leu	
			55						60					65		

aga	cag	cta	caa	gga	ttt	cca	ttt	tat	ggt	aaa	cca	atg	cga	ata	cag	417
Arg	Gln	Leu	Gln	Gly	Phe	Pro	Phe	Tyr	Gly	Lys	Pro	Met	Arg	Ile	Gln	
			70					75					80			

tat	gca	aaa	aca	gat	tcg	gat	ata	ata	tca	aaa	atg	cgt	gga	act	ttt	465
Tyr	Ala	Lys	Thr	Asp	Ser	Asp	Ile	Ile	Ser	Lys	Met	Arg	Gly	Thr	Phe	
			85				90					95				

gct	gac	aaa	gaa	aag	aaa	aaa	gaa	aag	aaa	aaa	gcc	aaa	act	gtg	gaa	513
Ala	Asp	Lys	Glu	Lys	Lys	Lys	Glu	Lys	Lys	Lys	Ala	Lys	Thr	Val	Glu	
			100				105				110					

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cag act gca aca acc aca aac aaa aag cct ggc ttc aag gaa gta cgt      561
Gln Thr Ala Thr Thr      Asn Lys Lys Pro Gly Phe Lys Glu Val Arg
115              120              125              130

ctg gta cca ggg agg cat gac att gct ttt gtt gaa ttt gaa aat gat      609
Leu Val Pro Gly Arg His Asp Ile Ala Phe Val Glu Phe Glu Asn Asp
              135              140              145

ggg cag gct gga gct gcc agg gat gct tta cag gga ttt aag atc aca      657
Gly Gln Ala Gly Ala Ala Arg Asp Ala Leu Gln Gly Phe Lys Ile Thr
              150              155              160

ccg tcc cat gct atg aag atc acc tat gcc aag aaa taa catttgggat      706
Pro Ser His Ala Met Lys Ile Thr Tyr Ala Lys Lys      *
              165              170              175

agtcgtcttt aaaagacttg gtgttattta cagtgtttgt tttgataaca tttggctggg      766

tcattttaat agttagagat gaggaggagt aaaagtgaaa tttttgtgaa ggacttaa      826

tatccagtgt ttcttttagcc ttggtgaact atgaaatacg aaggccttaa ttttgtacaa      886

taaactttta tttgtattct gtgtaaaaaa aaaaaaaaaa                        924

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<211> 1773
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<220>
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<222> (141)..(1667)

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ttctggtgct gcagtcagga      atg gag ctt gac agc gct ctg gaa gcc cca      170
                        Met Glu Leu Asp Ser Ala Leu Glu Ala Pro
                        1              5              10

tcg cag gaa gac tct aat ttg tcc gag gag ttg tct cac tcc gcc ttt      218
Ser Gln Glu Asp Ser Asn Leu Ser Glu Glu Leu Ser His Ser Ala Phe
              15              20              25

gga cag gcc ttc tcc aag att tta cac tgt ctt gcc cgc ccg gag gca      266
Gly Gln Ala Phe Ser Lys Ile Leu His Cys Leu Ala Arg Pro Glu Ala
              30              35              40

cga cga ggc aat gta aaa gat gca gtt ctt aaa gac ctc ggt gat cta      314
Arg Arg Gly Asn Val Lys Asp Ala Val Leu Lys Asp Leu Gly Asp Leu
              45              50              55

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ata gaa gcc aca gaa ttt gat agg tta ttt gag ggg act ggt gca cgg	362
Ile Glu Ala Thr Glu Phe Asp Arg Leu Phe Glu Gly Thr Gly Ala Arg	
60 65 70	
ctc cgc gga atg ccg gag aca ctg ggg cag gta gca aaa gcc ctg gag	410
Leu Arg Gly Met Pro Glu Thr Leu Gly Gln Val Ala Lys Ala Leu Glu	
75 80 85 90	
aag tat gca gcc ccc tcc aag gag gag gaa ggt gga ggt gat ggg cac	458
Lys Tyr Ala Ala Pro Ser Lys Glu Glu Glu Gly Gly Gly Asp Gly His	
95 100 105	
tcc gaa gcg gcc gag aaa gca gcc caa gtt ggg tta ctg ttt ctt aaa	506
Ser Glu Ala Ala Glu Lys Ala Ala Gln Val Gly Leu Leu Phe Leu Lys	
110 115 120	
ctg tta ggg aaa gtt gag act gct aag aat tcc ctg gtc ggc cct gca	554
Leu Leu Gly Lys Val Glu Thr Ala Lys Asn Ser Leu Val Gly Pro Ala	
125 130 135	
tgg cag acg ggc ctg cat cac ttg gca gga ccc gtt tat att ttt gcc	602
Trp Gln Thr Gly Leu His His Leu Ala Gly Pro Val Tyr Ile Phe Ala	
140 145 150	
atc aca cac agc ttg gag caa cca tgg acc act ccg aga tct cgg gaa	650
Ile Thr His Ser Leu Glu Gln Pro Trp Thr Thr Pro Arg Ser Arg Glu	
155 160 165 170	
gtt gct agg gag gtg ctc acc tca ctg ctt caa gtt act gaa tgc ggt	698
Val Ala Arg Glu Val Leu Thr Ser Leu Leu Gln Val Thr Glu Cys Gly	
175 180 185	
tct gtg gca gga ttc cta cat gga gaa aat gaa gat gag aaa ggg aga	746
Ser Val Ala Gly Phe Leu His Gly Glu Asn Glu Asp Glu Lys Gly Arg	
190 195 200	
ctt tcg gtg ata cta ggg ctt ctc aaa ccc gac ttg tat aag gaa tcc	794
Leu Ser Val Ile Leu Gly Leu Leu Lys Pro Asp Leu Tyr Lys Glu Ser	
205 210 215	
tgg aag aat aac cct gcc atc aaa cat gtt ttc tca tgg act ctg caa	842
Trp Lys Asn Asn Pro Ala Ile Lys His Val Phe Ser Trp Thr Leu Gln	
220 225 230	
cag gtc act cgg ccc tgg ctg agc cag cat ctg gaa agg gta ctt ccc	890
Gln Val Thr Arg Pro Trp Leu Ser Gln His Leu Glu Arg Val Leu Pro	
235 240 245 250	
gca tca ttg gtc att tca gat gac tat cag act gag aac aaa atc ctg	938
Ala Ser Leu Val Ile Ser Asp Asp Tyr Gln Thr Glu Asn Lys Ile Leu	
255 260 265	
ggg gta cac tgt ctc cat cac att gtg ctt aat gtg cca gct gct gat	986
Gly Val His Cys Leu His His Ile Val Leu Asn Val Pro Ala Ala Asp	
270 275 280	

ttg ctc cag tat aac aga gcc cag gtc cta tac cat gcc att tcc aac	1034
Leu Leu Gln Tyr Asn Arg Ala Gln Val Leu Tyr His Ala Ile Ser Asn	
285 290 295	
cac ctg tac aca cca gag cac cac ctc att cag gct gtg ctc ctg tgt	1082
His Leu Tyr Thr Pro Glu His His Leu Ile Gln Ala Val Leu Leu Cys	
300 305 310	
ctg ctg gat tta ttc ccc atc ctg gag aaa acc ctg cac tgg aaa gga	1130
Leu Leu Asp Leu Phe Pro Ile Leu Glu Lys Thr Leu His Trp Lys Gly	
315 320 325 330	
gat gga gct cga ccc acc acc cat tgt gat gag gtc ctg cgg ctg atc	1178
Asp Gly Ala Arg Pro Thr Thr His Cys Asp Glu Val Leu Arg Leu Ile	
335 340 345	
ctg acc cac atg gag cca gag cac cgc ctt ctt tta cgc agg acc tac	1226
Leu Thr His Met Glu Pro Glu His Arg Leu Leu Leu Arg Arg Thr Tyr	
350 355 360	
gca aga aac ctg ccg gct ttc gtg aac agg ttg ggg atc cta act gtc	1274
Ala Arg Asn Leu Pro Ala Phe Val Asn Arg Leu Gly Ile Leu Thr Val	
365 370 375	
cgg cac tta aag agg ctg gag aga gtc atc att ggt tat ctg gag gtt	1322
Arg His Leu Lys Arg Leu Glu Arg Val Ile Ile Gly Tyr Leu Glu Val	
380 385 390	
tat gat gga cct gag gag gaa gct aga ctg aag ata ttg gaa acc cta	1370
Tyr Asp Gly Pro Glu Glu Glu Ala Arg Leu Lys Ile Leu Glu Thr Leu	
395 400 405 410	
aaa ctt ctc atg caa cat act tgg ccc aga gtt tcc tgc aga ctt gtg	1418
Lys Leu Leu Met Gln His Thr Trp Pro Arg Val Ser Cys Arg Leu Val	
415 420 425	
gtc tta ctg aag gcc ctc ttg aaa ctg att tgt gat gta gca agg gat	1466
Val Leu Leu Lys Ala Leu Leu Lys Leu Ile Cys Asp Val Ala Arg Asp	
430 435 440	
cca aac ctt aca cct gag tct gtt aag agc gcc ctg cta cag gag gcc	1514
Pro Asn Leu Thr Pro Glu Ser Val Lys Ser Ala Leu Leu Gln Glu Ala	
445 450 455	
aca gac tgc ctg att ctc ctg gac cgc tgt tct caa gga cgg gta aag	1562
Thr Asp Cys Leu Ile Leu Leu Asp Arg Cys Ser Gln Gly Arg Val Lys	
460 465 470	
ggt ctc ctg gcc aaa att ccc caa agc tgt gaa gac aga aaa gtg gtg	1610
Gly Leu Leu Ala Lys Ile Pro Gln Ser Cys Glu Asp Arg Lys Val Val	
475 480 485 490	
aac tat atc aga aaa gtg cag cag gtt tct gaa ggc gca ccc tac aat	1658
Asn Tyr Ile Arg Lys Val Gln Gln Val Ser Glu Gly Ala Pro Tyr Asn	
495 500 505	
gga act taa gacttgt attactttcc caagaggaaa ggattttctt cccatcccaa	1714

Gly Thr *

tttgtatgaa tggagttatt taagaaaaaa agatatTTTT acacgaaaaa aaaaaaaaaa 1773

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<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (100)..(942)

<220>
<221> misc_feature
<222> (1)...(2242)
<223> n = a,t,c or g

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atccgaccac atttcactct caccgctgta ggaatccag atg cag gcc aag tac 114
Met Gln Ala Lys Tyr
1 5

agc agc acg agg gac atg ctg gat gat gat ggg gac acc acc atg agc 162
Ser Ser Thr Arg Asp Met Leu Asp Asp Asp Gly Asp Thr Thr Met Ser
10 15 20

ctg cat tct caa gcc tct gcc aca act cgg cat cca gag ccc cgg cgc 210
Leu His Ser Gln Ala Ser Ala Thr Thr Arg His Pro Glu Pro Arg Arg
25 30 35

aca gag cac agg gct ccc tct tca acg tgg cga cca gtg gcc ctg acc 258
Thr Glu His Arg Ala Pro Ser Ser Thr Trp Arg Pro Val Ala Leu Thr
40 45 50

ctg ctg act ttg tgc ttg gtg ctg ctg ata ggg ctg gca gcc ctg ggg 306
Leu Leu Thr Leu Cys Leu Val Leu Leu Ile Gly Leu Ala Ala Leu Gly
55 60 65

ctt ttg ttt ttt cag tac tac cag ctc tcc aat act ggt caa gac acc 354
Leu Leu Phe Phe Gln Tyr Tyr Gln Leu Ser Asn Thr Gly Gln Asp Thr
70 75 80 85

att tct caa atg gaa gaa aga tta gga aat acg tcc caa gag ttg caa 402
Ile Ser Gln Met Glu Glu Arg Leu Gly Asn Thr Ser Gln Glu Leu Gln
90 95 100

tct ctt caa gtc cag aat ata aag ctt gca gga agt ctg cag cat gtg 450
Ser Leu Gln Val Gln Asn Ile Lys Leu Ala Gly Ser Leu Gln His Val
105 110 115

gct gaa aaa ctc tgt cgt gag ctg tat aac aaa gct gga gca cac agg Ala Glu Lys Leu Cys Arg Glu Leu Tyr Asn Lys Ala Gly Ala His Arg 120 125 130	498
tgc agc cct tgt aca gaa caa tgg aaa tgg cat gga gac aat tgc tac Cys Ser Pro Cys Thr Glu Gln Trp Lys Trp His Gly Asp Asn Cys Tyr 135 140 145	546
cag ttc tat aaa gac agc aaa agt tgg gag gac tgt aaa tat ttc tgc Gln Phe Tyr Lys Asp Ser Lys Ser Trp Glu Asp Cys Lys Tyr Phe Cys 150 155 160 165	594
ctt agt gaa aac tct acc atg ctg aag ata aac aaa caa gaa gac ctg Leu Ser Glu Asn Ser Thr Met Leu Lys Ile Asn Lys Gln Glu Asp Leu 170 175 180	642
gaa ttt gcc gcg tct cag agc tac tct gag ttt ttc tac tct tat tgg Glu Phe Ala Ala Ser Gln Ser Tyr Ser Glu Phe Phe Tyr Ser Tyr Trp 185 190 195	690
aca ggg ctt ttg cgc cct gac agt ggc aag gcc tgg ctg tgg atg gat Thr Gly Leu Leu Arg Pro Asp Ser Gly Lys Ala Trp Leu Trp Met Asp 200 205 210	738
gga acc cct ttc act tct gaa ctg ttc cat att ata ata gat gtc acc Gly Thr Pro Phe Thr Ser Glu Leu Phe His Ile Ile Ile Asp Val Thr 215 220 225	786
agc cca aga agc aga gac tgt gtg gcc atc ctt aat ggg atg atc ttc Ser Pro Arg Ser Arg Asp Cys Val Ala Ile Leu Asn Gly Met Ile Phe 230 235 240 245	834
tca aag gac tgc aaa gaa ttg aag cgt tgt gtc tgt gag aga agg gca Ser Lys Asp Cys Lys Glu Leu Lys Arg Cys Val Cys Glu Arg Arg Ala 250 255 260	882
gga atg gtg aag cca gag agc ctc cat gtc ccc cct gaa aca tta ggc Gly Met Val Lys Pro Glu Ser Leu His Val Pro Pro Glu Thr Leu Gly 265 270 275	930
gaa ggt gac tga ttc gccctctgca actacaaata gcagagtgcg ccaggcggtg Glu Gly Asp * 280	985
ccaaagcaag ggctagttaga gacattggga aatggaacat aatcaggaaa gactatctct	1045
ctgactagta caaaatgggt tctcgtgttt cctgttcagg atcaccagca tttctgagct	1105
tgggttttatg cacgtattta acagtcacaa gaagtcttat ttacatgccca ccaaccaacc	1165
tcagaaaccc ataatgtcat ctgccttctt ggcttagaga taacttttag ctctctttct	1225
tctcaatgtc taatatcacc tcctgtttt catgtcttcc ttacacttgg tggaataaga	1285
aactttttga agtagaggaa atacattgag gtaacatcct tttctctgac agtcaagtag	1345
tccatcagaa attggcagtc acttcccaga ttgtaccagc aaatacacaa ggaattcttt	1405

ctg cat tct caa gcc tct gcc aca act cgg cat cca gag ccc cgg cgc	210
Leu His Ser Gln Ala Ser Ala Thr Thr Arg His Pro Glu Pro Arg Arg	
25 30 35	
aca gag cac agg gct ccc tct tca acg tgg cga cca gtg gcc ctg acc	258
Thr Glu His Arg Ala Pro Ser Ser Thr Trp Arg Pro Val Ala Leu Thr	
40 45 50	
ctg ctg act ttg tgc ttg gtg ctg ctg ata ggg ctg gca gcc ctg ggg	306
Leu Leu Thr Leu Cys Leu Val Leu Leu Ile Gly Leu Ala Ala Leu Gly	
55 60 65	
ctt ttg ttt ttt cag tac tac cag ctc tcc aat act ggt caa gac acc	354
Leu Leu Phe Phe Gln Tyr Tyr Gln Leu Ser Asn Thr Gly Gln Asp Thr	
70 75 80 85	
att tct caa atg gaa gaa aga tta gga aat acg tcc caa gag ttg caa	402
Ile Ser Gln Met Glu Glu Arg Leu Gly Asn Thr Ser Gln Glu Leu Gln	
90 95 100	
tct ctt caa gtc cag aat ata aag ctt gca gga agt ctg cag cat gtg	450
Ser Leu Gln Val Gln Asn Ile Lys Leu Ala Gly Ser Leu Gln His Val	
105 110 115	
gct gaa aaa ctc tgt cgt gag ctg tat aac aaa gct gga ggc tat aca	498
Ala Glu Lys Leu Cys Arg Glu Leu Tyr Asn Lys Ala Gly Gly Tyr Thr	
120 125 130	
aga aac atg gtg cca gca tct gct tct tct gag agc ctc agg cag ctt	546
Arg Asn Met Val Pro Ala Ser Ala Ser Ser Glu Ser Leu Arg Gln Leu	
135 140 145	
cca cac atg ggg gaa agt gca gca gca cac agg tgc agc cct tgt aca	594
Pro His Met Gly Glu Ser Ala Ala Ala His Arg Cys Ser Pro Cys Thr	
150 155 160 165	
gaa caa tgg aaa tgg cat gga gac aat tgc tac cag ttc tat aaa gac	642
Glu Gln Trp Lys Trp His Gly Asp Asn Cys Tyr Gln Phe Tyr Lys Asp	
170 175 180	
agc aaa agt tgg gag gac tgt aaa tat ttc tgc ctt agt gaa aac tct	690
Ser Lys Ser Trp Glu Asp Cys Lys Tyr Phe Cys Leu Ser Glu Asn Ser	
185 190 195	
acc atg ctg aag ata aac aaa caa gaa gac ctg gaa ttt gcc gcg tct	738
Thr Met Leu Lys Ile Asn Lys Gln Glu Asp Leu Glu Phe Ala Ala Ser	
200 205 210	
cag agc tac tct gag ttt ttc tac tct tat tgg aca ggg ctt ttg cgc	786
Gln Ser Tyr Ser Glu Phe Phe Tyr Ser Tyr Trp Thr Gly Leu Leu Arg	
215 220 225	
cct gac agt ggc aag gcc tgg ctg tgg atg gat gga acc cct ttc act	834
Pro Asp Ser Gly Lys Ala Trp Leu Trp Met Asp Gly Thr Pro Phe Thr	
230 235 240 245	
tct gaa ctg ttc cat att ata ata gat gtc acc agc cca aga agc aga	882

Ser Glu Leu Phe His Ile Ile Ile Asp Val Thr Ser Pro Arg Ser Arg	
250 255 260	
gac tgt gtg gcc atc ctt aat ggg atg atc ttc tca aag gac tgc aaa	930
Asp Cys Val Ala Ile Leu Asn Gly Met Ile Phe Ser Lys Asp Cys Lys	
265 270 275	
gaa ttg aag cgt tgt gtc tgt gag aga agg gca gga atg gtg aag cca	978
Glu Leu Lys Arg Cys Val Cys Glu Arg Arg Ala Gly Met Val Lys Pro	
280 285 290	
gag agc ctc cat gtc ccc cct gaa aca tta ggc gaa ggt gac tga ttc	1026
Glu Ser Leu His Val Pro Pro Glu Thr Leu Gly Glu Gly Asp *	
295 300 305	
gccctctgca actacaaata gcagagtgag ccaggcgggtg ccaaagcaag ggctagttga	1086
gacattggga aatggaacat aatcaggaaa gactatctct ctgactagta caaaatgggt	1146
tctcgtgttt cctgttcagg atcaccagca tttctgagct tgggtttatg cacgtattta	1206
acagtcacaa gaagtcttat ttacatgcca ccaaccaacc tcagaaaccc ataatgtcat	1266
ctgccttctt ggcttagaga taacttttag ctctctttct tctcaatgtc taatatcacc	1326
tccctgtttt catgtcttcc ttacacttgg tggaataaga aactttttga agtagaggaa	1386
atacattgag gtaacatcct tttctctgac agtcaagtag tccatcagaa attggcagtc	1446
acttcccaga ttgtaccagc aaatacacaa ggaattcttt ttgtttgttt cagttcatac	1506
tagtcccttc ccaatccatc agtaaagacc ccatctgcct tgtccatgcc gtttcccaac	1566
agggatgtca cttgatatga gaatctcaaa tctcaatgcc ttataagcat tccttcctgt	1626
gtccattaag actctgataa ttgtctcccc tccataggaa tttctcccag gaaagaaata	1686
tatccccatc tccgtttcat atcagaacta ccgtccccga tattcccttc agagagatta	1746
aagaccagaa aaaagtgagc ctcttcatct gcacctgtaa tagtttcagt tcctattttc	1806
ttccattgac ccatatttat acctttcagg tactgaagat ttaataataa taaatgtaaa	1866
tactgtgaag tgtgtgtgat ttacaatgg acttatgggt ggtgggaaaa ttcagcatgg	1926
aaatgctttt caaaatatga tagcggtcac tatttttgatt gtgccttact gaaagttttt	1986
ggggaattta caagagtact gattacatga ttatctggag aaaataagat gtctttgaaa	2046
tacatgttgg cttcaagaaa acagttttaa cgttttccta aaatgaaatc ttttgagggtg	2106
agcttatggc atcaacacat gggtgatgag gaagctgagt tgcattagtg cacatgattt	2166
ccagtcaggt catgggaaat gaacagagac agtgacatct ttgtagctgc tcctttgtga	2226
ggcacttctt tcttgagatg actccatgca caaatataac agggatcatt gggaatgaca	2286

ccatcacagc caccaagntt attgggttac tgataat

2323

<210> 143
<211> 971
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (72)..(767)

<400> 143

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atgtctactg a atg ttg act ggt gtt gga tgt ctt gtc tcc tca gaa tct	110
Met Leu Thr Gly Val Gly Cys Leu Val Ser Ser Glu Ser	
1 5 10	
ctg agc tgc gtg cag tgt aat tca tgg gaa aaa tcc tgt gtc aac agc	158
Leu Ser Cys Val Gln Cys Asn Ser Trp Glu Lys Ser Cys Val Asn Ser	
15 20 25	
att gcc tct gaa tgt ccc tca cat gcc aac acc agc tgt atc agc tcc	206
Ile Ala Ser Glu Cys Pro Ser His Ala Asn Thr Ser Cys Ile Ser Ser	
30 35 40 45	
tca gcc agc tcc tct cta gag aca cca gtc aga tta tac cag aat atg	254
Ser Ala Ser Ser Ser Leu Glu Thr Pro Val Arg Leu Tyr Gln Asn Met	
50 55 60	
ttc tgc tca gcg gag aac tgc agt gag gag aca cac att aca gcc ttc	302
Phe Cys Ser Ala Glu Asn Cys Ser Glu Glu Thr His Ile Thr Ala Phe	
65 70 75	
act gtc cac gtg tct gct gaa gaa cac ttt cat ttt gta agc cag tgc	350
Thr Val His Val Ser Ala Glu Glu His Phe His Phe Val Ser Gln Cys	
80 85 90	
tgc caa gga aag gaa tgc agc aac acc agc gat gcc ctg gac cct ccc	398
Cys Gln Gly Lys Glu Cys Ser Asn Thr Ser Asp Ala Leu Asp Pro Pro	
95 100 105	
ctg aag aac gtg tcc agc aac gca gag tgc cct gct tgt tat gaa tct	446
Leu Lys Asn Val Ser Ser Asn Ala Glu Cys Pro Ala Cys Tyr Glu Ser	
110 115 120 125	
aat gga act tcc tgt cgt ggg aag ccc tgg aaa tgc tat gaa gaa gaa	494
Asn Gly Thr Ser Cys Arg Gly Lys Pro Trp Lys Cys Tyr Glu Glu Glu	
130 135 140	
cag tgt gtc ttt cta gtt gca gaa ctt aag aat gac att gag tct aag	542
Gln Cys Val Phe Leu Val Ala Glu Leu Lys Asn Asp Ile Glu Ser Lys	
145 150 155	

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agt ctc gtg ctg aaa ggc tgt tcc aac gtc agt aac gcc acc tgt cag      590
Ser Leu Val Leu Lys Gly Cys Ser Asn Val Ser Asn Ala Thr Cys Gln
      160                      165                      170

ttc ctg tct ggt gaa aac aag act ctt gga gga gtc atc ttt cga aag      638
Phe Leu Ser Gly Glu Asn Lys Thr Leu Gly Gly Val Ile Phe Arg Lys
      175                      180                      185

ttt gag tgt gca aat gta aac agc tta acc ccc acg tct gca cca acc      686
Phe Glu Cys Ala Asn Val Asn Ser Leu Thr Pro Thr Ser Ala Pro Thr
      190                      195                      200                      205

act tcc cac aac gtg ggc tcc aaa gct tcc ctc tac ctc ttg gcc ctt      734
Thr Ser His Asn Val Gly Ser Lys Ala Ser Leu Tyr Leu Leu Ala Leu
      210                      215                      220

gcc agc ctc ctt ctt cgg gga ctg ctg ccc tga ggtcctgg ggctgcactt      785
Ala Ser Leu Leu Leu Arg Gly Leu Leu Pro *
      225                      230

tgcccagcac cccatttctg cttctctgag gtccagagca cccctgcgg tgctgacacc      845

ctctttccct gctctgcccc gtttaactgc ccagtaagtg ggagtcacag gtctccaggc      905

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aaaaaa                                                                971

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<210> 144
<211> 1689
<212> DNA
<213> Homo sapiens

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<221> CDS
<222> (354)..(1370)

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<220>
<221> misc_feature
<222> (1)...(1689)
<223> n = a,t,c or g

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<400> 144
cctgaatgct ttacgtaccg gcccggaatt cccgggtcga cccacgcgtc cgctcggcca      60

ccgaagccac cctgccctgg tgaaagggct cccgcaccgc ccggtgctcc ccatctgcct      120

ggcgtttgtgc gcagagctgg aaagcatggc tgttataaat gaattctgat tttggggagc      180

agatgccaac ttagagcctc gtaccaatct ctctgtcttt aaaagatgag gtgacttggt      240

gatttttctg gaaaattata ggtgcccagc taagacctga atgccatcac cctccccagg      300

gctctgcagt tttctcgtgg tgaacccttg atggatttgt tggttgcttga gaa atg      356

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[illegible][illegible]

210	215	220	225	
gag gca cgt ggc tcc agc cgg tgt gga cct ggg cct ctg ctg ccc acg				1076
Glu Ala Arg Gly Ser Ser Arg Cys Gly Pro Gly Pro Leu Leu Pro Thr	230	235	240	
tct gcc cct gtc ctc ctg cag cat tat cct ctg tat cgg aga agt gat				1124
Ser Ala Pro Val Leu Leu Gln His Tyr Pro Leu Tyr Arg Arg Ser Asp	245	250	255	
gct aac tgt tct ggg gaa gac gct gct cct gca gag gaa agg gac atc				1172
Ala Asn Cys Ser Gly Glu Asp Ala Ala Pro Ala Glu Glu Arg Asp Ile	260	265	270	
cca ttt aag gag aac tat gac gtg ctt tca cgg gag gca tca caa aag				1220
Pro Phe Lys Glu Asn Tyr Asp Val Leu Ser Arg Glu Ala Ser Gln Lys	275	280	285	
ctg ctg tgg tgg ctc cag ccg cgc ctg gtt ctc agt ggc cac acg cac				1268
Leu Leu Trp Trp Leu Gln Pro Arg Leu Val Leu Ser Gly His Thr His	290	295	300	305
agc gcc tgc gag gtg cac cac ggg ggc cga gtc ccc gag ctc agc gtc				1316
Ser Ala Cys Glu Val His His Gly Gly Arg Val Pro Glu Leu Ser Val	310	315	320	
cca tct ttc agt tgg agg aac aga aac aac ccc agt ttc atc atg gta				1364
Pro Ser Phe Ser Trp Arg Asn Arg Asn Asn Pro Ser Phe Ile Met Val	325	330	335	
ccg tga aagtttattt ttgtctgaaa gctttcataa gtatttaaata caacacagta				1420
Pro *				
atcaactatt taattgctgc aatcgggtcaa aatttataaaa agccacacac aaatttctct				1480
ccttctacac gtagctccat aactgcccc ttgccaaaca cccttccggg aaccaatcag				1540
catgacattc ctgggcagtt aatgtgagaa gcgagggcag ggcaccgtcc nagtggactt				1600
tatccttcag ggaggggagcgt atcctctctc ttacactctg tgtgtgggta aatttctaaa				1660
gaacaccatt taatccatag ctatatcag				1689

<210> 145
 <211> 480
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (104)..(298)

 <400> 145

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tttaagtttt ttttccttat tactgatctt atgcaatttg att  atg ttc ctt ggt      115
                                         Met Phe Leu Gly
                                         1

gta gct ttt cag tgt ttc ttc tgc ttt tgg ttt gtt gag ctt ttt gga      163
Val Ala Phe Gln Cys Phe Phe Cys Phe Trp Phe Val Glu Leu Phe Gly
   5              10              15              20

ttt gtg ggt tta cag tta tta tca aat ttg gaa aaa ttt cag ccc tta      211
Phe Val Gly Leu Gln Leu Leu Ser Asn Leu Glu Lys Phe Gln Pro Leu
          25              30              35

tgt ctt caa ata ttt ttt ctg tct ccc tgc ccc atc cgt agt ctt tat      259
Cys Leu Gln Ile Phe Phe Leu Ser Pro Cys Pro Ile Arg Ser Leu Tyr
          40              45              50

ata ttt gat cat cta aag ttg tct cac agc tca cag tga cactgcttgt      308
Ile Phe Asp His Leu Lys Leu Ser His Ser Ser Gln  *
          55              60              65

ttttccagtc tttttttccc tctaggtgtt tcattttgaa caattgctat tgctatgtct      368

tcaagatcct taatcttttc ttctgtagtg ccacatctta cccagtgaac ttttcacctc      428

agacatggta ttttttattt ctagaaatta ggactttttt tacatttccc ac      480

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<210> 146
 <211> 557
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (158)..(520)

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<400> 146
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ccttgggacc cagcacaggg agctggagag ccaactccac gtgcttcagt ccaaactgca      120
ggtaccaggc actgggggtg gggaggggaag acagggt atg ggg agg agg gat ggt      175
                                         Met Gly Arg Arg Asp Gly
                                         1              5

gat gaa aga agc tgt tct gga tta ggg act cca aag gca gct gac agc      223
Asp Glu Arg Ser Cys Ser Gly Leu Gly Thr Pro Lys Ala Ala Asp Ser
          10              15              20

atc tgg ctt tca gtt cct cag tca cca cta ctt tgt acc aaa ttc act      271
Ile Trp Leu Ser Val Pro Gln Ser Pro Leu Leu Cys Thr Lys Phe Thr
          25              30              35

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gtt ttg gct ctg aaa tct aat ttt gag ttt agc aag gat gtc tgc att 319
Val Leu Ala Leu Lys Ser Asn Phe Glu Phe Ser Lys Asp Val Cys Ile
40 45 50

gct cat gca aat gaa cta agc gtt cat tgg aat gac acc atc acc acc 367
Ala His Ala Asn Glu Leu Ser Val His Trp Asn Asp Thr Ile Thr Thr
55 60 65 70

caa atg aaa aga act ggc tgg aat att cat cag cct act aat gtc atc 415
Gln Met Lys Arg Thr Gly Trp Asn Ile His Gln Pro Thr Asn Val Ile
75 80 85

tcc caa ccc act ctc caa act cca tcc caa aaa agc atc cag ttc aga 463
Ser Gln Pro Thr Leu Gln Thr Pro Ser Gln Lys Ser Ile Gln Phe Arg
90 95 100

att gcc cac tgt tgg caa aga aag aat gtc act aat tta ttt aca ggg 511
Ile Ala His Cys Trp Gln Arg Lys Asn Val Thr Asn Leu Phe Thr Gly
105 110 115

agc aga tag cagggactta cagatgaacc aggcctgcg atttttg 557
Ser Arg *
120

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<213> Homo sapiens

<220>
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<222> (172)..(1071)

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gtccgggggct acacagccag gtgtcagatg tgtctctgct gatctgagtc tgcctgtggc 120
atggacctgc atcttccttg aagcatctcc agggctgaaa aatcactgac c atg gca 177
Met Ala
1

cca tgg tct cat cca tct gca cag ctg cag cca gtg gga gga gac gcc 225
Pro Trp Ser His Pro Ser Ala Gln Leu Gln Pro Val Gly Gly Asp Ala
5 10 15

gtg agc cct gcc ctc atg gtt ctg ctc tgc ctc ggg ctg agt ctg ggc 273
Val Ser Pro Ala Leu Met Val Leu Leu Cys Leu Gly Leu Ser Leu Gly
20 25 30

ccc agg acc cac gtg cag gca ggg aac ctc tcc aaa gcc acc ctc tgg 321
Pro Arg Thr His Val Gln Ala Gly Asn Leu Ser Lys Ala Thr Leu Trp
35 40 45 50

gct gag cca ggc tct gtg atc agc cgg ggg aac tct gtg acc atc cgg	369
Ala Glu Pro Gly Ser Val Ile Ser Arg Gly Asn Ser Val Thr Ile Arg	
55 60 65	
tgt cag ggg acc ctg gag gcc cag gaa tac cgt ctg gtt aaa gag gga	417
Cys Gln Gly Thr Leu Glu Ala Gln Glu Tyr Arg Leu Val Lys Glu Gly	
70 75 80	
agc cca gaa ccc tgg gac aca cag aac cca ctg gag ccc aag aac aag	465
Ser Pro Glu Pro Trp Asp Thr Gln Asn Pro Leu Glu Pro Lys Asn Lys	
85 90 95	
gcc aga ttc tcc atc cca tcc atg aca gag cac cat gca ggg aga tac	513
Ala Arg Phe Ser Ile Pro Ser Met Thr Glu His His Ala Gly Arg Tyr	
100 105 110	
cgc tgt tac tac tac agc cct gca ggc tgg tca gag ccc agc gac ccc	561
Arg Cys Tyr Tyr Tyr Ser Pro Ala Gly Trp Ser Glu Pro Ser Asp Pro	
115 120 125 130	
ctg gag ctg gtg gtg aca gga ttc tac aac aaa ccc acc ctc tca gcc	609
Leu Glu Leu Val Val Thr Gly Phe Tyr Asn Lys Pro Thr Leu Ser Ala	
135 140 145	
ctg ccc agt cct gtg gtg acc tca gga gag aac gtg acc ctc cag tgt	657
Leu Pro Ser Pro Val Val Thr Ser Gly Glu Asn Val Thr Leu Gln Cys	
150 155 160	
ggc tca cgg ctg aga ttc gac agg ttc att ctg act gag gaa gga gac	705
Gly Ser Arg Leu Arg Phe Asp Arg Phe Ile Leu Thr Glu Glu Gly Asp	
165 170 175	
cac aag ctc tcc tgg acc ttg gac tca cag ctg acc ccc agt ggg cag	753
His Lys Leu Ser Trp Thr Leu Asp Ser Gln Leu Thr Pro Ser Gly Gln	
180 185 190	
ttc cag gcc ctg ttc cct gtg ggc cct gtg acc ccc agc cac agg tgg	801
Phe Gln Ala Leu Phe Pro Val Gly Pro Val Thr Pro Ser His Arg Trp	
195 200 205 210	
atg ctc aga tgc tat ggc tct cgc agg cat atc ctg cag gta tgg tca	849
Met Leu Arg Cys Tyr Gly Ser Arg Arg His Ile Leu Gln Val Trp Ser	
215 220 225	
gaa ccc agt gac ctc ctg gag att ccg gtc tca gga gca gct gat aac	897
Glu Pro Ser Asp Leu Leu Glu Ile Pro Val Ser Gly Ala Ala Asp Asn	
230 235 240	
ctc agt ccg tca caa aac aag tct gac tct ggg act gcc tca cac ctt	945
Leu Ser Pro Ser Gln Asn Lys Ser Asp Ser Gly Thr Ala Ser His Leu	
245 250 255	
cag gat tac gca gta gag aat ctc atc cgc atg ggc atg gcc ggc ttg	993
Gln Asp Tyr Ala Val Glu Asn Leu Ile Arg Met Gly Met Ala Gly Leu	
260 265 270	

gtggactatg aggagaaata cggccgc	atg ttt cca cgt gag tgg tgc atg	231
	Met Phe Pro Arg Glu Trp Cys Met	
	1 5	
gct gag agg att gcg gtg gaa ttt tgc cat gtg aca agg gca gaa ctt	279	
Ala Glu Arg Ile Ala Val Glu Phe Cys His Val Thr Arg Ala Glu Leu		
10 15 20		
gcc aag att atg cgt acc aga gcg aag gaa att gaa gtg aaa ttg ctt	327	
Ala Lys Ile Met Arg Thr Arg Ala Lys Glu Ile Glu Val Lys Leu Leu		
25 30 35 40		
ctt ttt gct att caa aga aca act aac ttt gag ggg ttt ctt gca aaa	375	
Leu Phe Ala Ile Gln Arg Thr Thr Asn Phe Glu Gly Phe Leu Ala Lys		
45 50 55		
cgc ttc tcc ggc tgc acc ctg acc gat ggg acc ctg aaa aag ctt gag	423	
Arg Phe Ser Gly Cys Thr Leu Thr Asp Gly Thr Leu Lys Lys Leu Glu		
60 65 70		
tct cca ccc cca tct acc aat ccc ttc ctg gaa gat gag cca aca cca	471	
Ser Pro Pro Pro Ser Thr Asn Pro Phe Leu Glu Asp Glu Pro Thr Pro		
75 80 85		
gag atg gag gaa ctg gca acg gag aaa gga gat tta gat caa cca aag	519	
Glu Met Glu Glu Leu Ala Thr Glu Lys Gly Asp Leu Asp Gln Pro Lys		
90 95 100		
aag cct aaa gcc cca gac aat cca ttt cat ggc att gtt tcc aag tgt	567	
Lys Pro Lys Ala Pro Asp Asn Pro Phe His Gly Ile Val Ser Lys Cys		
105 110 115 120		
ttt gag cct cat ctc tac gtg tat atc gaa tcc caa gac aag aac ctc	615	
Phe Glu Pro His Leu Tyr Val Tyr Ile Glu Ser Gln Asp Lys Asn Leu		
125 130 135		
gga gag ctg ata gat cgg ttt gtg gct gat ttc aaa gcc cag ggg cca	663	
Gly Glu Leu Ile Asp Arg Phe Val Ala Asp Phe Lys Ala Gln Gly Pro		
140 145 150		
cct aag ccc aac act gat gaa ggg ggt gcc gtg ctc ccc agc tgc gcc	711	
Pro Lys Pro Asn Thr Asp Glu Gly Gly Ala Val Leu Pro Ser Cys Ala		
155 160 165		
gac ctc ttt gtc tac tac aag aag tgc atg gtg caa tgc tct cag ctc	759	
Asp Leu Phe Val Tyr Tyr Lys Lys Cys Met Val Gln Cys Ser Gln Leu		
170 175 180		
agt act ggg gag ccc atg atc gcc ctg acc acc att ttc cag aag tac	807	
Ser Thr Gly Glu Pro Met Ile Ala Leu Thr Thr Ile Phe Gln Lys Tyr		
185 190 195 200		
ctc cga gaa tac gcc tgg aaa atc ctc tct ggc aac ctg ccc aaa acc	855	
Leu Arg Glu Tyr Ala Trp Lys Ile Leu Ser Gly Asn Leu Pro Lys Thr		
205 210 215		
aca acc agc agt gga gga ctg act atc agc agc ctc ctc aag gaa aag	903	

Thr Thr Ser Ser Gly Gly Leu Thr Ile Ser Ser Leu Leu Lys Glu Lys	
220 225 230	
gag ggc tca gaa gta gcc aag ttc act ctg gag gag ctc tgc ctc atc	951
Glu Gly Ser Glu Val Ala Lys Phe Thr Leu Glu Glu Leu Cys Leu Ile	
235 240 245	
tgt aac atc ctg agc acg gca gag tac tgt ctg gcc acc acc cag cag	999
Cys Asn Ile Leu Ser Thr Ala Glu Tyr Cys Leu Ala Thr Thr Gln Gln	
250 255 260	
cta gaa gaa aaa ctc aaa gaa aaa gtg gat gta agt ctg att gaa cga	1047
Leu Glu Glu Lys Leu Lys Glu Lys Val Asp Val Ser Leu Ile Glu Arg	
265 270 275 280	
atc aat ctg act gga gag atg gac acg ttc agc acc gtc atc tcc agc	1095
Ile Asn Leu Thr Gly Glu Met Asp Thr Phe Ser Thr Val Ile Ser Ser	
285 290 295	
agt att cag ctg ctg gtt cag gat ctg gat gct gcc tgt gat cct gcc	1143
Ser Ile Gln Leu Leu Val Gln Asp Leu Asp Ala Ala Cys Asp Pro Ala	
300 305 310	
ctg act gcc atg agc aag atg cag tgg cag aac gtg gag cac gtt ggt	1191
Leu Thr Ala Met Ser Lys Met Gln Trp Gln Asn Val Glu His Val Gly	
315 320 325	
gac cag agc ccc tac gtc acc tct gtc att ctg cac atc aag cag aac	1239
Asp Gln Ser Pro Tyr Val Thr Ser Val Ile Leu His Ile Lys Gln Asn	
330 335 340	
gtc ccc atc atc cgt gac aac ctg gct tcc aca cgc aag tac ttc act	1287
Val Pro Ile Ile Arg Asp Asn Leu Ala Ser Thr Arg Lys Tyr Phe Thr	
345 350 355 360	
cag ttc tgc gtt aaa ttt gca aac tcc ttc att ccc aaa ttc atc acc	1335
Gln Phe Cys Val Lys Phe Ala Asn Ser Phe Ile Pro Lys Phe Ile Thr	
365 370 375	
cac ctc ttc aag tgc aag cca att agc atg gtg gga gca gaa cag gtg	1383
His Leu Phe Lys Cys Lys Pro Ile Ser Met Val Gly Ala Glu Gln Val	
380 385 390	
aga tgg acg tag tat caggcatttg cctgggcagct tttgtttag atcaagcaca	1438
Arg Trp Thr *	
395	
tattcttcta gtccagatct acttggcagg aataaaattg atgatgtccc ctgtttgggg	1498
acagtataat gactcaccgc gaaggtttct taattcggtc ttccatttat ttttaaaaat	1558
tttgtttgaa cgcctactaa gttctgggtg caggggtataa cacagcaagc accatggaaa	1618
ggtccttgct cctagtgtc acactccaat aagaagaagt ggctgggccc ggcacagcgg	1678
ctcacgtgt aaccccagca ttctgggagg cctgggcagg cagatcacct ggggtaagga	1738

atttgagagc agcctggcca acatggtgaa atcccatctc tactaaaaat acaaaaatta 1798
gctgggcatg ggggcaggct accggggagg ctgaggcagg agaatcactt gaacccggga 1858
ggtggagggtt gcagtgagcc gatatcacac cactgcactc cagcctgggt gacaaagtga 1918
gactccatct c 1929

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<213> Homo sapiens

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<222> (70)..(555)

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ggtctttcc atg gca ctg gcg tct tta cga aat ctc tac act cca aat 108
Met Ala Leu Ala Ser Leu Arg Asn Leu Tyr Thr Pro Asn
1 5 10

ata aag gtc agc cga ctg ctg att ttg gga ggt gcc aat att aat tac 156
Ile Lys Val Ser Arg Leu Leu Ile Leu Gly Gly Ala Asn Ile Asn Tyr
15 20 25

cgg aca gag gtt tta aat aat gct cca att cta tgt gtt cag tcc cat 204
Arg Thr Glu Val Leu Asn Asn Ala Pro Ile Leu Cys Val Gln Ser His
30 35 40 45

ctt ggt tac aca gaa atg gta gcc ctg ctg ctg gag ttc ggg gcc aac 252
Leu Gly Tyr Thr Glu Met Val Ala Leu Leu Leu Glu Phe Gly Ala Asn
50 55 60

gtg gat gcc tct tct gaa agt ggc ctg act ccc ctg gga tat gct gca 300
Val Asp Ala Ser Ser Glu Ser Gly Leu Thr Pro Leu Gly Tyr Ala Ala
65 70 75

gca gca ggg tac ctg agc att gtg gtg ctg ctg tgc aag aaa cgg gcc 348
Ala Ala Gly Tyr Leu Ser Ile Val Val Leu Leu Cys Lys Lys Arg Ala
80 85 90

aag gtg gat cat ttg gat aag aac ggg cag tgt gct ttg gtt cat gct 396
Lys Val Asp His Leu Asp Lys Asn Gly Gln Cys Ala Leu Val His Ala
95 100 105

gca ctc cga ggt cat ctg gag gtt gtc aag ttt ttg att cag tgt gac 444
Ala Leu Arg Gly His Leu Glu Val Val Lys Phe Leu Ile Gln Cys Asp
110 115 120 125

tgg acg atg gcc ggc cag cag caa gga gta ttt aag aag agc cat gcc 492
Trp Thr Met Ala Gly Gln Gln Gln Gly Val Phe Lys Lys Ser His Ala

130	135	140	
atc caa cag gcc ctc att gct gca gcc agc atg ggt tat act gag gta			540
Ile Gln Gln Ala Leu Ile Ala Ala Ser Met Gly Tyr Thr Glu Val			
145	150	155	
aga agt agg caa tag gattgttttt tcaagctctg tattgaagga cccaggaaac			595
Arg Ser Arg Gln *			
160			
caggagaaaa gattgcacga agacaaaatt gccaaccaaa ttaatgtgaa ttcgtgatcg			655
ctgctctgaa taataaggag attaaactcc atgaagcact ttactcaaat gccaaagtcc			715
ctcaaattat aggtatagaa aggtgctgagt tggaaaggac cgtggaaatg atataattat			775
tctccatggt ttcctccctg tttaacagac agtggcacca aggctcaaag agatgaatta			835
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cagaaggacc agatttgagt cccagcctcg ctattcatta actctagccc ttgaacaatt			955
tacctatctc ttagaagttt agtttcccat cagcaaagtg aagctaataa actcctttat			1015
acaaggctgt tgtaagggat gcttggtaaa ctgttaaaca ttatacagtt tatttattaa			1075
tgataataac aataatagtg gcaaagttag ggaattggta gtgtgctagg aaatgtttaa			1135
caaccaactg tgaagagggg tgtgggggtg aacaggggtg tgtgtttgtg tgtgcatacg			1195
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 <212> DNA
 <213> Homo sapiens

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 <222> (91)..(1257)

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gagggagccc gagccaggcc atctccaacc	atg ttc gac gag gcc tcg gcc	111
	Met Phe Asp Glu Ala Ser Ala	
	1 5	
atc act tcc tac gag aag ttt cta acc ccc gag gag ccc ttt cca ctc		159
Ile Thr Ser Tyr Glu Lys Phe Leu Thr Pro Glu Glu Pro Phe Pro Leu		
10 15 20		
ctg gga cct cct cgc ggg gtg ggc acc tgc ccg agc gag gag ccg ggc		207
Leu Gly Pro Pro Arg Gly Val Gly Thr Cys Pro Ser Glu Glu Pro Gly		

25	30	35	
tgc ctg gac atc agc gac ttc ggc tgc cag ctg tcc tcc tgc cat cgc			255
Cys Leu Asp Ile Ser Asp Phe Gly Cys Gln Leu Ser Ser Cys His Arg			
40	45	50	55
acc gac ccg ctc cac cgc ttc cac acc aac agg tgg aac cta act tct			303
Thr Asp Pro Leu His Arg Phe His Thr Asn Arg Trp Asn Leu Thr Ser			
	60	65	70
tgt gga aca agt gtt gcc agc tca gaa ggc agt gag gag ctg ttt tca			351
Cys Gly Thr Ser Val Ala Ser Ser Glu Gly Ser Glu Glu Leu Phe Ser			
	75	80	85
tct gtg tct gtt gga gat caa gat gat tgc tat tcc ctg tta gat gat			399
Ser Val Ser Val Gly Asp Gln Asp Asp Cys Tyr Ser Leu Leu Asp Asp			
	90	95	100
cag gac ttc act tct ttt gat tta ttt cct gag ggg agt gtc tgc agt			447
Gln Asp Phe Thr Ser Phe Asp Leu Phe Pro Glu Gly Ser Val Cys Ser			
	105	110	115
gat gtc tct tct tct att agc act tac tgg gat tgg tca gat agc gag			495
Asp Val Ser Ser Ser Ile Ser Thr Tyr Trp Asp Trp Ser Asp Ser Glu			
	120	125	130
ttt gaa tgg cag tta cca ggc agt gac att gcc agt ggg agt gat gta			543
Phe Glu Trp Gln Leu Pro Gly Ser Asp Ile Ala Ser Gly Ser Asp Val			
	140	145	150
ctt tct gat gtc ata ccc agt att cca agt tca cct tgc ctg ctt cct			591
Leu Ser Asp Val Ile Pro Ser Ile Pro Ser Ser Pro Cys Leu Leu Pro			
	155	160	165
aaa aag aaa aac aag cac cgg aat tta gat gaa ctc cct tgg agt gca			639
Lys Lys Lys Asn Lys His Arg Asn Leu Asp Glu Leu Pro Trp Ser Ala			
	170	175	180
atg aca aat gat gag cag gtg gaa tat att gag tat ctg agt cgg aaa			687
Met Thr Asn Asp Glu Gln Val Glu Tyr Ile Glu Tyr Leu Ser Arg Lys			
	185	190	195
gtg agt act gag atg ggt ctt cgg gag caa ctt gat att att aag atc			735
Val Ser Thr Glu Met Gly Leu Arg Glu Gln Leu Asp Ile Ile Lys Ile			
	200	205	210
att gat cct tct gct cag atc tcc cct aca gac agg gag ttt att att			783
Ile Asp Pro Ser Ala Gln Ile Ser Pro Thr Asp Arg Glu Phe Ile Ile			
	220	225	230
gaa ctt aac tgt ctc aca gat gaa aaa ctg aag cag gtc aga aac tat			831
Glu Leu Asn Cys Leu Thr Asp Glu Lys Leu Lys Gln Val Arg Asn Tyr			
	235	240	245
atc aag gaa cat agc cct cgc caa cgg cct gca aga gag gcc tgg aag			879
Ile Lys Glu His Ser Pro Arg Gln Arg Pro Ala Arg Glu Ala Trp Lys			
	250	255	260

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aga agc aac ttt agt tgt gca agc acc agt gga gtg agc ggt gcc agt      927
Arg Ser Asn Phe Ser Cys Ala Ser Thr Ser Gly Val Ser Gly Ala Ser
    265                      270                      275

gcc agc gcc agc agc agc agt gcc agc atg gtc agt tct gca agc agc      975
Ala Ser Ala Ser Ser Ser Ser Ala Ser Met Val Ser Ser Ala Ser Ser
    280                      285                      290                      295

agt ggg tcc agt gtt gga aac tct gct tca aac tcc agt gcc aac atg      1023
Ser Gly Ser Ser Val Gly Asn Ser Ala Ser Asn Ser Ser Ala Asn Met
    300                      305                      310

agt cga gca cac agt gac agc aac ctg tct gca agt gca gca gag cgg      1071
Ser Arg Ala His Ser Asp Ser Asn Leu Ser Ala Ser Ala Ala Glu Arg
    315                      320                      325

att cgg gat tca aaa aag cga tcc aag cag cgg aag tta cag cag aag      1119
Ile Arg Asp Ser Lys Lys Arg Ser Lys Gln Arg Lys Leu Gln Gln Lys
    330                      335                      340

gcc ttc cgc aag agg cag ctg aag gag cag agg cag gcc cgg aag gag      1167
Ala Phe Arg Lys Arg Gln Leu Lys Glu Gln Arg Gln Ala Arg Lys Glu
    345                      350                      355

agg ctc agt ggg ctc ttc ctt aac gaa gag gtg ctg tcc ttg aaa gtg      1215
Arg Leu Ser Gly Leu Phe Leu Asn Glu Glu Val Leu Ser Leu Lys Val
    360                      365                      370                      375

act gag gaa gac cat gaa gca gat gtt gat gtt ttg atg taa taagggt      1264
Thr Glu Glu Asp His Glu Ala Asp Val Asp Val Leu Met *
    380                      385

gaatttatca acgttctttg tgagcattaa aatactccat ccttatgggt ttacatgcaa      1324

aaaaaaaaa a                                                                1335

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 <211> 2251
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (203)..(1582)

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gatgcaggaa ttcatctaatt tttactgcc gggcgaggtg tgagagccct agcatctgaa      180

agtggtcgac ttgcgagttg tt atg gag aaa act tgt ata gat gca ctt cct      232

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	Met	Glu	Lys	Thr	Cys	Ile	Asp	Ala	Leu	Pro	
	1				5					10	
ctt act atg aat tct tca gaa aag caa gag act gta tgt att ttt gga											280
Leu Thr Met Asn Ser Ser Glu Lys Gln Glu Thr Val Cys Ile Phe Gly											
	15				20				25		
act ggt gat ttt gga aga tca ctg gga ttg aaa atg ctc cag tgt ggt											328
Thr Gly Asp Phe Gly Arg Ser Leu Gly Leu Lys Met Leu Gln Cys Gly											
	30				35				40		
tat tct gtt gtt ttt gga agt cga aac ccc cag aag acc acc cta ctg											376
Tyr Ser Val Val Phe Gly Ser Arg Asn Pro Gln Lys Thr Thr Leu Leu											
	45				50				55		
ccc agt ggt gca gaa gtc ttg agc tat tca gaa gca gcc aag aag tct											424
Pro Ser Gly Ala Glu Val Leu Ser Tyr Ser Glu Ala Ala Lys Lys Ser											
	60				65				70		
ggc atc ata atc ata gca atc cac aga gag cat tat gat ttt ctc aca											472
Gly Ile Ile Ile Ile Ala Ile His Arg Glu His Tyr Asp Phe Leu Thr											
	75				80				85		90
gaa tta act gag gtt ctc aat gga aaa ata ttg gta gac atc agc aac											520
Glu Leu Thr Glu Val Leu Asn Gly Lys Ile Leu Val Asp Ile Ser Asn											
	95								100		105
aac ctc aaa atc aat caa tat cca gaa tct aat gca gag tac ctt gct											568
Asn Leu Lys Ile Asn Gln Tyr Pro Glu Ser Asn Ala Glu Tyr Leu Ala											
	110								115		120
cat ttg gtg cca gga gcc cac gtg gta aaa gca ttt aac acc atc tca											616
His Leu Val Pro Gly Ala His Val Val Lys Ala Phe Asn Thr Ile Ser											
	125								130		135
gcc tgg gct ctc cag tca gga gca ctg gat gca agt cgg cag gtg ttt											664
Ala Trp Ala Leu Gln Ser Gly Ala Leu Asp Ala Ser Arg Gln Val Phe											
	140								145		150
gtg tgt gga aat gac agc aaa gcc aag caa aga gtg atg gat att gtt											712
Val Cys Gly Asn Asp Ser Lys Ala Lys Gln Arg Val Met Asp Ile Val											
	155								160		165
cgt aat ctt gga ctt act cca atg gat caa gga tca ctc atg gca gcc											760
Arg Asn Leu Gly Leu Thr Pro Met Asp Gln Gly Ser Leu Met Ala Ala											
	175								180		185
aaa gaa att gaa aag tac ccc ctg cag cta ttt cca atg tgg agg ttc											808
Lys Glu Ile Glu Lys Tyr Pro Leu Gln Leu Phe Pro Met Trp Arg Phe											
	190								195		200
ccc ttc tat ttg tct gct gtg ctg tgt gtc ttc ttg ttt ttc tat tgt											856
Pro Phe Tyr Leu Ser Ala Val Leu Cys Val Phe Leu Phe Phe Tyr Cys											
	205								210		215
gtt ata aga gac gta atc tac cct tat gtt tat gaa aag aaa gat aat											904
Val Ile Arg Asp Val Ile Tyr Pro Tyr Val Tyr Glu Lys Lys Asp Asn											

220	225	230	
aca ttt cgt atg gct att tcc att cca aat cgt atc ttt cca ata aca			952
Thr Phe Arg Met Ala Ile Ser Ile Pro Asn Arg Ile Phe Pro Ile Thr			
235	240	245	250
gca ctt aca ctg ctt gct ttg gtt tac ctc cct ggt gtt att gct gcc			1000
Ala Leu Thr Leu Leu Ala Leu Val Tyr Leu Pro Gly Val Ile Ala Ala			
	255	260	265
att cta caa ctg tac cga ggc aca aaa tac cgt cga ttc cca gac tgg			1048
Ile Leu Gln Leu Tyr Arg Gly Thr Lys Tyr Arg Arg Phe Pro Asp Trp			
	270	275	280
ctt gac cac tgg atg ctt tgc cga aag cag ctt ggc ttg gta gct ctg			1096
Leu Asp His Trp Met Leu Cys Arg Lys Gln Leu Gly Leu Val Ala Leu			
	285	290	295
gga ttt gcc ttc ctt cat gtc ctc tac aca ctt gtg att cct att cga			1144
Gly Phe Ala Phe Leu His Val Leu Tyr Thr Leu Val Ile Pro Ile Arg			
	300	305	310
tat tat gta cga tgg aga ttg gga aac tta acc gtt acc cag gca ata			1192
Tyr Tyr Val Arg Trp Arg Leu Gly Asn Leu Thr Val Thr Gln Ala Ile			
	315	320	325
ctc aag aag gag aat cca ttt agc acc tcc tca gcc tgg ctc agt gat			1240
Leu Lys Lys Glu Asn Pro Phe Ser Thr Ser Ser Ala Trp Leu Ser Asp			
	335	340	345
tca tat gtg gct ttg gga ata ctt ggg ttt ttt ctg ttt gta ctc ttg			1288
Ser Tyr Val Ala Leu Gly Ile Leu Gly Phe Phe Leu Phe Val Leu Leu			
	350	355	360
gga atc act tct ttg cca tct gtt agc aat gca gtc aac tgg aga gag			1336
Gly Ile Thr Ser Leu Pro Ser Val Ser Asn Ala Val Asn Trp Arg Glu			
	365	370	375
ttc cga ttt gtc cag tcc aaa ctg ggt tat ttg acc ctg atc ttg tgt			1384
Phe Arg Phe Val Gln Ser Lys Leu Gly Tyr Leu Thr Leu Ile Leu Cys			
	380	385	390
aca gcc cac acc ctg gtg tac ggt ggg aag aga ttc ctc agc cct tca			1432
Thr Ala His Thr Leu Val Tyr Gly Gly Lys Arg Phe Leu Ser Pro Ser			
	395	400	405
aat ctc aga tgg tat ctt cct gca gcc tac gtg tta ggg ctt atc att			1480
Asn Leu Arg Trp Tyr Leu Pro Ala Ala Tyr Val Leu Gly Leu Ile Ile			
	415	420	425
cct tgc act gtg ctg gtg atc aag ttt gtc cta atc atg cca tgt gta			1528
Pro Cys Thr Val Leu Val Ile Lys Phe Val Leu Ile Met Pro Cys Val			
	430	435	440
gac aac acc ctt aca agg atc cgc cag ggc tgg gaa agg aac tca aaa			1576
Asp Asn Thr Leu Thr Arg Ile Arg Gln Gly Trp Glu Arg Asn Ser Lys			
	445	450	455

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cac tag aaaaagcatt gaatggaaaa tcaatattta aaacaaagtt caatttagct      1632
His *
    460

ggatttctga actatggttt tgaatgttta aagaagaatg atgggtacag ttaggaaagt      1692
ttttttctta caccgtgact gagggaaaca ttgcttgtct ttgagaaatt gactgacata      1752
ctggaagaga acaccatttt atctcagggt agtgaagaat cagtgcaggt ccctgactct      1812
tattttccca gaggccatgg agctgagatt gagactagcc ttgtggtttc aactaaaga      1872
gtttccttgt tatgggcaac atgcatgacc taatgtcttg caaatccaa tagaagtatt      1932
gcagcttcct tctctggctc aagggtgag ttaagtgaaa ggaaaaacag cacaatgggtg      1992
accactgata aaggctttat taggtatatc tgaggaagtg ggtcacatga aatgtaaaaa      2052
gggaatgagg tttttgttgt tttttggaag taaaggcaaa cataaatatt accatgatga      2112
attctagtga aatgaccctt tgactttgct tttcttaata cagatattta ctgagaggaa      2172
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tacgtaaaaa aaaaaaaaaa                                         2251
    
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cttctcccca ggaccccagg gccaactccc cctgccggcc ctctgccatc aaattggcag      180
tggtccagg ggagtccctt ggggatgggg gaccactgtt ggggaccct ctgcgtgcac      240
ccctgtagtt ggggaagcag gacagggggc tggggagacg gaagggcgcc aggggttgag      300
agagg      atg gtg gac gtt gtt gga ctt gaa agg gaa aca ggc cct cgg      347
            Met Val Asp Val Val Gly Leu Glu Arg Glu Thr Gly Pro Arg
            1             5             10

gga agc ccc tgg cca ggc ctg cct ctc ccc tcc ctg gtg ggc cca gcg      395
Gly Ser Pro Trp Pro Gly Leu Pro Leu Pro Ser Leu Val Gly Pro Ala
15             20             25             30
    
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ccc ctg ctc act tgt ctc tgc cca cag tgc ctg tct gtg gag gac gcc	443
Pro Leu Leu Thr Cys Leu Cys Pro Gln Cys Leu Ser Val Glu Asp Ala	
35 40 45	
ctg ggc ctg ggc gag cct gag ggg tca ggg ctg ccc ccg ggc ccg gtc	491
Leu Gly Leu Gly Glu Pro Glu Gly Ser Gly Leu Pro Pro Gly Pro Val	
50 55 60	
ctg gag gcc agg tac gtc gcc cgc ctc agt gcc gcc gcc gtc ctg tac	539
Leu Glu Ala Arg Tyr Val Ala Arg Leu Ser Ala Ala Ala Val Leu Tyr	
65 70 75	
ctc agc aac ccc gag ggc acc tgt gag gac gct cgg gct ggc ctc tgg	587
Leu Ser Asn Pro Glu Gly Thr Cys Glu Asp Ala Arg Ala Gly Leu Trp	
80 85 90	
gcc tct cat gca gac cac ctc ctg gcc ctg ctc gag agc ccc aag gcc	635
Ala Ser His Ala Asp His Leu Leu Ala Leu Leu Glu Ser Pro Lys Ala	
95 100 105 110	
ctg acc ccg ggc ctg agc tgg ctg ctg cag agg atg cag gcc ccg gct	683
Leu Thr Pro Gly Leu Ser Trp Leu Leu Gln Arg Met Gln Ala Arg Ala	
115 120 125	
gcc ggc cag acc ccc aag acg gcc tgc gta gat atc cct cag ctg ctg	731
Ala Gly Gln Thr Pro Lys Thr Ala Cys Val Asp Ile Pro Gln Leu Leu	
130 135 140	
gag gag gcg gtg ggg gcg ggg gct ccg ggc agt gct ggc ggc gtc ctg	779
Glu Glu Ala Val Gly Ala Gly Ala Pro Gly Ser Ala Gly Gly Val Leu	
145 150 155	
gct gcc ctg ctg gac cat gtc agg agc ggg tct tgc ttc cac gcc ttg	827
Ala Ala Leu Leu Asp His Val Arg Ser Gly Ser Cys Phe His Ala Leu	
160 165 170	
ccg agc cct cag tac ttc gtg gac ttt gtg ttc cag cag cac agc agc	875
Pro Ser Pro Gln Tyr Phe Val Asp Phe Val Phe Gln Gln His Ser Ser	
175 180 185 190	
gag gtc cct atg acg ctg gcc gag ctg tca gcc ttg atg cag cgc ctg	923
Glu Val Pro Met Thr Leu Ala Glu Leu Ser Ala Leu Met Gln Arg Leu	
195 200 205	
ggg gtg ggc agg gag gcc cac agt gac cac agt cat cgg cac agg gga	971
Gly Val Gly Arg Glu Ala His Ser Asp His Ser His Arg His Arg Gly	
210 215 220	
gcc agc agc ccg gac cct gtg ccc ctc atc agc tcc agc aac agc tcc	1019
Ala Ser Ser Arg Asp Pro Val Pro Leu Ile Ser Ser Ser Asn Ser Ser	
225 230 235	
agt gtg tgg gac acg gta tgc ctg agt gcc agg gac gtg atg gct gca	1067
Ser Val Trp Asp Thr Val Cys Leu Ser Ala Arg Asp Val Met Ala Ala	
240 245 250	

tat gga ctg tcg gaa cag gct ggg gtg acc ccg gag gcc tgg gcc caa	1115
Tyr Gly Leu Ser Glu Gln Ala Gly Val Thr Pro Glu Ala Trp Ala Gln	
255 260 265 270	
ctg agc cct gcc ctg ctc caa cag cag ctg agt gga gcc tgc acc tcc	1163
Leu Ser Pro Ala Leu Leu Gln Gln Gln Leu Ser Gly Ala Cys Thr Ser	
275 280 285	
cag tcc agg ccc ccc gtc cag gac cag ctc agc cag tca gag agg tat	1211
Gln Ser Arg Pro Pro Val Gln Asp Gln Leu Ser Gln Ser Glu Arg Tyr	
290 295 300	
ctg tac ggc tcc ctg gcc acg ctg ctc atc tgc ctc tgc gcg gtc ttt	1259
Leu Tyr Gly Ser Leu Ala Thr Leu Leu Ile Cys Leu Cys Ala Val Phe	
305 310 315	
ggc ctc ctg ctg ctg acc tgc act ggc tgc agg ggg gtc gcc cac tac	1307
Gly Leu Leu Leu Leu Thr Cys Thr Gly Cys Arg Gly Val Ala His Tyr	
320 325 330	
atc ctg cag acc ttc ctg agc ctg gca gtg ggt gca ctc act ggg gac	1355
Ile Leu Gln Thr Phe Leu Ser Leu Ala Val Gly Ala Leu Thr Gly Asp	
335 340 345 350	
gct gtc ctg cat ctg acg ccc aag gtg ctg ggg ctg cat aca cac agc	1403
Ala Val Leu His Leu Thr Pro Lys Val Leu Gly Leu His Thr His Ser	
355 360 365	
gaa gag ggc ctc agc cca cag ccc acc tgg cgc ctc ctg gct atg ctg	1451
Glu Glu Gly Leu Ser Pro Gln Pro Thr Trp Arg Leu Leu Ala Met Leu	
370 375 380	
gcc ggg ctc tac gcc ttc ttc ctg ttt gag aac ctc ttc aat ctc ctg	1499
Ala Gly Leu Tyr Ala Phe Phe Leu Phe Glu Asn Leu Phe Asn Leu Leu	
385 390 395	
ctg ccc agg gac ccg gag gac ctg gag gac ggg ccc tgc ggc cac agc	1547
Leu Pro Arg Asp Pro Glu Asp Leu Glu Asp Gly Pro Cys Gly His Ser	
400 405 410	
agc cat agc cac ggg ggc cac agc cac ggt gtg tcc ctg cag ctg gca	1595
Ser His Ser His Gly Gly His Ser His Gly Val Ser Leu Gln Leu Ala	
415 420 425 430	
ccc agc gag ctc cgg cag ccc aag ccc ccc cac gag ggc tcc cgc gca	1643
Pro Ser Glu Leu Arg Gln Pro Lys Pro Pro His Glu Gly Ser Arg Ala	
435 440 445	
gac ctg gtg gcg gag gag agc ccg gag ctg ctg aac cct gag ccc agg	1691
Asp Leu Val Ala Glu Glu Ser Pro Glu Leu Leu Asn Pro Glu Pro Arg	
450 455 460	
aga ctg agc cca gag ttg agg cta ctg ccc tat atg atc act ctg ggc	1739
Arg Leu Ser Pro Glu Leu Arg Leu Leu Pro Tyr Met Ile Thr Leu Gly	
465 470 475	
gac gcc gtg cac aac ttc gcc gac ggg ctg gcc gtg ggc gcc gcc ttc	1787

Asp Ala Val His Asn Phe Ala Asp Gly Leu Ala Val Gly Ala Ala Phe
 480 485 490

gcg tcc tcc tgg aag acc ggg ctg gcc acc tcg ctg gcc gtg ttc tgc 1835
 Ala Ser Ser Trp Lys Thr Gly Leu Ala Thr Ser Leu Ala Val Phe Cys
 495 500 505 510

cac gag ttg cca cac gag ctg ggg gac ttc gcc gcc ttg ctg cac gcg 1883
 His Glu Leu Pro His Glu Leu Gly Asp Phe Ala Ala Leu Leu His Ala
 515 520 525

ggg ctg tcc gtg cgc caa gca ctg ctg ctg aac ctg gcc tcc gcg ctc 1931
 Gly Leu Ser Val Arg Gln Ala Leu Leu Leu Asn Leu Ala Ser Ala Leu
 530 535 540

acg gcc ttc gct ggt ctc tac gtg gca ctc gcg gtt gga gtc agc gag 1979
 Thr Ala Phe Ala Gly Leu Tyr Val Ala Leu Ala Val Gly Val Ser Glu
 545 550 555

gag agc gag gcc tgg atc ctg gca gtg gcc acc ggc ctg ttc ctc tac 2027
 Glu Ser Glu Ala Trp Ile Leu Ala Val Ala Thr Gly Leu Phe Leu Tyr
 560 565 570

gta gca ctc tgc gac atg ctc ccg gcg atg ttg aaa gta cgg gac ccg 2075
 Val Ala Leu Cys Asp Met Leu Pro Ala Met Leu Lys Val Arg Asp Pro
 575 580 585 590

cgg ccc tgg ctc ctc ttc ctg ctg cac aac gtg ggc ctg ctg ggc ggc 2123
 Arg Pro Trp Leu Leu Phe Leu Leu His Asn Val Gly Leu Leu Gly Gly
 595 600 605

tgg acc gtc ctg ctg ctg ctg tcc ctg tac gag gat gac atc acc ttc 2171
 Trp Thr Val Leu Leu Leu Leu Ser Leu Tyr Glu Asp Asp Ile Thr Phe
 610 615 620

tga tacc ctgccctagt ccccccacctt tgacttaaga tcccacacct cacaaaccta 2228
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cagcccagaa accagaagcc cctatagagg cccaggtccc aactccagta aagacactct 2288

tgtccttgga aaaaaaaaaa aa 2310

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ccgcgggctg ggacc atg ggc tgc ttc ttc tcc aag aga cgg aag gct gac	171
Met Gly Cys Phe Phe Ser Lys Arg Arg Lys Ala Asp	
1 5 10	
aag gag tgc cgg ccc gag aac gag gag gag cgg cca aag cag tac agc	219
Lys Glu Ser Arg Pro Glu Asn Glu Glu Glu Arg Pro Lys Gln Tyr Ser	
15 20 25	
tgg gat cag cgc gag aag gtt gat cca aaa gac tac atg ttc agt gga	267
Trp Asp Gln Arg Glu Lys Val Asp Pro Lys Asp Tyr Met Phe Ser Gly	
30 35 40	
ctg aag gat gaa aca gta ggt cgc tta cct ggg acg gta gca gga caa	315
Leu Lys Asp Glu Thr Val Gly Arg Leu Pro Gly Thr Val Ala Gly Gln	
45 50 55 60	
cag ttt ctc att caa gac tgt gag aac tgt aac atc tat att ttt gat	363
Gln Phe Leu Ile Gln Asp Cys Glu Asn Cys Asn Ile Tyr Ile Phe Asp	
65 70 75	
cac tct gct aca gtt acc att gat gac tgt act aac tgc ata att ttt	411
His Ser Ala Thr Val Thr Ile Asp Asp Cys Thr Asn Cys Ile Ile Phe	
80 85 90	
ctg gga ccc gtg aaa ggc agc gtg ttt ttc cgg aat tgc aga gat tgc	459
Leu Gly Pro Val Lys Gly Ser Val Phe Phe Arg Asn Cys Arg Asp Cys	
95 100 105	
aag tgc aca tta gcc tgc caa caa ttt cgt gtg cga gat tgt aga aag	507
Lys Cys Thr Leu Ala Cys Gln Gln Phe Arg Val Arg Asp Cys Arg Lys	
110 115 120	
ctg gaa gtc ttt ttg tgt tgt gcc act caa ccc atc att gag tct tcc	555
Leu Glu Val Phe Leu Cys Cys Ala Thr Gln Pro Ile Ile Glu Ser Ser	
125 130 135 140	
tca aat atc aaa ttt gga tgt ttt caa tgg tac tat cct gaa tta gct	603
Ser Asn Ile Lys Phe Gly Cys Phe Gln Trp Tyr Tyr Pro Glu Leu Ala	
145 150 155	
ttc cag ttc aaa gat gca ggg cta agt atc ttc gac aat aca tgg agt	651
Phe Gln Phe Lys Asp Ala Gly Leu Ser Ile Phe Asp Asn Thr Trp Ser	
160 165 170	
aac att cat gac ttt aca cct gtg tca gga gaa ctc aac tgg agc ctt	699
Asn Ile His Asp Phe Thr Pro Val Ser Gly Glu Leu Asn Trp Ser Leu	
175 180 185	
ctt cca gaa gat gct gtg gtt cag gac tat gtt cct ata cct act acc	747
Leu Pro Glu Asp Ala Val Val Gln Asp Tyr Val Pro Ile Pro Thr Thr	
190 195 200	
gaa gag ctc aaa gct gtt cgt gtt tcc aca gaa gcc aat aga agc att	795
Glu Glu Leu Lys Ala Val Arg Val Ser Thr Glu Ala Asn Arg Ser Ile	

205	210	215	220	
gtt cca ata tcc cgg ggt cag aga cag aag agc agc gat gaa tca tgc				843
Val Pro Ile Ser Arg Gly Gln Arg Gln Lys Ser Ser Asp Glu Ser Cys	225	230	235	
tta gtg gta tta ttt gct ggt gat tac act att gca aat gcc aga aaa				891
Leu Val Val Leu Phe Ala Gly Asp Tyr Thr Ile Ala Asn Ala Arg Lys	240	245	250	
cta att gat gag atg gtt ggt aaa ggc ttt ttc cta gtt cag aca aag				939
Leu Ile Asp Glu Met Val Gly Lys Gly Phe Phe Leu Val Gln Thr Lys	255	260	265	
gaa gtg tcc atg aaa gct gag gat gct caa agg gtt ttt cgg gaa aaa				987
Glu Val Ser Met Lys Ala Glu Asp Ala Gln Arg Val Phe Arg Glu Lys	270	275	280	
gca cct gac ttc ctt cct ctt ctg aac aaa ggt cct gtt att gcc ttg				1035
Ala Pro Asp Phe Leu Pro Leu Leu Asn Lys Gly Pro Val Ile Ala Leu	285	290	295	300
gag ttt aat ggg gat ggt gct gta gaa gta tgt caa ctt att gta aac				1083
Glu Phe Asn Gly Asp Gly Ala Val Glu Val Cys Gln Leu Ile Val Asn	305	310	315	
gag ata ttc aat ggg acc aag atg ttt gta tct gaa agc aag gag aca				1131
Glu Ile Phe Asn Gly Thr Lys Met Phe Val Ser Glu Ser Lys Glu Thr	320	325	330	
ggt ttc tgg aga tgt aga cac gct cta aca ctt ggc tga tatacagatg				1180
Gly Phe Trp Arg Cys Arg His Ala Leu Thr Leu Gly *	335	340	345	
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cctttttag tag tctgatgaa taatttcatt ttctcaagt ttatgacact cggaacgtca	180
agaactggag gtttgtgcaa tttgagaccg gtcggcactg tgcagagatc agagtactaa	240

gagacagaga ttaaa atg gct tcc aga gga aag aca gag aca agc aaa tta	291
Met Ala Ser Arg Gly Lys Thr Glu Thr Ser Lys Leu	
1 5 10	
aag cag aat tta gaa gaa cag ttg gat aga ctc atg caa caa tta caa	339
Lys Gln Asn Leu Glu Glu Gln Leu Asp Arg Leu Met Gln Gln Leu Gln	
15 20 25	
gat ctg gag gaa tgc aga gag gaa ctt gat aca gat gaa tat gaa gaa	387
Asp Leu Glu Glu Cys Arg Glu Glu Leu Asp Thr Asp Glu Tyr Glu Glu	
30 35 40	
acc aaa aag gaa act ctg gag caa cta agt gaa ttt aat gat tca cta	435
Thr Lys Lys Glu Thr Leu Glu Gln Leu Ser Glu Phe Asn Asp Ser Leu	
45 50 55 60	
aag aaa att atg tct gga aat atg act ttg gta gat gaa cta agt gga	483
Lys Lys Ile Met Ser Gly Asn Met Thr Leu Val Asp Glu Leu Ser Gly	
65 70 75	
atg cag ctg gct att cag gca gct atc agc cag gcc ttt aaa acc cca	531
Met Gln Leu Ala Ile Gln Ala Ala Ile Ser Gln Ala Phe Lys Thr Pro	
80 85 90	
gag gtc atc aga ttg ttt gca aag aaa caa cca ggt cag ctt cgg aca	579
Glu Val Ile Arg Leu Phe Ala Lys Lys Gln Pro Gly Gln Leu Arg Thr	
95 100 105	
agg tta gca gag atg gat aga gat ctg atg gta gga aag ctg gaa aga	627
Arg Leu Ala Glu Met Asp Arg Asp Leu Met Val Gly Lys Leu Glu Arg	
110 115 120	
gac ctg tac act caa cag aaa gtg gag ata cta aca gct ctt agg aaa	675
Asp Leu Tyr Thr Gln Gln Lys Val Glu Ile Leu Thr Ala Leu Arg Lys	
125 130 135 140	
ctt gga gag aag ctg act gca gat gat gag gcc ttc ttg tca gca aat	723
Leu Gly Glu Lys Leu Thr Ala Asp Asp Glu Ala Phe Leu Ser Ala Asn	
145 150 155	
gca ggt gct ata ctc agc cag ttt gag aaa gtc tct aca gac ctt gga	771
Ala Gly Ala Ile Leu Ser Gln Phe Glu Lys Val Ser Thr Asp Leu Gly	
160 165 170	
cgg ccc cca agt tac atg aac tac ctg cta gac tca cac ccc agc aaa	819
Arg Pro Pro Ser Tyr Met Asn Tyr Leu Leu Asp Ser His Pro Ser Lys	
175 180 185	
aat att gat gtc ccc agc aag att agc ttc ctg tta aag atc cag gac	867
Asn Ile Asp Val Pro Ser Lys Ile Ser Phe Leu Leu Lys Ile Gln Asp	
190 195 200	
ctg tga atacatgcgt aactgcaaga atggaagcaa aggatgaacc caagttaaag	923
Leu *	
205	
cccagcacaa gaatatgatg taagcgcttt tgggaaatgc agagattttc ttttctcttc	983

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1021

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Glu Gly Thr Glu Gln Thr Leu Asp Ala Glu Glu Glu Gln Glu Glu Ser	
20 25 30	
gaa gaa gcg gcc tgt ggc agc aag aag cgg gta gtg cca ggt att gtg	144
Glu Glu Ala Ala Cys Gly Ser Lys Lys Arg Val Val Pro Gly Ile Val	
35 40 45	
tac ctg ggc cat atc ccg ccg cgc ttc cgg ccc ctg cac gtc cgc aac	192
Tyr Leu Gly His Ile Pro Pro Arg Phe Arg Pro Leu His Val Arg Asn	
50 55 60	
ctt ctc agc gcc tat ggc gag gtc gga cgc gtc ttc ttt cag gct gag	240
Leu Leu Ser Ala Tyr Gly Glu Val Gly Arg Val Phe Phe Gln Ala Glu	
65 70 75 80	
gac cgg ttc gtg aga cgc aag aag aag gca gca gca gct gcc gga gga	288
Asp Arg Phe Val Arg Arg Lys Lys Lys Ala Ala Ala Ala Ala Gly Gly	
85 90 95	
aaa aag cgg tcc tac acc aag gac tac acc gag gga tgg gtg gag ttc	336
Lys Lys Arg Ser Tyr Thr Lys Asp Tyr Thr Glu Gly Trp Val Glu Phe	
100 105 110	
cgt gac aag cgc ata gcc aag cgc gtg gcg gcc agt cta cac aac acg	384
Arg Asp Lys Arg Ile Ala Lys Arg Val Ala Ala Ser Leu His Asn Thr	
115 120 125	
cct atg ggt gcc cgc agg cgc agc ccc ttc cgt tat gat ctt tgg aac	432
Pro Met Gly Ala Arg Arg Arg Ser Pro Phe Arg Tyr Asp Leu Trp Asn	
130 135 140	
ctc aag tac ttg cac cgt ttc acc tgg tcc cac ctc agc gag cac ctc	480
Leu Lys Tyr Leu His Arg Phe Thr Trp Ser His Leu Ser Glu His Leu	
145 150 155 160	
gcc ttt gag cgc cag gtg cgc agg cag cgc ttg aga gcg gag gtt gct	528

Ala Phe Glu Arg Gln Val Arg Arg Gln Arg Leu Arg Ala Glu Val Ala	
165 170 175	
caa gcc aag cgt gag acc gac ttc tat ctt caa agt gtg gaa cgg gga	576
Gln Ala Lys Arg Glu Thr Asp Phe Tyr Leu Gln Ser Val Glu Arg Gly	
180 185 190	
caa cgc ttt ctt gcg gcc gat ggg gac cct gct cgc cca gat ggc tcc	624
Gln Arg Phe Leu Ala Ala Asp Gly Asp Pro Ala Arg Pro Asp Gly Ser	
195 200 205	
tgg aca ttt gcc cag cgt cct act gag cag gaa ctg agg gcc cgt aaa	672
Trp Thr Phe Ala Gln Arg Pro Thr Glu Gln Glu Leu Arg Ala Arg Lys	
210 215 220	
gca gca cgg cca ggg gga cgt gaa cgg gct cgc ctg gca act gcc cag	720
Ala Ala Arg Pro Gly Gly Arg Glu Arg Ala Arg Leu Ala Thr Ala Gln	
225 230 235 240	
gac aag gcc cgc tcc aac aaa ggg ctc ctg gcc agg atc ttt gga gcc	768
Asp Lys Ala Arg Ser Asn Lys Gly Leu Leu Ala Arg Ile Phe Gly Ala	
245 250 255	
ccg cca ccc tca gag agc atg gag gga cct tcc ctt gtc agg gac tcc	816
Pro Pro Pro Ser Glu Ser Met Glu Gly Pro Ser Leu Val Arg Asp Ser	
260 265 270	
tga gggc ctgggtggcc ccttccattt cctggccctg ctctgcttcc tgtctacctc	873
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atactagaat gatcgtgact acccgggcag acattttact gtgttttctca gaccaagtgt	933
ctactgatgg cccaaacatg gagttttgtg ggcttccact gtccccactc cgaactcctg	993
tatgtgcctg gctgagtcac ctaattcata ctgtcatact agcataatta tgactattgc	1053
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cttctgccc ccagaaaggg cctttatttc caactaggag gataatgcct agtccaggca	1173
atctttctct gtttagcagt cacaggtagg ggtggtatta gcatcttttt tatgtagaaa	1233
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cctggcacc accttactgt ttaacctgga ttttttttcc tatttaattt ttgtctaata	1473
tattagccca gtttatcaat cagttatctt aagtcagcat tttctaagcc attgtttgag	1533
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<400> 157

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aaggatcctt aattaaatta atcccccccc cccccccgag tagcggcagc ggcgacgacg      60
gcggcggcag cgctccaact ggctcctcgc tccgggctcc gccgtcgagc cgggagagag      120
cctccgccag cggccaggca ccagccagac gacgccagcg accccggcct ctcggcggca      180
ccgcgctaac tcaggggctg cataggcacc cagagccgaa ctccaag  atg gga ggc      236
                                     Met Gly Gly
                                     1

aag ctc agc aag aag aag aag ggc tac aat gtg aac gac gag aaa gcc      284
Lys Leu Ser Lys Lys Lys Lys Gly Tyr Asn Val Asn Asp Glu Lys Ala
      5                      10                      15

aag gag aaa gac aag aag gcc gag ggc gcg gcg acg gaa gag gag ggg      332
Lys Glu Lys Asp Lys Lys Ala Glu Gly Ala Ala Thr Glu Glu Glu Gly
      20                      25                      30                      35

acc ccg aag gag agt gag ccc cag gcg gcc gca gag ccc gcc gag gcc      380
Thr Pro Lys Glu Ser Glu Pro Gln Ala Ala Ala Glu Pro Ala Glu Ala
                      40                      45                      50

aag gag ggc aag gag aag ccc gac cag gac gcc gag ggc aag gcc gag      428
Lys Glu Gly Lys Glu Lys Pro Asp Gln Asp Ala Glu Gly Lys Ala Glu
                      55                      60                      65

gag aag gag ggc gag aag gac gcg gcg gct gcc aag gag gag gcc ccg      476
Glu Lys Glu Gly Glu Lys Asp Ala Ala Ala Lys Glu Glu Ala Pro
      70                      75                      80

aag gcg gag ccc gag aag acg gag ggc gcg gca gag gcc aag gct gag      524
Lys Ala Glu Pro Glu Lys Thr Glu Gly Ala Ala Glu Ala Lys Ala Glu
      85                      90                      95

ccc ccg aag gcg ccc gag cag gag cag gcg gcc ccc ggc ccc gct gcg      572
Pro Pro Lys Ala Pro Glu Gln Glu Gln Ala Ala Pro Gly Pro Ala Ala
      100                      105                      110                      115

ggc ggc gag gcc ccc aaa gct gct gag gcc gcc gcg gcc ccg gcc gag      620
Gly Gly Glu Ala Pro Lys Ala Ala Glu Ala Ala Ala Ala Pro Ala Glu
                      120                      125                      130

agc gcg gcc cct gcc gcc ggg gag gag ccc agc aag gag gaa ggg gaa      668
Ser Ala Ala Pro Ala Ala Gly Glu Glu Pro Ser Lys Glu Glu Gly Glu
      135                      140                      145

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ccc aaa aag act gag gcg ccc gca gct cct gcc gcc cag gag acc aaa      716
Pro Lys Lys Thr Glu Ala Pro Ala Ala Pro Ala Ala Gln Glu Thr Lys
      150                      155                      160

agt gac ggg gcc cca gct tca gac tca aaa ccc gcc agc tcg gag gct      764
Ser Asp Gly Ala Pro Ala Ser Asp Ser Lys Pro Gly Ser Ser Glu Ala
      165                      170                      175

gcc ccc tct tcc aag gag acc ccc gca gcc acg gaa gcg cct agt tcc      812
Ala Pro Ser Ser Lys Glu Thr Pro Ala Ala Thr Glu Ala Pro Ser Ser
      180                      185                      190                      195

aca ccc aag gcc cag gcc ccc gca gcc tct gca gaa gag ccc aag ccg      860
Thr Pro Lys Ala Gln Gly Pro Ala Ala Ser Ala Glu Glu Pro Lys Pro
      200                      205                      210

gtg gag gcc ccg gca gct aat tcc gac caa acc gta acc gtg aaa gag      908
Val Glu Ala Pro Ala Ala Asn Ser Asp Gln Thr Val Thr Val Lys Glu
      215                      220                      225

tga caag gacagcctat aggaaaaaca ataccactta aaacaatctc ctctctctct      965
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ctctctctct ctctatctct ctctctatct cctctctctc tctcctctcc tatctctcct      1025

ctctctctct cctatactaa cttgtttcaa attggaagta atgatatgta ttgcccaagg      1085

aaaaatacag gatgttgtcc catcaaggga gggagggggg gggagaatcc aaatagtatt      1145

tttgtgggga aatatctaata ataccttcag tcaactttac caagaagtcc tggatttcca      1205

agatccgcgt ctgaaagtgc agtacatcgt ttgtacctga aactgccgcc acatgcactc      1265

ctccaccgct gagagttgaa tagcttttct tctgcaatgg gagttgggag tgatgcgttt      1325

gattctgccc acagggcctg tgccaaggca atcagatctt tatgagagca gtattttctg      1385

tgtttttctt ttaatttaca gcctttctta ttttgatatt tttttaatgt tgtggatgaa      1445

tgccagcttt cagacagagc ccacttagct tgtccacatg gatctcaatg ccaatcctcc      1505

attcttctct tccagatatt tttgggagtg acaaacattc tctcatccta cttagcctac      1565

ctagatttct catgacgagt taatgcatgt ccgtggttgg gtgcacctgt agttctgttt      1625

attggtcagt ggaaatg      1642

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<210> 158
 <211> 1521
 <212> DNA
 <213> Homo sapiens

 <220>

<221> CDS
 <222> (417)..(1403)

<400> 158

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gggtcaccac cctggggcgac cgggaggtgg cgctccgcc ggccgcagct ggagaggagc      180
gtgtcccca gccgggggag caggacttga gcaggcacgc ggggtcaccg ccgggcagcg      240
tggaggagcc atctcctgga ggagaaaact cacctggtgg cggaggctcc ccttgtttgt      300
cctcccgag cctggcggtgg ggttcttctg cggaagaga gagtgcgcgc ggagatagca      360

gtgtggaaac gcgcgaggag tcggagggca cgggcggcca gcgctcagcc tgcgcc      416
atg ggt ggt ccc ggg acc aag agc ggg gag cct ttg tgt cct ccg tta      464
Met Gly Gly Pro Gly Thr Lys Ser Gly Glu Pro Leu Cys Pro Pro Leu
  1             5             10             15

ctg tgt aat cag gac aaa gaa acc ttg act ctg ctc att cag gtg cct      512
Leu Cys Asn Gln Asp Lys Glu Thr Leu Thr Leu Leu Ile Gln Val Pro
          20             25             30

cgg atc cag ccg caa agt ctt caa gga gat ttg aat ccc ctc tgg tac      560
Arg Ile Gln Pro Gln Ser Leu Gln Gly Asp Leu Asn Pro Leu Trp Tyr
          35             40             45

aaa tta cgc ttc tcc gca caa gac tta gtt tat tcc ttc ttt ttg caa      608
Lys Leu Arg Phe Ser Ala Gln Asp Leu Val Tyr Ser Phe Phe Leu Gln
          50             55             60

ttt gct cca gag aat aaa ttg agt acc aca gaa cct gtg att agc att      656
Phe Ala Pro Glu Asn Lys Leu Ser Thr Thr Glu Pro Val Ile Ser Ile
          65             70             75             80

tct tca aac aat gca gtg ata gaa ctg gca aaa tct cca gag agc cat      704
Ser Ser Asn Asn Ala Val Ile Glu Leu Ala Lys Ser Pro Glu Ser His
          85             90             95

gga cat tgg aga gag tgg tat tat ggt gta aac aac gat tct ttg gag      752
Gly His Trp Arg Glu Trp Tyr Tyr Gly Val Asn Asn Asp Ser Leu Glu
          100            105            110

gaa agg tta ttt gtc aat gaa gaa aat gtt aat gag ttt ctt gaa gag      800
Glu Arg Leu Phe Val Asn Glu Glu Asn Val Asn Glu Phe Leu Glu Glu
          115            120            125

gtc ctg agc tct cca ttc aaa cag tct atg tcc ttg acc cca cca tta      848
Val Leu Ser Ser Pro Phe Lys Gln Ser Met Ser Leu Thr Pro Pro Leu
          130            135            140

att gaa gtt ctt caa gtt act gat aat aag att caa att aat gca aag      896
Ile Glu Val Leu Gln Val Thr Asp Asn Lys Ile Gln Ile Asn Ala Lys
          145            150            155            160

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ttg caa gaa tgt agt aac tct gat cag cta caa gga aag gag gaa aga	944
Leu Gln Glu Cys Ser Asn Ser Asp Gln Leu Gln Gly Lys Glu Glu Arg	
165 170 175	
gta aat gaa gaa agt cat cta act gaa aag gaa tat ata gaa cat tgt	992
Val Asn Glu Glu Ser His Leu Thr Glu Lys Glu Tyr Ile Glu His Cys	
180 185 190	
aac acc cct aca act gat tct gat tca tct ata gca gtt aaa gca cta	1040
Asn Thr Pro Thr Thr Asp Ser Asp Ser Ser Ile Ala Val Lys Ala Leu	
195 200 205	
caa ata gat agc ttt ggt tta gtt aca tgc ttt caa caa gag tct ctt	1088
Gln Ile Asp Ser Phe Gly Leu Val Thr Cys Phe Gln Gln Glu Ser Leu	
210 215 220	
gat gtt tct caa atg ata ctt gga aaa tct cag caa cct gag tca aaa	1136
Asp Val Ser Gln Met Ile Leu Gly Lys Ser Gln Gln Pro Glu Ser Lys	
225 230 235 240	
atg caa tct gaa ttt ata aaa gaa aaa agt gct act tgt tca aat gag	1184
Met Gln Ser Glu Phe Ile Lys Glu Lys Ser Ala Thr Cys Ser Asn Glu	
245 250 255	
gaa aaa ggt aac tta aac gag tca gta ata act gaa gag aaa gaa aca	1232
Glu Lys Gly Asn Leu Asn Glu Ser Val Ile Thr Glu Glu Lys Glu Thr	
260 265 270	
gat gga gat cac cta tct tca tta ctg aac aaa act acg gtt cac aat	1280
Asp Gly Asp His Leu Ser Ser Leu Leu Asn Lys Thr Thr Val His Asn	
275 280 285	
ata cct gga ttc gac agc ata aaa gaa acc aat atg cag gat ggt agt	1328
Ile Pro Gly Phe Asp Ser Ile Lys Glu Thr Asn Met Gln Asp Gly Ser	
290 295 300	
gtg cag gtc att aaa gat cat gtg acc aat tgt gca ttc agt ttt cag	1376
Val Gln Val Ile Lys Asp His Val Thr Asn Cys Ala Phe Ser Phe Gln	
305 310 315 320	
aat tct ttg cta tat gat ttg gat taa ttcta tataattttg gactttttaa	1428
Asn Ser Leu Leu Tyr Asp Leu Asp *	
325	
tattaagggtt aaaaaatacc tgtatctaaa attgattctg ttaactgttg tcttaaaact	1488
aaagggtatta aagtataaaa ttaaaatttg caa	1521

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 <211> 1377
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
 <222> (417)..(1259)

<400> 159

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gggtcaccac cctggggcgac cgggaggtgg cgctccgcc ggccgcagct ggagaggagc      180
gtgtcccca gcccgggggag caggacttga gcaggcacgc ggggtcaccg ccgggcagcg      240
tggaggagcc atctcctgga ggagaaaact cacctggtgg cggaggctcc ccttgtttgt      300
cctccccgag cctggcggtgg ggttcttctg cgggaagaga gagtgcgcgc ggagatagca      360

gtgtggaaac gcgcgaggag tcggagggca cgggcggcca gcgctcagcc tgcgcc      416
atg ggt ggt ccc ggg acc aag agc ggg gag cct ttg tgt cct ccg tta      464
Met Gly Gly Pro Gly Thr Lys Ser Gly Glu Pro Leu Cys Pro Pro Leu
  1             5             10             15

ctg tgt aat cag gac aaa gaa acc ttg act ctg ctc att cag gtg cct      512
Leu Cys Asn Gln Asp Lys Glu Thr Leu Thr Leu Leu Ile Gln Val Pro
             20             25             30

cgg atc cag ccg caa agt ctt caa gga gat ttg aat ccc ctc tgg tac      560
Arg Ile Gln Pro Gln Ser Leu Gln Gly Asp Leu Asn Pro Leu Trp Tyr
             35             40             45

aaa tta cgc ttc tcc gca caa gac tta gtt tat tcc ttc ttt ttg caa      608
Lys Leu Arg Phe Ser Ala Gln Asp Leu Val Tyr Ser Phe Phe Leu Gln
             50             55             60

ttt gct cca gag aat aaa ttg agt acc aca gaa cct gtg att agc att      656
Phe Ala Pro Glu Asn Lys Leu Ser Thr Thr Glu Pro Val Ile Ser Ile
             65             70             75             80

tct tca aac aat gca gtg ata gaa ctg gca aaa tct cca gag agc cat      704
Ser Ser Asn Asn Ala Val Ile Glu Leu Ala Lys Ser Pro Glu Ser His
             85             90             95

gga cat tgg aga gag tgg tat tat ggt gta aac aac gat tct ttg gag      752
Gly His Trp Arg Glu Trp Tyr Tyr Gly Val Asn Asn Asp Ser Leu Glu
             100             105             110

ttg caa gaa tgt agt aac tct gat cag cta caa gga aag gag gaa aga      800
Leu Gln Glu Cys Ser Asn Ser Asp Gln Leu Gln Gly Lys Glu Glu Arg
             115             120             125

gta aat gaa gaa agt cat cta act gaa aag gaa tat ata gaa cat tgt      848
Val Asn Glu Glu Ser His Leu Thr Glu Lys Glu Tyr Ile Glu His Cys
             130             135             140

aac acc cct aca act gat tct gat tca tct ata gca gtt aaa gca cta      896
Asn Thr Pro Thr Thr Asp Ser Asp Ser Ser Ile Ala Val Lys Ala Leu
             145             150             155             160

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caa ata gat agc ttt ggt tta gtt aca tgc ttt caa caa gag tct ctt 944
Gln Ile Asp Ser Phe Gly Leu Val Thr Cys Phe Gln Gln Glu Ser Leu
165 170 175

gat gtt tct caa atg ata ctt gga aaa tct cag caa cct gag tca aaa 992
Asp Val Ser Gln Met Ile Leu Gly Lys Ser Gln Gln Pro Glu Ser Lys
180 185 190

atg caa tct gaa ttt ata aaa gaa aaa agt gct act tgt tca aat gag 1040
Met Gln Ser Glu Phe Ile Lys Glu Lys Ser Ala Thr Cys Ser Asn Glu
195 200 205

gaa aaa ggt aac tta aac gag tca gta ata act gaa gag aaa gaa aca 1088
Glu Lys Gly Asn Leu Asn Glu Ser Val Ile Thr Glu Glu Lys Glu Thr
210 215 220

gat gga gat cac cta tct tca tta ctg aac aaa act acg gtt cac aat 1136
Asp Gly Asp His Leu Ser Ser Leu Leu Asn Lys Thr Thr Val His Asn
225 230 235 240

ata cct gga ttc gac agc ata aaa gaa acc aat atg cag gat ggt agt 1184
Ile Pro Gly Phe Asp Ser Ile Lys Glu Thr Asn Met Gln Asp Gly Ser
245 250 255

gtg cag gtc att aaa gat cat gtg acc aat tgt gca ttc agt ttt cag 1232
Val Gln Val Ile Lys Asp His Val Thr Asn Cys Ala Phe Ser Phe Gln
260 265 270

aat tct ttg cta tat gat ttg gat taa ttcta tataattttg gactttttaa 1284
Asn Ser Leu Leu Tyr Asp Leu Asp *
275 280

tattaagggtt aaaaaatacc tgtatctaaa attgattctg ttaactgttg tcttaaaact 1344

aaagggtatta aagtataaaa ttaaaatttg caa 1377

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<212> DNA
<213> Homo sapiens

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<222> (510)..(1112)

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ttgactgcaa ggccagccca cgccgagggt ccaagcatcg ggatatgccg ccagcacctg 180
gctgctgcag caccgcgctg gacatgagcg ctccgccc aa cccgacggcg tcagctggcg 240

cgcgcgccccg cgaccgacgt ggcgaggcgc ccacggggccg cgcagccgcc attgctctcc	300
tgccacgggag gggagcgcctt ggtggcagtc cgcggggcccg gacggaaggc tgaggcgacg	360
cctcgacgac agcggaccgg agctgcaggg gcaacacatt cagggcgggg tgccccattt	420
aggcctggct gaccggagta agaaactaca acccccgaag tgccttgccg ctcaagggtta	480
cggaggcagt gaccacccac cctggagcc atg gtc cac gcc ttc ctc att cac	533
Met Val His Ala Phe Leu Ile His	
1 5	
acc ttg agg gcc ccg aat act gag gac acg ggc ctt tgc cga gtg ctg	581
Thr Leu Arg Ala Pro Asn Thr Glu Asp Thr Gly Leu Cys Arg Val Leu	
10 15 20	
tac tcc tgc gtc ttc ggt gct gag aag tca cct gat gac cca cgg ccg	629
Tyr Ser Cys Val Phe Gly Ala Glu Lys Ser Pro Asp Asp Pro Arg Pro	
25 30 35 40	
cat ggt gcc gag agg gac agg ctt ctc cgg aag gaa cag att tta gct	677
His Gly Ala Glu Arg Asp Arg Leu Leu Arg Lys Glu Gln Ile Leu Ala	
45 50 55	
gtg gcc agg cag gta gag tca atg tgt cgg ctg cag cag cag gca tct	725
Val Ala Arg Gln Val Glu Ser Met Cys Arg Leu Gln Gln Gln Ala Ser	
60 65 70	
ggc cgg ccc ccc atg gac ctg cag ccg caa tcc tca gat gag caa gtg	773
Gly Arg Pro Pro Met Asp Leu Gln Pro Gln Ser Ser Asp Glu Gln Val	
75 80 85	
ccg ctg cac gag gcc cca cgt ggg gct ttc cgc ctg gca gca gag aac	821
Pro Leu His Glu Ala Pro Arg Gly Ala Phe Arg Leu Ala Ala Glu Asn	
90 95 100	
cct ttc cag gag cca cgg acg gtg gtg tgg ctg ggc gtg ctc tcg tta	869
Pro Phe Gln Glu Pro Arg Thr Val Val Trp Leu Gly Val Leu Ser Leu	
105 110 115 120	
ggc ttt gcc ctg gtg ctg gat gcc cat gag aac ctg cta ctg gct gag	917
Gly Phe Ala Leu Val Leu Asp Ala His Glu Asn Leu Leu Leu Ala Glu	
125 130 135	
ggc acg ctc cgg ctg ctg aca cgc ctc ctc ctt gac cac ctc cgg ctg	965
Gly Thr Leu Arg Leu Leu Thr Arg Leu Leu Leu Asp His Leu Arg Leu	
140 145 150	
ctg gcg ccc agc acc agc ctt ctg ctg cgg gct gac cgc att gag ggc	1013
Leu Ala Pro Ser Thr Ser Leu Leu Leu Arg Ala Asp Arg Ile Glu Gly	
155 160 165	
atc ctc acc cgc ttc ctg cca cat ggt cag ctg ctt ttc ctc aac gac	1061
Ile Leu Thr Arg Phe Leu Pro His Gly Gln Leu Phe Leu Asn Asp	
170 175 180	
cag ttt gtc caa ggc ctg gag aag gaa ttc agt gcc gct tgg ccc cgc	1109

Gln	Phe	Val	Gln	Gly	Leu	Glu	Lys	Glu	Phe	Ser	Ala	Ala	Trp	Pro	Arg
185					190					195					200

tga ttcc tcgttgggat ggtgcttctg agggcaggca gagggtagac acacagccag 1166
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atgaagcttg gcatctccct cctaccacagc agctctgatg tgctgctata ccaggacaag 1226
tgggtgacac aagcctgcag aaagggggct gggcagaggg tggaggaggt cctgcctgtc 1286
ctcagggttag tggaaccaca gaacttctctg agcctagagc tgctgtgtta cttagaccgc 1346
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atgcctggcc tcaatctttt cttttaaaca attattccta tattttattg taatgcagtt 1526
aaccgtgttt gtcagattca atactctgtg acccgtaac caagtctctg tatgtttatt 1586
actgcaattc aagtggccct gtatt 1611

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<212> DNA
<213> Homo sapiens

<220>
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<222> (193)..(555)

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accgccgccg agtcgcgcgg aggcggaggc ttgggtgctg tcaagattca gcttcacccg 180
taaccacccg cc atg gcc gag gaa ggc att gct gct gga ggt gta atg 228
Met Ala Glu Glu Gly Ile Ala Ala Gly Gly Val Met
1 5 10
gac gtt aat act gct tta caa gag gtt ctg aag act gcc ctc atc cac 276
Asp Val Asn Thr Ala Leu Gln Glu Val Leu Lys Thr Ala Leu Ile His
15 20 25
gat ggc cta gca cgt gga att cgc gaa gct gcc aaa gcc tta gac aag 324
Asp Gly Leu Ala Arg Gly Ile Arg Glu Ala Ala Lys Ala Leu Asp Lys
30 35 40
cgc caa gcc cat ctt tgt gtg ctt gca tcc aac tgt gat gag cct atg 372
Arg Gln Ala His Leu Cys Val Leu Ala Ser Asn Cys Asp Glu Pro Met
45 50 55 60

tat gtc aag ttg gtg gag gcc ctt tgt gct gaa cac caa atc aac cta	420
Tyr Val Lys Leu Val Glu Ala Leu Cys Ala Glu His Gln Ile Asn Leu	
65 70 75	
att aag gtt gat gac aac aag aaa cta gga gaa tgg gta ggc ctt tgt	468
Ile Lys Val Asp Asp Asn Lys Lys Leu Gly Glu Trp Val Gly Leu Cys	
80 85 90	
aaa att gac aga gag ggg tgt att gcg gcc gct cta gag gat cca agc	516
Lys Ile Asp Arg Glu Gly Cys Ile Ala Ala Ala Leu Glu Asp Pro Ser	
95 100 105	
tta cgt acg cgt gca tgc gac gtc ata gct ctt cta tag tgtcacctaa	565
Leu Arg Thr Arg Ala Cys Asp Val Ile Ala Leu Leu *	
110 115 120	
att	568

<210> 162
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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (784)..(1473)

<400> 162	
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aggaaacttc tggttaccaa ttccatctgc ctctttctca gtgactcctg acgagctgct	180
catttacaca cacctgctcc cccccacc ccacagtctg gattgcgaaa cctaccgcac	240
cccccccca gtgcaggaag aaggtgacct tggctctgggg tggggacaga gagtctggga	300
gggggtggtg gctggcagtc tcggtggctg gcgacgcctc ttccgctctt ccttctctggg	360
aggaggcggg caaggcgaag cctctccgct cagtcgatgg ttcccttcag gacgtctcat	420
agaggtgtgg gtgagatccc aggtctgggc cgcaatttct agccacgctg cccaaccttc	480
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agagggagtg gtctgtaaata gcgtcgggac aagagtggcc tcctaactcc acctggagct	600
ggcgtcaggg cgatctctgg atgccagcc cataagcctg gcctgtctgt gaggaggctg	660
cgtctggctc ccgctctcac agccattgca gtacattgag ctccatagag acagcgccgg	720
ggcaagtgag agccggacgg gcactgggag actctgtgcc tcgctgagga aaaataacta	780

aac atg ggc aaa gga gat cct aag aag ccg aga ggc aaa atg tca tca	828
Met Gly Lys Gly Asp Pro Lys Lys Pro Arg Gly Lys Met Ser Ser	
1 5 10 15	
tat gca ttt ttt gtg caa act tgt cgg gag gag cat aag aag aag cac	876
Tyr Ala Phe Phe Val Gln Thr Cys Arg Glu Glu His Lys Lys Lys His	
20 25 30	
cca gat gct tca gtc aac ttc tca gag ttt tct aag aag tgc tca gag	924
Pro Asp Ala Ser Val Asn Phe Ser Glu Phe Ser Lys Lys Cys Ser Glu	
35 40 45	
agg tgg aag acc atg tct gct aaa gag aaa gga aaa ttt gaa gat atg	972
Arg Trp Lys Thr Met Ser Ala Lys Glu Lys Gly Lys Phe Glu Asp Met	
50 55 60	
gca aag gcg gac aag gcc cgt tat gaa aga gaa atg aaa acc tat atc	1020
Ala Lys Ala Asp Lys Ala Arg Tyr Glu Arg Glu Met Lys Thr Tyr Ile	
65 70 75	
cct ccc aaa ggg gag aca aaa aag aag ttc aag gat ccc aat gca ccc	1068
Pro Pro Lys Gly Glu Thr Lys Lys Lys Phe Lys Asp Pro Asn Ala Pro	
80 85 90 95	
aag agg cct cct tgc gcc ttc ttc ctc ttc tgc tct gag tat cgc cca	1116
Lys Arg Pro Pro Ser Ala Phe Phe Leu Phe Cys Ser Glu Tyr Arg Pro	
100 105 110	
aaa atc aaa gga gaa cat cct ggc ctg tcc att ggt gat gtt gcg aag	1164
Lys Ile Lys Gly Glu His Pro Gly Leu Ser Ile Gly Asp Val Ala Lys	
115 120 125	
aaa ctg gga gag atg tgg aat aac act gct gca gat gac aag cag cct	1212
Lys Leu Gly Glu Met Trp Asn Asn Thr Ala Ala Asp Asp Lys Gln Pro	
130 135 140	
tat gaa aag aag gct gcg aag ctg aag gaa aaa tac gaa aag gat att	1260
Tyr Glu Lys Lys Ala Ala Lys Leu Lys Glu Lys Tyr Glu Lys Asp Ile	
145 150 155	
gct gca tat cga gct aaa gga aag cct gat gca gca aaa aag gga gtt	1308
Ala Ala Tyr Arg Ala Lys Gly Lys Pro Asp Ala Ala Lys Lys Gly Val	
160 165 170 175	
gtc aag gct gaa aaa agc aaa aaa aag aag gaa gag gag gaa gat gag	1356
Val Lys Ala Glu Lys Ser Lys Lys Lys Lys Glu Glu Glu Glu Asp Glu	
180 185 190	
gaa gat gaa gag gat gag gag gag gag gaa gat gaa gaa gat gaa gat	1404
Glu Asp Glu Glu Asp Glu Glu Glu Glu Glu Asp Glu Glu Asp Glu Asp	
195 200 205	
gaa gaa gaa gaa gat gat gat atg atg aat aag ttg gtt cta gcg cag	1452
Glu Glu Glu Glu Asp Asp Asp Met Met Asn Lys Leu Val Leu Ala Gln	
210 215 220	

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ttt ttt ttt tct tgt cta taa ag catttaaccc ccctgttaca caactcactc 1505
Phe Phe Phe Ser Cys Leu *
    225                      230

cttttaaaga aaaaaattga aatgtaaggc tgtgtaagat ttgttttttaa actgtacagt 1565

gtctttttttt gtatagttaa cacactaccg aatgtgtctt tagatagccc tgtcctgggtg 1625

gtatttttcaa tagccactaa ccttgccctgg tacagtatgg gggttgtaaa ttggcatgga 1685

aatttaaagc aggttcttgt tgggtgcacag cacaaattag ttatatatgg ggatggtagt 1745

tttttcatct tcagttgtct ctgatgcagc ttatacgaaa taattgttgt tctgttaact 1805

gaataccact ctgtaattgc aaaaaaaaaa aa 1837

<210> 163
<211> 1454
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (269)..(718)

<400> 163
ccaccttggt ccggtttatt tcagtttaat ggttatgtaa caacgggtccg tctctcctac 60

caaccggtac cccgcccacg ccagcagcca cgggtcgcca gcgccacgca gcggaggcgg 120

gcggcatggc tggcccaagg tgccgaggcg cactagccct gggggtgctt ccgtgtctgc 180

gccctgagac atttttggcg ccggccccag cctgagcggg gacggcggcc gggagggcgc 240

ggccccgggtt cccgttcccc gcggagcc atg cgg tac aac gag aag gag ctg 292
                        Met Arg Tyr Asn Glu Lys Glu Leu
                        1                      5

cag gct ctg tcc cgg cag ccg gcc gag atg gcg gcc gag ctg ggc atg 340
Gln Ala Leu Ser Arg Gln Pro Ala Glu Met Ala Ala Glu Leu Gly Met
    10                      15                      20

agg ggc ccc aag aag ggc agc gtg ctg aag cgg cgg ctg gtg aag ctg 388
Arg Gly Pro Lys Lys Gly Ser Val Leu Lys Arg Arg Leu Val Lys Leu
    25                      30                      35                      40

gtg gtg aat ttc ctc ttc tac ttt cgg aca gac gag gcc gag ccc gtc 436
Val Val Asn Phe Leu Phe Tyr Phe Arg Thr Asp Glu Ala Glu Pro Val
                45                      50                      55

gga gcc ctg ctg ctg gag cgc tgc aga gtc gtc cgg gaa gag ccc ggc 484
Gly Ala Leu Leu Leu Glu Arg Cys Arg Val Val Arg Glu Glu Pro Gly
                60                      65                      70

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<400> 164
acggcgcg atg gcg gcg gct gcc gcc gag acc ccc gaa gtc ctt cgg gaa 50
Met Ala Ala Ala Ala Ala Glu Thr Pro Glu Val Leu Arg Glu
1 5 10

tgc ggt tgc aag ggc atc cgg acc tgt ctg atc tgc gag cgg cag cgc 98
Cys Gly Cys Lys Gly Ile Arg Thr Cys Leu Ile Cys Glu Arg Gln Arg
15 20 25 30

ggc agt gac ccg ccc tgg gag ctg ccc cca gcg aaa aca tac cgt ttc 146
Gly Ser Asp Pro Pro Trp Glu Leu Pro Pro Ala Lys Thr Tyr Arg Phe
35 40 45

att tac tgc tcc gac acc ggc tgg gcc gtg ggc aca gag gag tct gac 194
Ile Tyr Cys Ser Asp Thr Gly Trp Ala Val Gly Thr Glu Glu Ser Asp
50 55 60

ttt gag ggc tgg gcc ttc ccc ttc cca gga gtg atg ctg atc gag gac 242
Phe Glu Gly Trp Ala Phe Pro Phe Pro Gly Val Met Leu Ile Glu Asp
65 70 75

ttt gtg acc cgg gag gaa gaa gcc gag ttg gtg cgg ctc atg gac cgt 290
Phe Val Thr Arg Glu Glu Glu Ala Glu Leu Val Arg Leu Met Asp Arg
80 85 90

gac ccc tgg aag ctc tcc cag tct gga cgg agg aag cag gac tat ggc 338
Asp Pro Trp Lys Leu Ser Gln Ser Gly Arg Arg Lys Gln Asp Tyr Gly
95 100 105 110

ccc aaa gtc aac ttt cgg aaa cag aag cta aag acc gag ggc ttc tgc 386
Pro Lys Val Asn Phe Arg Lys Gln Lys Leu Lys Thr Glu Gly Phe Cys
115 120 125

ggc ctc ccc agc ttc agc cgg gag gtg gtg cgg agg atg ggc ctc tac 434
Gly Leu Pro Ser Phe Ser Arg Glu Val Val Arg Arg Met Gly Leu Tyr
130 135 140

ccg ggg ctg gag ggc ttc cgg ccc gtc gag cag tgc aac ctg gac tac 482
Pro Gly Leu Glu Gly Phe Arg Pro Val Glu Gln Cys Asn Leu Asp Tyr
145 150 155

tgc ccc gag cgg ggc tct gcc att gac ccc cac ctg gac gac gcc tgg 530
Cys Pro Glu Arg Gly Ser Ala Ile Asp Pro His Leu Asp Asp Ala Trp
160 165 170

ctg tgg ggg gag cgg ctg gtc agc ctc aac ctc ctg tcc ccc acc gtg 578
Leu Trp Gly Glu Arg Leu Val Ser Leu Asn Leu Leu Ser Pro Thr Val
175 180 185 190

ctg tcc atg tgt cgg gag gcg ccc ggg agc ctg ctc ctc tgc tcg gcc 626
Leu Ser Met Cys Arg Glu Ala Pro Gly Ser Leu Leu Leu Cys Ser Ala
195 200 205

ccg tcg gct gcc ccg gag gcc ttg gtg gac agc gtg ata gca ccc agc 674
Pro Ser Ala Ala Pro Glu Ala Leu Val Asp Ser Val Ile Ala Pro Ser
210 215 220

cgg tcg gtg cta tgc cag gag gtg gag gtg gcc atc ccc tta ccc gcc Arg Ser Val Leu Cys Gln Glu Val Glu Val Ala Ile Pro Leu Pro Ala 225 230 235	722
cgc tcc ctg ctg gtc ctc acc ggg gcg gca cgg cac cag tgg aag cat Arg Ser Leu Leu Val Leu Thr Gly Ala Ala Arg His Gln Trp Lys His 240 245 250	770
gcc atc cac cgc aga cac atc gag gcc cgc cgc gtc tgc gtc act ttc Ala Ile His Arg Arg His Ile Glu Ala Arg Arg Val Cys Val Thr Phe 255 260 265 270	818
cgg gag ctg tcg gct gag ttt ggc cct gga ggg agg cag caa gag ctg Arg Glu Leu Ser Ala Glu Phe Gly Pro Gly Gly Arg Gln Gln Glu Leu 275 280 285	866
ggc cag gaa ctg ctg cgg atc gcc ctc tcc ttc cag gga aga ccc gtg Gly Gln Glu Leu Leu Arg Ile Ala Leu Ser Phe Gln Gly Arg Pro Val 290 295 300	914
tga accg cctccttggc tccagacttg actgatcccg ggattgaaat gaggagcaca *	971
gaacaggggcc tcctgcaact cacgggggttt caagagaaga tggctgaccc ctgatgctgt	1031
gagcagtgtg agccctgccc aggagcaggt tttgatggga acgtacctcc aggcagcccc	1091
cttcacactg gaccgtggcc acactttttt ggttatttag tttgtcacag tcttggggac	1151
atgggatcat t	1162

<210> 165
<211> 1018
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (40)..(747)

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ccg tgg gac ccg gcg tcc gcg cct aac ggc gct ggg cta gtg cta ggc Pro Trp Asp Pro Ala Ser Ala Pro Asn Gly Ala Gly Leu Val Leu Gly 10 15 20	102	
cac ttc ata gct tcg ggg atg gtc aat cag gag atg tta aac atg tct His Phe Ile Ala Ser Gly Met Val Asn Gln Glu Met Leu Asn Met Ser 25 30 35	150	

aag aaa aca gtt tct tgt ttt gtg aac ttc acc aga cta cag cag atc	198
Lys Lys Thr Val Ser Cys Phe Val Asn Phe Thr Arg Leu Gln Gln Ile	
40 45 50	
aca aat att caa gct gaa atc tac cag aaa aac ctg gaa att gaa ctc	246
Thr Asn Ile Gln Ala Glu Ile Tyr Gln Lys Asn Leu Glu Ile Glu Leu	
55 60 65	
ctg aaa cta gaa aaa gat aca gca gat gtt gtt cat cct ttc ttt ttg	294
Leu Lys Leu Glu Lys Asp Thr Ala Asp Val Val His Pro Phe Phe Leu	
70 75 80 85	
gct cag aag tgt cat act ctg caa agc atg aat aat cat ttg gaa gca	342
Ala Gln Lys Cys His Thr Leu Gln Ser Met Asn Asn His Leu Glu Ala	
90 95 100	
gtg ctg aaa gag aag aga tcc ctt agg caa aga ctg ttg aaa ccc atg	390
Val Leu Lys Glu Lys Arg Ser Leu Arg Gln Arg Leu Leu Lys Pro Met	
105 110 115	
tgc cag gaa aac tta cct att gaa gct gtt tat cac aga tat atg gta	438
Cys Gln Glu Asn Leu Pro Ile Glu Ala Val Tyr His Arg Tyr Met Val	
120 125 130	
cat ttg ctg gag ttg gct gtg act ttc att gag aga tta gaa acc cac	486
His Leu Leu Glu Leu Ala Val Thr Phe Ile Glu Arg Leu Glu Thr His	
135 140 145	
ctt gaa aca att aga aat att cct cat tta gct gca aat cta aag aaa	534
Leu Glu Thr Ile Arg Asn Ile Pro His Leu Ala Ala Asn Leu Lys Lys	
150 155 160 165	
atg aac cag gct tta gca aag atg gat ata ttg gtg act gag aca gaa	582
Met Asn Gln Ala Leu Ala Lys Met Asp Ile Leu Val Thr Glu Thr Glu	
170 175 180	
gaa ctg gca gag aat ata ctc aag tgg cgt aaa caa caa aac gaa gtt	630
Glu Leu Ala Glu Asn Ile Leu Lys Trp Arg Lys Gln Gln Asn Glu Val	
185 190 195	
tcg tct tgt atc ccc aaa ata tta gct gaa gaa agt tat ctt tat aaa	678
Ser Ser Cys Ile Pro Lys Ile Leu Ala Glu Glu Ser Tyr Leu Tyr Lys	
200 205 210	
cat gat att ata atg cct cct tta cct ttt act tct aaa gtt cat gtc	726
His Asp Ile Ile Met Pro Pro Leu Pro Phe Thr Ser Lys Val His Val	
215 220 225	
caa act att aat gcc aag tag tc atcaacttta tttttgctta attatgtgta	779
Gln Thr Ile Asn Ala Lys *	
230 235	
gtcatatgaa gtctatttct agttgactgt aacatgggta ttaatagtct ttgctgctgg	839
taatactgaa agaacctgct ttatatggga gtatcaagat ctcagggttca ttaagaccaa	899

actgactttt cctttgtttt tcatatattt ttattctacc tttcagtaaa actagagaag 959
 ctaaaaaata gccatgacaa tttattaata taagtgaatt aaccattaaa aaaaaaaaaa 1018

<210> 166
 <211> 925
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (40)..(654)

<400> 166
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 Met Ala Ala Ala Asn
 1 5
 ccg tgg gac ccg gcg tcc gcg cct aac ggc gct ggg cta gtg cta ggc 102
 Pro Trp Asp Pro Ala Ser Ala Pro Asn Gly Ala Gly Leu Val Leu Gly
 10 15 20
 cac ttc ata gct tcg ggg atg gtc aat cag aaa aac ctg gaa att gaa 150
 His Phe Ile Ala Ser Gly Met Val Asn Gln Lys Asn Leu Glu Ile Glu
 25 30 35
 ctc ctg aaa cta gaa aaa gat aca gca gat gtt gtt cat cct ttc ttt 198
 Leu Leu Lys Leu Glu Lys Asp Thr Ala Asp Val Val His Pro Phe Phe
 40 45 50
 ttg gct cag aag tgt cat act ctg caa agc atg aat aat cat ttg gaa 246
 Leu Ala Gln Lys Cys His Thr Leu Gln Ser Met Asn Asn His Leu Glu
 55 60 65
 gca gtg ctg aaa gag aag aga tcc ctt agg caa aga ctg ttg aaa ccc 294
 Ala Val Leu Lys Glu Lys Arg Ser Leu Arg Gln Arg Leu Leu Lys Pro
 70 75 80 85
 atg tgc cag gaa aac tta cct att gaa gct gtt tat cac aga tat atg 342
 Met Cys Gln Glu Asn Leu Pro Ile Glu Ala Val Tyr His Arg Tyr Met
 90 95 100
 gta cat ttg ctg gag ttg gct gtg act ttc att gag aga tta gaa acc 390
 Val His Leu Leu Glu Leu Ala Val Thr Phe Ile Glu Arg Leu Glu Thr
 105 110 115
 cac ctt gaa aca att aga aat att cct cat tta gct gca aat cta aag 438
 His Leu Glu Thr Ile Arg Asn Ile Pro His Leu Ala Ala Asn Leu Lys
 120 125 130
 aaa atg aac cag gct tta gca aag atg gat ata ttg gtg act gag aca 486
 Lys Met Asn Gln Ala Leu Ala Lys Met Asp Ile Leu Val Thr Glu Thr
 135 140 145

gaa gaa ctg gca gag aat ata ctc aag tgg cgt aaa caa caa aac gaa 534
 Glu Glu Leu Ala Glu Asn Ile Leu Lys Trp Arg Lys Gln Gln Asn Glu
 150 155 160 165

gtt tcg tct tgt atc ccc aaa ata tta gct gaa gaa agt tat ctt tat 582
 Val Ser Ser Cys Ile Pro Lys Ile Leu Ala Glu Glu Ser Tyr Leu Tyr
 170 175 180

aaa cat gat att ata atg cct cct tta cct ttt act tct aaa gtt cat 630
 Lys His Asp Ile Ile Met Pro Pro Leu Pro Phe Thr Ser Lys Val His
 185 190 195

gtc caa act att aat gcc aag tag tcatcaactt tatttttgct taattatgtg 684
 Val Gln Thr Ile Asn Ala Lys *
 200 205

tagtcatatg aagtctatatt ctagttgact gtaacatggg tattaatagt ctttgctgct 744

ggtaataactg aaagaacctg ctttatattg gagtatcaag atctcagggt cattaagacc 804

aaactgactt ttcctttggt tttcatatat ttttattcta ccttttcagta aaactagaga 864

agctaaaaaa tagccatgac aatttattaa tataagtga ttaaccatta aaaaaaaaaa 924

a 925

<210> 167
 <211> 1058
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (190)..(828)

<400> 167
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ctgagtttgc gaccgtagct gtcgctttcc ggccaacaca gaggtgcctg aaggctgggt 120

gggggtggtga ggcccagggc agctcttggt cagcttctgg aatttctgag cagccctcgt 180

cagtacaag atg gac ccc gta gtc ttg agt tac atg gac agt cta ctg 228
 Met Asp Pro Val Val Leu Ser Tyr Met Asp Ser Leu Leu
 1 5 10

cgg caa tca gat gtc tca cta ttg gat ccg cca agc tgg ctc aat gac 276
 Arg Gln Ser Asp Val Ser Leu Leu Asp Pro Pro Ser Trp Leu Asn Asp
 15 20 25

cat att att ggg ttt gcg ttt gag tac ttt gcc aac agt cag ttt cat 324
 His Ile Ile Gly Phe Ala Phe Glu Tyr Phe Ala Asn Ser Gln Phe His
 30 35 40 45

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (99)..(5618)

<400> 168

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gccgctcctg cactgcgccg gccctgagcg gacctgtggc tcggactatc tattacatcg      60

cagccgagct ggtccggctg gtgggggtctg tggactcc      atg aag ccc gtg ctc      113
               Met Lys Pro Val Leu
                   1           5

cag tcc ctc tac cac cga gtg ctg ctc tac ccc cca ccc cag cac cgg      161
Gln Ser Leu Tyr His Arg Val Leu Leu Tyr Pro Pro Pro Gln His Arg
              10              15              20

gtg gaa gcc atc aaa ata atg aaa gag ata ctt ggg agc cca cag cgt      209
Val Glu Ala Ile Lys Ile Met Lys Glu Ile Leu Gly Ser Pro Gln Arg
              25              30              35

ctc tgt gac ttg gca gga ccc agc tcc act gaa tca gag tcc aga aaa      257
Leu Cys Asp Leu Ala Gly Pro Ser Ser Thr Glu Ser Glu Ser Arg Lys
              40              45              50

aga tca att tca aaa aga aag tct cat ctg gat ctc ctc aaa ctc atc      305
Arg Ser Ile Ser Lys Arg Lys Ser His Leu Asp Leu Leu Lys Leu Ile
              55              60              65

atg gat ggc atg acc gaa gca tgc atc aag ggt ggc atc gaa gct tgc      353
Met Asp Gly Met Thr Glu Ala Cys Ile Lys Gly Gly Ile Glu Ala Cys
              70              75              80              85

tat gca gcc gtg tcc tgt gtc tgc acc ttg ctg ggt gcc ctg gat gag      401
Tyr Ala Ala Val Ser Cys Val Cys Thr Leu Leu Gly Ala Leu Asp Glu
              90              95              100

ctc agc cag ggg aag ggc ttg agc gaa ggt cag gtg caa ctg ctg ctt      449
Leu Ser Gln Gly Lys Gly Leu Ser Glu Gly Gln Val Gln Leu Leu Leu
              105              110              115

ctg cgc ctt gag gag ctg aag gat ggg gct gag tgg agc cga gat tcc      497
Leu Arg Leu Glu Glu Leu Lys Asp Gly Ala Glu Trp Ser Arg Asp Ser
              120              125              130

atg gag atc aat gag gct gac ttc cgc tgg cag cgg cga gtg ctg tcc      545
Met Glu Ile Asn Glu Ala Asp Phe Arg Trp Gln Arg Arg Val Leu Ser
              135              140              145

tca gaa cac acg ccg tgg gag tca ggg aac gag agg agc ctt gac atc      593
Ser Glu His Thr Pro Trp Glu Ser Gly Asn Glu Arg Ser Leu Asp Ile
              150              155              160              165

agc atc agt gtc acc aca gac aca ggc cag acc act ctc gag gga gag      641
Ser Ile Ser Val Thr Thr Asp Thr Gly Gln Thr Thr Leu Glu Gly Glu
              170              175              180

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ttg ggt cag act aca ccc gag gac cat tcg gga aac cac aag aac agt	689
Leu Gly Gln Thr Thr Pro Glu Asp His Ser Gly Asn His Lys Asn Ser	
185 190 195	
ctc aag tcg cca gcc atc cca gag ggt aag gag acg ctg agc aaa gta	737
Leu Lys Ser Pro Ala Ile Pro Glu Gly Lys Glu Thr Leu Ser Lys Val	
200 205 210	
ttg gaa aca gag gcg gta gac cag cca gat gtc gtg cag aga agc cac	785
Leu Glu Thr Glu Ala Val Asp Gln Pro Asp Val Val Gln Arg Ser His	
215 220 225	
acg gtc cct tac cct gac ata act aac ttc ctg tca gta gac tgc agg	833
Thr Val Pro Tyr Pro Asp Ile Thr Asn Phe Leu Ser Val Asp Cys Arg	
230 235 240 245	
aca agg tcc tat gga tct agg tat agt gag agc aat ttt agc gtt gat	881
Thr Arg Ser Tyr Gly Ser Arg Tyr Ser Glu Ser Asn Phe Ser Val Asp	
250 255 260	
gac caa gac ctt tct agg aca gag ttt gat tcc tgt gat cag tac tct	929
Asp Gln Asp Leu Ser Arg Thr Glu Phe Asp Ser Cys Asp Gln Tyr Ser	
265 270 275	
atg gca gca gaa aag gac tcg ggc agg tcc gac gtg tca gac att ggg	977
Met Ala Ala Glu Lys Asp Ser Gly Arg Ser Asp Val Ser Asp Ile Gly	
280 285 290	
tcg gac aac tgt tca cta gcc gat gaa gag cag aca ccc cgg gac tgc	1025
Ser Asp Asn Cys Ser Leu Ala Asp Glu Glu Gln Thr Pro Arg Asp Cys	
295 300 305	
cta ggc cac cgg tcc ctg cga act gcc gcc ctg tct cta aaa ctg ctg	1073
Leu Gly His Arg Ser Leu Arg Thr Ala Ala Leu Ser Leu Lys Leu Leu	
310 315 320 325	
aag aac cag gag gcg gat cag cac agc gcc agg ctg ttc ata cag tcc	1121
Lys Asn Gln Glu Ala Asp Gln His Ser Ala Arg Leu Phe Ile Gln Ser	
330 335 340	
ctg gaa ggc ctc ctc cct cgg ctc ctg gct ctc tcc aat gta gag gag	1169
Leu Glu Gly Leu Leu Pro Arg Leu Leu Ala Leu Ser Asn Val Glu Glu	
345 350 355	
gtg gac acc gct ctg cag aac ttt gcc tct act ttc tgc tca ggc atg	1217
Val Asp Thr Ala Leu Gln Asn Phe Ala Ser Thr Phe Cys Ser Gly Met	
360 365 370	
atg cac tct cct ggc ttt gac ggg aat agc agc ctc agc ttc cag atg	1265
Met His Ser Pro Gly Phe Asp Gly Asn Ser Ser Leu Ser Phe Gln Met	
375 380 385	
ctg atg aac gca gac agc ctc tac aca gct gca cac tgc gcc ctg ctc	1313
Leu Met Asn Ala Asp Ser Leu Tyr Thr Ala Ala His Cys Ala Leu Leu	
390 395 400 405	

ctc aac ctg aag ctc tcc cac ggt gac tac tac agg aag cgg ccg acc	1361
Leu Asn Leu Lys Leu Ser His Gly Asp Tyr Tyr Arg Lys Arg Pro Thr	
410 415 420	
ctg gcg cca ggc gtg atg aag gac ttc atg aag cag gtg cag acc agc	1409
Leu Ala Pro Gly Val Met Lys Asp Phe Met Lys Gln Val Gln Thr Ser	
425 430 435	
ggc gtg ctg atg gtc ttc tct cag gcc tgg att gag gag ctc tac cat	1457
Gly Val Leu Met Val Phe Ser Gln Ala Trp Ile Glu Glu Leu Tyr His	
440 445 450	
cag gtg ctc gac agg aac atg ctt gga gag gct ggc tat tgg ggc agc	1505
Gln Val Leu Asp Arg Asn Met Leu Gly Glu Ala Gly Tyr Trp Gly Ser	
455 460 465	
cca gaa gat aac agc ctt ccc ctc atc aca atg ctg acc gat att gac	1553
Pro Glu Asp Asn Ser Leu Pro Leu Ile Thr Met Leu Thr Asp Ile Asp	
470 475 480 485	
ggc tta gag agc agt gcc att ggt ggc cag ctg atg gcc tcg gct gct	1601
Gly Leu Glu Ser Ser Ala Ile Gly Gly Gln Leu Met Ala Ser Ala Ala	
490 495 500	
aca gag tct cct ttc gcc cag agc agg aga att gat gac tcc aca gtg	1649
Thr Glu Ser Pro Phe Ala Gln Ser Arg Arg Ile Asp Asp Ser Thr Val	
505 510 515	
gca ggc gtg gca ttt gct cgc tat att ctg gtg ggc tgc tgg aag aac	1697
Ala Gly Val Ala Phe Ala Arg Tyr Ile Leu Val Gly Cys Trp Lys Asn	
520 525 530	
ttg atc gat act tta tca acc cca ctg act ggt cga atg gcg ggg agc	1745
Leu Ile Asp Thr Leu Ser Thr Pro Leu Thr Gly Arg Met Ala Gly Ser	
535 540 545	
tcc aaa ggg ctg gcc ttc att ctg gga gct gaa ggc atc aaa gag cag	1793
Ser Lys Gly Leu Ala Phe Ile Leu Gly Ala Glu Gly Ile Lys Glu Gln	
550 555 560 565	
aac cag aag gag cgg gac gcc atc tgc atg agc ctc gac ggg ctg cgg	1841
Asn Gln Lys Glu Arg Asp Ala Ile Cys Met Ser Leu Asp Gly Leu Arg	
570 575 580	
aaa gcc gca cgg ctg agc tgc gct cta ggc gtt gct gct aac tgc gcc	1889
Lys Ala Ala Arg Leu Ser Cys Ala Leu Gly Val Ala Ala Asn Cys Ala	
585 590 595	
tca gcc ctt gcc cag atg gca gct gcc tcc tgt gtc caa aaa aaa aaa	1937
Ser Ala Leu Ala Gln Met Ala Ala Ser Cys Val Gln Lys Lys Lys	
600 605 610	
gaa gag agg gag gcc caa gaa ccc agt gat gcc atc aca caa gtg aaa	1985
Glu Glu Arg Glu Ala Gln Glu Pro Ser Asp Ala Ile Thr Gln Val Lys	
615 620 625	
cta aaa gtg gag cag aaa ctg gag cag att ggg aag gtg cag ggg gtg	2033

Leu 630	Lys	Val	Glu	Gln	Lys 635	Leu	Glu	Gln	Ile	Gly 640	Lys	Val	Gln	Gly	Val 645	
tgg Trp	ctg Leu	cac His	act Thr	gcc Ala 650	cac His	gtc Val	ttg Leu	tgc Cys	atg Met 655	gag Glu	gcc Ala	atc Ile	ctc Leu	agc Ser 660	gta Val	2081
ggc Gly	ctg Leu	gag Glu	atg Met 665	gga Gly	agc Ser	cac His	aac Asn	ccg Pro 670	gac Asp	tgc Cys	tgg Trp	cca Pro	cac His 675	gtg Val	ttc Phe	2129
agg Arg	gtg Val	tgt Cys 680	gaa Glu	tac Tyr	gtg Val	ggc Gly	acc Thr 685	ctg Leu	gag Glu	cac His	aac Asn 690	cac His	ttc Phe	agc Ser	gat Asp	2177
ggt Gly	gcc Ala 695	tcg Ser	cag Gln	ccc Pro	cct Pro	ctg Leu 700	acc Thr	atc Ile	agc Ser	cag Gln	ccc Pro 705	cag Gln	aag Lys	gcc Ala	act Thr	2225
gga Gly 710	agc Ser	gct Ala	ggc Gly	ctc Leu	ctt Leu 715	ggg Gly	gac Asp	ccc Pro	gag Glu	tgt Cys 720	gag Glu	ggc Gly	tcg Ser	ccc Pro	ccc Pro 725	2273
gag Glu	cac His	agc Ser	ccg Pro	gag Glu 730	cag Gln	ggg Gly	cgc Arg	tcc Ser	ctg Leu 735	agc Ser	acg Thr	gcc Ala	cct Pro	gtc Val 740	gtc Val	2321
cag Gln	ccc Pro	ctg Leu	tcc Ser	atc Ile	cag Gln	gac Asp	ctc Leu	gtc Val 750	cgg Arg	gaa Glu	ggc Gly	agc Ser	cgg Arg 755	ggg Gly	cgg Arg	2369
gcc Ala	tcc Ser	gac Asp 760	ttc Phe	cgc Arg	ggc Gly	ggg Gly	agc Ser 765	ctc Leu	atg Met	agc Ser	ggg Gly	agc Ser 770	agc Ser	gcg Ala	gcc Ala	2417
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gct Ala 790	acg Thr	gat Asp	aag Lys	ttg Leu	aac Asn 795	ctc Leu	atg Met	gcc Ala	ttg Leu	gga Gly 800	ggg Gly	ttt Phe	ctt Leu	tac Tyr	cag Gln 805	2513
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ctaagaaggg agataaaata agtagaaaat atgcccttat agtctggaaa tagagatgaa 1096
gtagagcacc ataactga gataacagct taagttagta cataattgac tagagttgta 1156
gcagttcttt cttgctatca cttagcgaac aaataactta gaactaaaag cctaatagtt 1216
taatctatctt gcttcaagt taacaaatta tattttcaat taatattccc aatgaaatcc 1276
tggtctttta tattctttgt ccaggaatga cagcaccatt gttgtaagcc agaaacctta 1336
aagcttgatt atccatttga taaagacttt acccatttgc tccctcagcc cttttgattc 1396

taccacagcct attctcttcc tcattttctg aatgagctcc ctgtaaccca attctcttat 1456
 ttgatattgt ccgtctatgt cttagatctc tgttactttt aggttgattt caaactcctt 1516
 atgtaaaagg tacattaact ttatgatttg ttcagtacct atctctccca tctcttttat 1576
 tttattttatt attcctagag aaaaagaatg agaaaaattc taccttcttt tatgggtcaaa 1636
 ctgaaaaaca ttattcctct atgaaacttt ctgagcctgt ggaagactga gaaaagcatg 1696
 aatacctttc ttttccatt atatcacatt ctttttagatt tagacatctc tgagagaagt 1756
 gaccttgcta gcataaaaca ccatctaatt tcttcaaaga aaaaaaatg gaggcaggtc 1816
 taagagacag agacaacttt tttccccaat atatcatacc agcttttgga ggtagagatt 1876
 tttttcttat taaaaaatgg cttttctttt ttttttgcc aggtaagggtg gctcacgcct 1936
 gtggctcctag gactttggga ggctgaggca ggcagattgc ttgagctcag gagttcgaga 1996
 ccagcctggg caacatgggtg agaccccgtc tctacaaagg tacaaaaatt ggccaggcgt 2056
 ggtggcactt gtctgtagtc caggggtactt gagggcctga ggtgggggga tcacttgaac 2116
 ctgggtgggc gaggtgcag tgagccgaga tcgcgccact actccagcct gggtgacaaa 2176
 gtaagaccct gcctc 2191

<210> 171
 <211> 874
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (141)..(401)

<400> 171
 gtagttcgcg acctcggatt cgatacgcg gtgcaaggcg gcacctgctt caccagggcg 60
 cccaacgtag aggttgagca tcagcggcag catggccgac ccttcgga agtgcagcca 120
 ttgcacgtat tcgtcatagg atg ctg tgg ccc ggc gca gga ttg gag gga 170
 Met Leu Trp Pro Gly Ala Gly Leu Glu Gly
 1 5 10
 cat aga cct ggt gga agg cgt ggg gct gcc ctg acc cag gga ttt ggc 218
 His Arg Pro Gly Gly Arg Arg Gly Ala Ala Leu Thr Gln Gly Phe Gly
 15 20 25
 tcc tgt agc gct gct ggg cag agg tcc gca gga gct gca ggt act tct 266
 Ser Cys Ser Ala Ala Gly Gln Arg Ser Ala Gly Ala Ala Gly Thr Ser
 30 35 40

tgg cca act cta gct gct gct tct tgc act gct tcc ggc ggg gtg agg	314
Trp Pro Thr Leu Ala Ala Ala Ser Cys Thr Ala Ser Gly Gly Val Arg	
45 50 55	
acc cac agc tct gat gtg ggc gct tca ggc cat ggt gga gct gag att	362
Thr His Ser Ser Asp Val Gly Ala Ser Gly His Gly Gly Ala Glu Ile	
60 65 70	
cag gtt ggc ttt tcc cct cag ctc cca gct ggc tgg tga acccatcatc	411
Gln Val Gly Phe Ser Pro Gln Leu Pro Ala Gly Trp *	
75 80 85	
atagccaaaa gtactcagca gcagcacctc caggtccaga ggcacctcca gctgcatgca	471
cacacaatga atgaaagact gccaggtgtc cgaaccctgg acatgcagct tgttgagttg	531
caggatgact ctctgttcag ggtccaaggt ctcgttcctg gaatccaggt cctgtgtggg	591
gaggaagaac ttcattcttg cggttcagcca ttctgggtct ttggtgagca gcctcacaag	651
acagctccac aggttcttgt tgccgagctg gaggccaacg ggggtccatga ggagccagcc	711
ttggtctcct cgttcatgat aggtgctcta ggggtcccccac ggagaggggtc tcatgggtgt	771
ctgggctatg tgtgccttga gctggattga caggttgttt ccatagtgca gactccctca	831
gagctcccg cactcacct cagcgctcgc ggctcctccg cgc	874
<210> 172	
<211> 1297	
<212> DNA	
<213> Homo sapiens	
<220>	
<221> CDS	
<222> (15)..(1052)	
<400> 172	
agccagagggc cccg atg gca aag ggt aaa agc acc acc tta acg cag gac	50
Met Ala Lys Gly Lys Ser Thr Thr Leu Thr Gln Asp	
1 5 10	
atg agc acc agc ctc cag gaa ggc cag gag gac ggg ccg gca gga tgg	98
Met Ser Thr Ser Leu Gln Glu Gly Gln Glu Asp Gly Pro Ala Gly Trp	
15 20 25	
aga gcg aat ctg aag ccc gtg gac agg aga agc cca gct gag agg act	146
Arg Ala Asn Leu Lys Pro Val Asp Arg Arg Ser Pro Ala Glu Arg Thr	
30 35 40	
ctg aag ccc aag gaa cca cgg gcc ctg gca gag ccg agg gcg ggg gag	194
Leu Lys Pro Lys Glu Pro Arg Ala Leu Ala Glu Pro Arg Ala Gly Glu	
45 50 55 60	

gcc ccc agg aag gtc tca ggc agc ttt gct ggg agt gtc cac atc acc	242
Ala Pro Arg Lys Val Ser Gly Ser Phe Ala Gly Ser Val His Ile Thr	
65 70 75	
ctg acc ccc gtg agg cct gac agg acc cca cgc cca gcc agc cca gga	290
Leu Thr Pro Val Arg Pro Asp Arg Thr Pro Arg Pro Ala Ser Pro Gly	
80 85 90	
ccc agc ctc cca gcc agg tcc ccc tcc cca ccc cgc cgc agg aga ctg	338
Pro Ser Leu Pro Ala Arg Ser Pro Ser Pro Pro Arg Arg Arg Arg Leu	
95 100 105	
gcc gtc cct gcc agc ctc gac gtt tgt gac aac tgg ctt cgg ccg gag	386
Ala Val Pro Ala Ser Leu Asp Val Cys Asp Asn Trp Leu Arg Pro Glu	
110 115 120	
ccc cct ggc cag gaa gcc cga gtg cag agc tgg aag gag gag gag aag	434
Pro Pro Gly Gln Glu Ala Arg Val Gln Ser Trp Lys Glu Glu Glu Lys	
125 130 135 140	
aaa cct cac ctt cag ggc aaa cca ggg aga ccc ttg tcc ccg gcc aat	482
Lys Pro His Leu Gln Gly Lys Pro Gly Arg Pro Leu Ser Pro Ala Asn	
145 150 155	
gtc cct gct ctg cct ggc gag acg gtg acc tcc cca gtc agg ctg cac	530
Val Pro Ala Leu Pro Gly Glu Thr Val Thr Ser Pro Val Arg Leu His	
160 165 170	
ccc gac tac ctc tcc ccg gag gag ata cag agg cag ctg cag gac atc	578
Pro Asp Tyr Leu Ser Pro Glu Glu Ile Gln Arg Gln Leu Gln Asp Ile	
175 180 185	
gag agg cgg ctg gac gcc ctg gag ctc cgc ggc gtg gag ctg gag aag	626
Glu Arg Arg Leu Asp Ala Leu Glu Leu Arg Gly Val Glu Leu Glu Lys	
190 195 200	
cga ctg cgg gcg gcc gag gga gat gac gct gag gat agc ctc atg gtg	674
Arg Leu Arg Ala Ala Glu Gly Asp Asp Ala Glu Asp Ser Leu Met Val	
205 210 215 220	
gac tgg ttc tgg ctc att cac gag aag cag ctt ctg ctg aga cag gag	722
Asp Trp Phe Trp Leu Ile His Glu Lys Gln Leu Leu Leu Arg Gln Glu	
225 230 235	
tca gag ctg atg tac aag tcc aag gcc cag cgt ctg gag gag cag cag	770
Ser Glu Leu Met Tyr Lys Ser Lys Ala Gln Arg Leu Glu Glu Gln Gln	
240 245 250	
ctg gac atc gag ggc gag ctg cgc cgg ctc atg gcc aag ccc gag gct	818
Leu Asp Ile Glu Gly Glu Leu Arg Arg Leu Met Ala Lys Pro Glu Ala	
255 260 265	
ctg aag tca ctg cag gag cgg cgg cgg gag cag gag ctg ctg gag cag	866
Leu Lys Ser Leu Gln Glu Arg Arg Arg Glu Gln Glu Leu Leu Glu Gln	
270 275 280	

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tac gtg agc acc gtg aac gac cgc agt gac atc gtg gac tcg ctg gac      914
Tyr Val Ser Thr Val Asn Asp Arg Ser Asp Ile Val Asp Ser Leu Asp
285                290                295                300

gag gac cgg ctc cgg gaa caa gag gag gat cag atg ctg cgg gac atg      962
Glu Asp Arg Leu Arg Glu Gln Glu Glu Asp Gln Met Leu Arg Asp Met
                305                310                315

att gag aag ctg ggc ctc cag agg aag aag tcc aag ttc cgc ttg tcc    1010
Ile Glu Lys Leu Gly Leu Gln Arg Lys Lys Ser Lys Phe Arg Leu Ser
                320                325                330

aag atc tgg tca cca aaa agc aaa agc agc ccc tcc cag tag tagccag    1059
Lys Ile Trp Ser Pro Lys Ser Lys Ser Ser Pro Ser Gln *
                335                340                345

tagggccgtg ggctcggccc ggacctggca tccggacttg gactcggggc catgggcttg    1119

gccccgaccc ggaacccgga cttgtactcg gggccgtggg ctcggccccg acccggcatt    1179

cggacttgga ctcgggaagg gcctcctgtc cctacaaggg gcatgtggac agcagggacc    1239

tgcgctaccg tctgtggtct caataaagaa accgaccaca tggaaaaaaaa aaaaaaaaa    1297

<210> 173
<211> 546
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (131)..(502)

<400> 173
ctgccgtgag aaaattagcc tctgggggtac ggccgacttt tgtccactgg gtgtcgcaga    60

tcccagtcct cagggcctca agacagctct gcaatccgcc gcacagaatt caagttcgga    120

ttcggctttg   atg acc tta atc cag gca aat cct aaa tcc tat cca gtc    169
             Met Thr Leu Ile Gln Ala Asn Pro Lys Ser Tyr Pro Val
               1               5               10

ggc agc atc cag atg aac cac aac tcc ttc ctc agc gca acc agg cca    217
Gly Ser Ile Gln Met Asn His Asn Ser Phe Leu Ser Ala Thr Arg Pro
             15             20             25

agg gag tgc tcc atc ccc tgc ctc gca gtt act gat tct cca agc cgg    265
Arg Glu Cys Ser Ile Pro Cys Leu Ala Val Thr Asp Ser Pro Ser Arg
             30             35             40             45

gcg ccg ccc agt cct ggc ggg gct tcc ccc acc cct ctc cgc gcc ggg    313
Ala Pro Pro Ser Pro Gly Gly Ala Ser Pro Thr Pro Leu Arg Ala Gly
             50             55             60

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caa tcg cgc gtt ctt tct tta ctt gtg ctc cac tgg tgg gca gca tgt	361
Gln Ser Arg Val Leu Ser Leu Leu Val Leu His Trp Trp Ala Ala Cys	
65 70 75	
gct ccc gcg tcc aca gct ctg ttt cgc ctt ccg gtc ccc gta gct ctg	409
Ala Pro Ala Ser Thr Ala Leu Phe Arg Leu Pro Val Pro Val Ala Leu	
80 85 90	
cag ggg aac ggg atc tct gcc gcc tcc tcg gcc gct aag cga ccc ggg	457
Gln Gly Asn Gly Ile Ser Ala Ala Ser Ser Ala Ala Lys Arg Pro Gly	
95 100 105	
gct gcc cga cct agc gag tgc gca cga ccg ccc agc gag ggg tag ccg	505
Ala Ala Arg Pro Ser Glu Cys Ala Arg Pro Pro Ser Glu Gly *	
110 115 120	
agtcgaggca gcacggttcc caaggcagcc aaggctgcgc c	546

<210> 174
 <211> 1009
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (50)..(793)

<400> 174

gcacgagggc acgagctgta tgagtggtag cttttccct caaccagca	atg gag	55
	Met Glu	
	1	
gag cag ccc cag atg caa gac gcc gac gag ccc gcg gac tcc gga ggg	103	
Glu Gln Pro Gln Met Gln Asp Ala Asp Glu Pro Ala Asp Ser Gly Gly		
5 10 15		
gaa ggc cgg gca ggc ggg cca ccg cag gtc gcc ggc gcc cag gcg gcg	151	
Glu Gly Arg Ala Gly Gly Pro Pro Gln Val Ala Gly Ala Gln Ala Ala		
20 25 30		
tgc agc gag gac cgc atg acc ctg ctc ctc agg ctg aga gca cag aca	199	
Cys Ser Glu Asp Arg Met Thr Leu Leu Leu Arg Leu Arg Ala Gln Thr		
35 40 45 50		
aaa caa caa ctc tta gaa tat aaa tca atg gtt gat gca agt gaa gaa	247	
Lys Gln Gln Leu Leu Glu Tyr Lys Ser Met Val Asp Ala Ser Glu Glu		
55 60 65		
aaa act cca gaa caa att atg caa gaa aag caa atc gaa gct aaa att	295	
Lys Thr Pro Glu Gln Ile Met Gln Glu Lys Gln Ile Glu Ala Lys Ile		
70 75 80		
gaa gac ctg gaa aat gaa att gaa gag gta aaa gtt gct ttt gag ata	343	
Glu Asp Leu Glu Asn Glu Ile Glu Glu Val Lys Val Ala Phe Glu Ile		

85	90	95	
aaa aag ctt gca tta gac agg atg aga ctt tca act gca ctt aaa aaa			391
Lys Lys Leu Ala Leu Asp Arg Met Arg Leu Ser Thr Ala Leu Lys Lys			
100	105	110	
aac ctg gag aaa att agc aga cag tct agt gtg ctc atg gat aac atg			439
Asn Leu Glu Lys Ile Ser Arg Gln Ser Ser Val Leu Met Asp Asn Met			
115	120	125	130
aaa cac cta tta gag cta aat aaa tta ata atg aaa tca cag cag gaa			487
Lys His Leu Leu Glu Leu Asn Lys Leu Ile Met Lys Ser Gln Gln Glu			
135	140	145	
tct tgg gat tta gag gaa aaa ctg ctt gat att aga aag aag aga ttg			535
Ser Trp Asp Leu Glu Glu Lys Leu Leu Asp Ile Arg Lys Lys Arg Leu			
150	155	160	
caa tta aaa caa gct tca gaa agt aag ctt tta gaa ata cag act gaa			583
Gln Leu Lys Gln Ala Ser Glu Ser Lys Leu Leu Glu Ile Gln Thr Glu			
165	170	175	
aag aac aaa cag aag att gat ttg gac agt atg gaa aac tca gag agg			631
Lys Asn Lys Gln Lys Ile Asp Leu Asp Ser Met Glu Asn Ser Glu Arg			
180	185	190	
ata aag atc ata cga caa aac cta cag atg gag ata aaa att act act			679
Ile Lys Ile Ile Arg Gln Asn Leu Gln Met Glu Ile Lys Ile Thr Thr			
195	200	205	210
gtt att caa cat gtg ttc cag aac ctt att ttg ggg agt aaa gtc aat			727
Val Ile Gln His Val Phe Gln Asn Leu Ile Leu Gly Ser Lys Val Asn			
215	220	225	
tgg gca gag gat cct gcc ctt aag gaa att gtt ctg cag ctt gag aag			775
Trp Ala Glu Asp Pro Ala Leu Lys Glu Ile Val Leu Gln Leu Glu Lys			
230	235	240	
aat gtt gac atg atg taa taagaa ttcatttctg acatatttta catttctggc			829
Asn Val Asp Met Met *			
245			
aatctcaact cttatttgga atacttctgt gcatttgtct gtccaccgta attttagaaa			889
agcatatcca taacgttttac agttgtagta cagttgtggt tagttatttg tagtgggatt			949
gaaagtaatt tttttctttt tatatttcta tattcagggtt ggtttttttg tgccgttcgc			1009

<210> 175
 <211> 834
 <212> DNA
 <213> Homo sapiens
 <220>

<221> CDS
 <222> (12)..(833)

<400> 175

tttcgtcaag g atg aca tcc att cga gct gta ttt ata ttc ctg tgg ctg	50
Met Thr Ser Ile Arg Ala Val Phe Ile Phe Leu Trp Leu	
1 5 10	
cag ctg gac ttg gtg aat gga gag aat gtg gag cag cat cct tca acc	98
Gln Leu Asp Leu Val Asn Gly Glu Asn Val Glu Gln His Pro Ser Thr	
15 20 25	
ctg agt gtc cag gag gga gac agc gct gtt atc aag tgt act tat tca	146
Leu Ser Val Gln Glu Gly Asp Ser Ala Val Ile Lys Cys Thr Tyr Ser	
30 35 40 45	
gac agt gcc tca aac tac ttc cct tgg tat aag caa gaa ctt gga aaa	194
Asp Ser Ala Ser Asn Tyr Phe Pro Trp Tyr Lys Gln Glu Leu Gly Lys	
50 55 60	
aga cct cag ctt att ata gac att cgt tca aat gtg ggc gaa aag aaa	242
Arg Pro Gln Leu Ile Ile Asp Ile Arg Ser Asn Val Gly Glu Lys Lys	
65 70 75	
gac caa cga att gct gtt aca ttg aac aag aca gcc aaa cat ttc tcc	290
Asp Gln Arg Ile Ala Val Thr Leu Asn Lys Thr Ala Lys His Phe Ser	
80 85 90	
ctg cac atc aca gag acc caa cct gaa gac tcg gct gtc tac ttc tgt	338
Leu His Ile Thr Glu Thr Gln Pro Glu Asp Ser Ala Val Tyr Phe Cys	
95 100 105	
gca gca agt aac ggc cag gca gga act gct ctg atc ttt ggg aag gga	386
Ala Ala Ser Asn Gly Gln Ala Gly Thr Ala Leu Ile Phe Gly Lys Gly	
110 115 120 125	
acc acc tta tca gtg agt tcc aat atc cag aac cct gac cct gcc gtg	434
Thr Thr Leu Ser Val Ser Ser Asn Ile Gln Asn Pro Asp Pro Ala Val	
130 135 140	
tac cag ctg aga gac tct aaa tcc agt gac aag tct gtc tgc cta ttc	482
Tyr Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe	
145 150 155	
acc gat ttt gat tct caa aca aat gtg tca caa agt aag gat tct gat	530
Thr Asp Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp	
160 165 170	
gtg tat atc aca gac aaa act gtg cta gac atg agg tct atg gac ttc	578
Val Tyr Ile Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp Phe	
175 180 185	
aag agc aac agt gct gtg gcc tgg agc aac aaa tct gac ttt gca tgt	626
Lys Ser Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys	
190 195 200 205	
gca aac gcc ttc aac aac agc att att cca gaa gac acc ttc ttc ccc	674

Ala Asn Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro	
210 215 220	
agc cca gaa agt tcc tgt gat gtc aag ctg gtc gag aaa agc ttt gaa	722
Ser Pro Glu Ser Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu	
225 230 235	
aca gat acg aac cta aac ttt caa aac ctg tca gtg att ggg ttc cga	770
Thr Asp Thr Asn Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe Arg	
240 245 250	
atc ctc ctc ctg aaa gtg gcc ggg ttt aat ctg ctc atg acg ctg cgg	818
Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg	
255 260 265	
ctg tgg tcc agc tga g	834
Leu Trp Ser Ser *	
270	

<210> 176
 <211> 778
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (34)..(576)

 <220>
 <221> misc_feature
 <222> (1)...(778)
 <223> n = a,t,c or g

<400> 176	
tttcgtagac ctctctgtct tgtagcatct gcc atg aga atc agg ctc ctg tgc	54
Met Arg Ile Arg Leu Leu Cys	
1 5	
tgt gtg gcc ttt tct ctc ctg tgg gca ggt cca gtg att gct ggg atc	102
Cys Val Ala Phe Ser Leu Leu Trp Ala Gly Pro Val Ile Ala Gly Ile	
10 15 20	
acc cag gca cca aca tct cag atc ctg gca gca gga cgg cgc atg aca	150
Thr Gln Ala Pro Thr Ser Gln Ile Leu Ala Ala Gly Arg Arg Met Thr	
25 30 35	
ctg aga tgt acc cag gat atg aga cat aat gcc atg tac tgg tat aga	198
Leu Arg Cys Thr Gln Asp Met Arg His Asn Ala Met Tyr Trp Tyr Arg	
40 45 50 55	
caa gat cta gga ctg ggg cta agg ctc atc cat tat tca aat act gca	246
Gln Asp Leu Gly Leu Gly Leu Arg Leu Ile His Tyr Ser Asn Thr Ala	
60 65 70	

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ggt acc act ggc aaa gga gaa gtc cct gat ggt tat agt gtc tcc aga      294
Gly Thr Thr Gly Lys Gly Glu Val Pro Asp Gly Tyr Ser Val Ser Arg
      75                      80                      85

gca aac aca gat gat ttc ccc ctc acg ttg gcg tct gct gta ccc tct      342
Ala Asn Thr Asp Asp Phe Pro Leu Thr Leu Ala Ser Ala Val Pro Ser
      90                      95                      100

cag aca tct gtg tac ttc tgt gcc agc agt gac ggg gct agc ggg agt      390
Gln Thr Ser Val Tyr Phe Cys Ala Ser Ser Asp Gly Ala Ser Gly Ser
      105                      110                      115

ccc cac acc ggg gag ctg ttt ttt gga gaa ggc tct agg ctg acc gta      438
Pro His Thr Gly Glu Leu Phe Phe Gly Glu Gly Ser Arg Leu Thr Val
      120                      125                      130                      135

ctg gag gac ctg aaa aac gtg ttc cca ccc gag gtc gct gtg ttt gag      486
Leu Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala Val Phe Glu
      140                      145                      150

cca tca gaa gca gag atc tcc cac acc caa aag gcc aca ctg gtg tgc      534
Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val Cys
      155                      160                      165

ctg gcc aca ggc ttc tac ccc gac cac gtg gag ctg agc tga ttttttc      583
Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser *
      170                      175                      180

atagactatg agcttctaaa aaatcatccc catattcgtc attacattct tgggatcaaa      643

tatactgcat gaaaaaagat gctcagaaaa gtctatgtta agttaatgta gaatatatga      703

atgagtgaag gaaagtgttt tgaaaccatc ataggaata taataagata anattacact      763

agaataaaat gaaac                                                    778

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<210> 177
 <211> 708
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (176)..(493)

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<400> 177
gagggcgggga gaggcagatg agtaaatgga tccttacact aagtgtgatg agcagaaacc      60

caggcgctct ggggcatgag cagggaatac taaccagcc ctgggggctc aatctctccc      120

caccctgca ggagaggctt ggggtgagtt ttgggaataa ggaccatcca gccac atg      178
Met
1

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acg aag ggg aag gaa aat ccc cat caa ggc aaa aac aca gtc caa ggc 226
Thr Lys Gly Lys Glu Asn Pro His Gln Gly Lys Asn Thr Val Gln Gly
      5              10              15

tct gag gcc caa att ccg ggg aga ggg gtg aag gtt gtt tgt cgc acc 274
Ser Glu Ala Gln Ile Pro Gly Arg Gly Val Lys Val Val Cys Arg Thr
      20              25              30

tgg gtt aaa ggg tgg ggg tgg aga gta gga gaa gag gct aca cag gtg 322
Trp Val Lys Gly Trp Gly Trp Arg Val Gly Glu Glu Ala Thr Gln Val
      35              40              45

aga agg tgt cag atc aca aag ggc ctt gta tgc caa act aag aag act 370
Arg Arg Cys Gln Ile Thr Lys Gly Leu Val Cys Gln Thr Lys Lys Thr
      50              55              60              65

gaa ctt gac cat gaa gtt agg cag acc ctc tgg aga gtt tta aag caa 418
Glu Leu Asp His Glu Val Arg Gln Thr Leu Trp Arg Val Leu Lys Gln
      70              75              80

gga gtc gtg tgg atg aac aaa cct gtg atg ggc tgg ggt tac caa gga 466
Gly Val Val Trp Met Asn Lys Pro Val Met Gly Trp Gly Tyr Gln Gly
      85              90              95

ggg ctt cct gga gga ggt cag act tga gctga gggaaggata ggatttggag 518
Gly Leu Pro Gly Gly Gly Gln Thr *
      100              105

agctgacatt ctgatgagcg gcttcggtta aagctcacia aaacccttcc ctcccccatg 578

ccctttgaaa tcatttgaat caaagattgc gtgtgttaaa gacatgtttg tctgttatct 638

gaaagctgtg gtttctcttt aacagattca gggcctcatc ctttgactcg gaccaagaag 698

gaattatgag 708

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<210> 178
 <211> 1463
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (120)..(1175)

<220>
 <221> misc_feature
 <222> (1)...(1463)
 <223> n = a,t,c or g

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<400> 178
tttcgtgcaa agaaaactgt gagagagaga atttttaaaa agcagctggg gcctgaggtt 60

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tctccccag taccctgggt cacctcagcc cagagctggc ggcaggcccc cagcccctc	119
atg tca gag ccc cct gtg tac tgt aac ctg gtg gac ctt cgc cgc tgt	167
Met Ser Glu Pro Pro Val Tyr Cys Asn Leu Val Asp Leu Arg Arg Cys	
1 5 10 15	
cct cgg tcc cca ccc cca ggc cct gca tgc ccc ctg ctg cag agg ctg	215
Pro Arg Ser Pro Pro Pro Gly Pro Ala Cys Pro Leu Leu Gln Arg Leu	
20 25 30	
gat gcc tgg gag cag cac ctg gac ccc aac tct gga cgc tgc ttc tac	263
Asp Ala Trp Glu Gln His Leu Asp Pro Asn Ser Gly Arg Cys Phe Tyr	
35 40 45	
ata aat tca ctg act ggc tgc aag tcc tgg aag ccc ccg cgc cgc agt	311
Ile Asn Ser Leu Thr Gly Cys Lys Ser Trp Lys Pro Pro Arg Arg Ser	
50 55 60	
cgc agc gag acg aac cct ggc tcc atg gag ggg aca cag acc ctg aag	359
Arg Ser Glu Thr Asn Pro Gly Ser Met Glu Gly Thr Gln Thr Leu Lys	
65 70 75 80	
agg aac aat gat gtc ctg caa cct cag gca aag ggc ttc aga tct gac	407
Arg Asn Asn Asp Val Leu Gln Pro Gln Ala Lys Gly Phe Arg Ser Asp	
85 90 95	
aca ggg acc cca gaa ccg ctt gac cca cag ggt tca ctc agc ctc agc	455
Thr Gly Thr Pro Glu Pro Leu Asp Pro Gln Gly Ser Leu Ser Leu Ser	
100 105 110	
caa cgc acc tcg cag ctt gac cct cca gcc ttg cag gcc cct cga cct	503
Gln Arg Thr Ser Gln Leu Asp Pro Pro Ala Leu Gln Ala Pro Arg Pro	
115 120 125	
ctg ccg cag ctc ctg gac gac ccc cat gag gtg gaa aag tcg ggt ctg	551
Leu Pro Gln Leu Leu Asp Asp Pro His Glu Val Glu Lys Ser Gly Leu	
130 135 140	
ctc aac atg acc aag att gcc caa ggg ggg cgc aag ctc agg aag aac	599
Leu Asn Met Thr Lys Ile Ala Gln Gly Gly Arg Lys Leu Arg Lys Asn	
145 150 155 160	
tgg ggc ccg tct tgg gtg gtg tta acg ggt aac agc ctg gtg ttc tac	647
Trp Gly Pro Ser Trp Val Val Leu Thr Gly Asn Ser Leu Val Phe Tyr	
165 170 175	
cga gag cca ccg ccg aca gcg ccc tcc tca ggc tgg gga cca gcg ggt	695
Arg Glu Pro Pro Pro Thr Ala Pro Ser Ser Gly Trp Gly Pro Ala Gly	
180 185 190	
agc cgg ccc gaa agt agc gtg gac ctg cgc ggg gcg gcc ctg gcg cac	743
Ser Arg Pro Glu Ser Ser Val Asp Leu Arg Gly Ala Ala Leu Ala His	
195 200 205	
ggc cgc cac ctg tcc agc cgc cgc aac gtc ctg cac atc cgc acg atc	791
Gly Arg His Leu Ser Ser Arg Arg Asn Val Leu His Ile Arg Thr Ile	
210 215 220	

cct ggc cac gag ttc ctg ctg cag tgc gac cac gag aca gag ctg cga 839
 Pro Gly His Glu Phe Leu Leu Gln Ser Asp His Glu Thr Glu Leu Arg
 225 230 235 240

gcc tgg cac cgc gcg ctg cgg act gtc atc gag cgg ctg gat cgg gag 887
 Ala Trp His Arg Ala Leu Arg Thr Val Ile Glu Arg Leu Asp Arg Glu
 245 250 255

aac ccc ctg gag ctg cgt ctg tgc ggc tct gga ccc gcg gag ctg agc 935
 Asn Pro Leu Glu Leu Arg Leu Ser Gly Ser Gly Pro Ala Glu Leu Ser
 260 265 270

gcc ggg gag gac gaa gaa gag gag tgc gag ctg gtg tcc aag ccg ctg 983
 Ala Gly Glu Asp Glu Glu Glu Glu Ser Glu Leu Val Ser Lys Pro Leu
 275 280 285

ctg cgc ctc agc agc cgc cgg agc tcc att cgg ggg ccc gaa ggc acc 1031
 Leu Arg Leu Ser Ser Arg Arg Ser Ser Ile Arg Gly Pro Glu Gly Thr
 290 295 300

gag cag aac cgc gtg cgc aac aaa cta aag cgg ctc atc gcg aag aga 1079
 Glu Gln Asn Arg Val Arg Asn Lys Leu Lys Arg Leu Ile Ala Lys Arg
 305 310 315 320

ccg ccc tta caa agc ctg cag gag cgg ggt ctg ctc cga ggt gag ggg 1127
 Pro Pro Leu Gln Ser Leu Gln Glu Arg Gly Leu Leu Arg Gly Glu Gly
 325 330 335

gct ggg cca ggt tca tgg ata aga aaa ctc cag cga ggc tca gag tag 1175
 Ala Gly Pro Gly Ser Trp Ile Arg Lys Leu Gln Arg Gly Ser Glu *
 340 345 350

agcttcccag aactagacca caaccttctg tgactgtctg tttcccacta cccagattg 1235

tttaggggag aagctggggg gacctgtacc cctttgccag attgtttgaa gcanggggaag 1295

ggaggtggag tgtatttctt tgcccaggcc tggcacaggc agccaggagg accagcctca 1355

cttaaggata aagacctatg ctgagaagag ctctgtgtgag tgacgctggc acttggcttc 1415

cgctcactc tacttcccca gaccaggtgt tcggctggca gatggaat 1463

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Pro Ala Ile Lys Ala Leu Met Arg Pro Asp Pro Arg Leu Lys Trp Ala	
35 40 45	
gtg ctg gtg ctg gtg ctg gtg cag atg ctg gcc tgc tgg ctg gtg cgc	253
Val Leu Val Leu Val Leu Val Gln Met Leu Ala Cys Trp Leu Val Arg	
50 55 60	
ggg ctg gcc tgg cgc tgg ctg ctg ttc tgg gcc tac gcc ttt ggt ggc	301
Gly Leu Ala Trp Arg Trp Leu Leu Phe Trp Ala Tyr Ala Phe Gly Gly	
65 70 75	
tgc gtg aac cac tcg ctg acg ctg gcc atc cac gac atc tcg cac aac	349
Cys Val Asn His Ser Leu Thr Leu Ala Ile His Asp Ile Ser His Asn	
80 85 90	
gcg gcc ttc ggc acg ggc cgt gcg gca cgc aac cgc tgg ctg gcc gtg	397
Ala Ala Phe Gly Thr Gly Arg Ala Ala Arg Asn Arg Trp Leu Ala Val	
95 100 105 110	
ttc gcc aac ctg ccc gtg ggt gtg ccc tac gcc gcc tcc ttc aag aag	445
Phe Ala Asn Leu Pro Val Gly Val Pro Tyr Ala Ala Ser Phe Lys Lys	
115 120 125	
tac cac gtg gac cac cac cgc tac ctg ggc ggc gac ggg ctg gac gtg	493
Tyr His Val Asp His His Arg Tyr Leu Gly Gly Asp Gly Leu Asp Val	
130 135 140	
gac gtg ccc acg cgt ctg gag ggc tgg ttc ttc tgc acg ccc gcc cgc	541
Asp Val Pro Thr Arg Leu Glu Gly Trp Phe Phe Cys Thr Pro Ala Arg	
145 150 155	
aag ctg ctc tgg ctg gtg ctg cag ccc ttc ttc tac tca cta cgg ccg	589
Lys Leu Leu Trp Leu Val Leu Gln Pro Phe Phe Tyr Ser Leu Arg Pro	
160 165 170	
ctc tgc gtc cac ccc aag gcc gtg acc cgc atg gag gtg ctc aac acg	637
Leu Cys Val His Pro Lys Ala Val Thr Arg Met Glu Val Leu Asn Thr	
175 180 185 190	
ctg gtg cag ctg gcg gcc gac ctg gcc atc ttt gcc ctt tgg ggg ctc	685
Leu Val Gln Leu Ala Ala Asp Leu Ala Ile Phe Ala Leu Trp Gly Leu	
195 200 205	
aag ccc gtg gtc tac ctg ctg gcc agc tcc ttc ctg ggc ctg ggc ctg	733
Lys Pro Val Val Tyr Leu Leu Ala Ser Ser Phe Leu Gly Leu Gly Leu	
210 215 220	
cac ccc atc tcg ggc cac ttc gtg gcc gag cac tac atg ttc ctc aag	781
His Pro Ile Ser Gly His Phe Val Ala Glu His Tyr Met Phe Leu Lys	
225 230 235	
ggc cac gag acc tac tcc tac tat ggg cct ctc aac tgg atc acc ttc	829
Gly His Glu Thr Tyr Ser Tyr Tyr Gly Pro Leu Asn Trp Ile Thr Phe	
240 245 250	
aat gtg ggc tac cac gtg gag cac cac gac ttc ccc agc atc ccg ggc	877

Asn Val Gly Tyr His Val Glu His His Asp Phe Pro Ser Ile Pro Gly	
255 260 265 270	
tac aac ctg ccg ctg gtg cgg aag atc gcg ccc gag tac tac gac cac	925
Tyr Asn Leu Pro Leu Val Arg Lys Ile Ala Pro Glu Tyr Tyr Asp His	
275 280 285	
ctg ccg cag cac cac tcc tgg gtg aag gtg ctc tgg gat ttt gtg ttt	973
Leu Pro Gln His His Ser Trp Val Lys Val Leu Trp Asp Phe Val Phe	
290 295 300	
gag gac tcc ctg ggg ccc tat gcc agg gtg aag cgg gtg tac agg ctg	1021
Glu Asp Ser Leu Gly Pro Tyr Ala Arg Val Lys Arg Val Tyr Arg Leu	
305 310 315	
gca aaa gat ggt ctg tga gcccgg gctgcctcct ggtggtggcc attgtcccc	1075
Ala Lys Asp Gly Leu *	
320	
atcgccccct cagccttgca cccagcact gagaagctac atttccttcc tgtgctctgg	1135
actgctgccc ttgtccccga ggagtgtccc gcgcagccac acctggcaac agcagtgtgg	1195
gctgcagggc tccgtctgca cgtggacttg ccctggacct tgagtgtggc cctccctttc	1255
tgggcoctccc caggtgagggc ctggccctgc cccaccatga cctgggtgct ctgagcccac	1315
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gag ctg tgg acc ttc gcg ggt tcc cgg gac ccg agc gca ccg cgg cta	99
Glu Leu Trp Thr Phe Ala Gly Ser Arg Asp Pro Ser Ala Pro Arg Leu	
15 20 25	
gcc tac ggc tac ggc ccg ggc agc ctg cgc gag ctg cgg gcg cgc gag	147
Ala Tyr Gly Tyr Gly Pro Gly Ser Leu Arg Glu Leu Arg Ala Arg Glu	
30 35 40	
ttc agc cgc ctg gca gga act gtc tat ctt gac cat gca ggt gcc acc	195

Phe	Ser	Arg	Leu	Ala	Gly	Thr	Val	Tyr	Leu	Asp	His	Ala	Gly	Ala	Thr		
		45					50					55					
ttg	ttc	tcc	cag	agc	cag	ctc	gaa	agc	ttc	act	agt	gat	ctc	atg	gaa	243	
Leu	Phe	Ser	Gln	Ser	Gln	Leu	Glu	Ser	Phe	Thr	Ser	Asp	Leu	Met	Glu		
	60					65				70							
aac	act	tat	ggg	aat	cct	cac	agc	cag	aac	atc	agc	agc	aag	ctc	acc	291	
Asn	Thr	Tyr	Gly	Asn	Pro	His	Ser	Gln	Asn	Ile	Ser	Ser	Lys	Leu	Thr		
	75				80				85					90			
cat	gac	act	gtg	gag	cag	gtg	cgc	tac	aga	atc	ctg	gcg	cac	ttc	cac	339	
His	Asp	Thr	Val	Glu	Gln	Val	Arg	Tyr	Arg	Ile	Leu	Ala	His	Phe	His		
			95					100						105			
acc	acc	gca	gaa	gac	tac	act	gtg	atc	ttc	act	gcc	ggg	agc	acg	gct	387	
Thr	Thr	Ala	Glu	Asp	Tyr	Thr	Val	Ile	Phe	Thr	Ala	Gly	Ser	Thr	Ala		
		110					115					120					
gct	ctc	aaa	ctg	gtg	gca	gag	gcc	ttt	cca	tgg	gtg	tcc	cag	ggc	cca	435	
Ala	Leu	Lys	Leu	Val	Ala	Glu	Ala	Phe	Pro	Trp	Val	Ser	Gln	Gly	Pro		
	125					130					135						
gag	agc	agt	ggg	agt	cgc	ttc	tgt	tac	ctc	acc	gac	agc	cac	acc	tcc	483	
Glu	Ser	Ser	Gly	Ser	Arg	Phe	Cys	Tyr	Leu	Thr	Asp	Ser	His	Thr	Ser		
	140				145					150							
gta	gtg	ggg	atg	agg	aac	gtg	acc	atg	gct	ata	aat	gtc	ata	tcc	atc	531	
Val	Val	Gly	Met	Arg	Asn	Val	Thr	Met	Ala	Ile	Asn	Val	Ile	Ser	Ile		
	155				160				165					170			
ccg	gtc	agg	cca	gag	gac	ctg	tgg	tct	gca	gag	gaa	cgt	ggg	gct	tca	579	
Pro	Val	Arg	Pro	Glu	Asp	Leu	Trp	Ser	Ala	Glu	Glu	Arg	Gly	Ala	Ser		
			175					180						185			
gcc	agc	aac	cca	gac	tgc	cag	ctg	ccg	cat	ctc	ttc	tgc	tac	cca	gct	627	
Ala	Ser	Asn	Pro	Asp	Cys	Gln	Leu	Pro	His	Leu	Phe	Cys	Tyr	Pro	Ala		
		190						195					200				
cag	agt	aac	ttt	tct	gga	gtc	aga	tac	ccc	ctg	tcc	tgg	ata	gaa	gag	675	
Gln	Ser	Asn	Phe	Ser	Gly	Val	Arg	Tyr	Pro	Leu	Ser	Trp	Ile	Glu	Glu		
	205					210					215						
gtc	aag	tct	ggg	cgg	ttg	cgc	cct	gtg	agc	acg	cct	ggg	aag	tgg	ttt	723	
Val	Lys	Ser	Gly	Arg	Leu	Arg	Pro	Val	Ser	Thr	Pro	Gly	Lys	Trp	Phe		
	220				225						230						
gtg	ctg	ctg	gat	gca	gcc	tcc	tac	gtg	agc	acc	tgc	cct	ttg	gac	ctg	771	
Val	Leu	Leu	Asp	Ala	Ala	Ser	Tyr	Val	Ser	Thr	Ser	Pro	Leu	Asp	Leu		
	235				240					245				250			
tca	gct	cac	cag	gcc	gac	ttt	gtc	ccc	atc	tcc	ttc	tat	aag	atc	ttc	819	
Ser	Ala	His	Gln	Ala	Asp	Phe	Val	Pro	Ile	Ser	Phe	Tyr	Lys	Ile	Phe		
			255					260					265				
ggg	ttt	cct	aca	ggc	ctg	ggc	gct	ctg	ctg	gtc	cat	aat	cgt	gcg	gct	867	
Gly	Phe	Pro	Thr	Gly	Leu	Gly	Ala	Leu	Leu	Val	His	Asn	Arg	Ala	Ala		

270	275	280	
cct cta ctg agg aag acc tac ttt gga gga ggg aca gcc tct gcg tac			915
Pro Leu Leu Arg Lys Thr Tyr Phe Gly Gly Gly Thr Ala Ser Ala Tyr			
285	290	295	
cta gca gga gaa gac ttc tac atc ccg agg cag tcg gta gct cag agg			963
Leu Ala Gly Glu Asp Phe Tyr Ile Pro Arg Gln Ser Val Ala Gln Arg			
300	305	310	
ttt gaa gat ggc acc atc tca ttc ctt gat gtt atc gcg cta aaa cat			1011
Phe Glu Asp Gly Thr Ile Ser Phe Leu Asp Val Ile Ala Leu Lys His			
315	320	325	330
gga ttt gac acc cta gag cgc ctc aca ggt gga atg gag aat ata aag			1059
Gly Phe Asp Thr Leu Glu Arg Leu Thr Gly Gly Met Glu Asn Ile Lys			
335	340	345	
cag cac acc ttc acc ttg gct cag tat acc tac atg gcc ctg tcc tct			1107
Gln His Thr Phe Thr Leu Ala Gln Tyr Thr Tyr Met Ala Leu Ser Ser			
350	355	360	
ctc cag tac ccc aat gga gcc cct gtg gtg cgg att tac agc gat tct			1155
Leu Gln Tyr Pro Asn Gly Ala Pro Val Val Arg Ile Tyr Ser Asp Ser			
365	370	375	
gag ttc agc agc cct gag gtt cag ggc ccg atc atc aat ttt aat gtg			1203
Glu Phe Ser Ser Pro Glu Val Gln Gly Pro Ile Ile Asn Phe Asn Val			
380	385	390	
ctg gat gac aaa ggg aac atc att ggt tac tcc cag gtg gac aaa atg			1251
Leu Asp Asp Lys Gly Asn Ile Ile Gly Tyr Ser Gln Val Asp Lys Met			
395	400	405	410
gcc agt ctt tac aac atc cac ctg cga act ggc tgc ttc tgt aac act			1299
Ala Ser Leu Tyr Asn Ile His Leu Arg Thr Gly Cys Phe Cys Asn Thr			
415	420	425	
ggg gcc tgc cag agg cac ctg ggc ata agc aac gag atg gtc agg aag			1347
Gly Ala Cys Gln Arg His Leu Gly Ile Ser Asn Glu Met Val Arg Lys			
430	435	440	
cat ttt cag gct ggt cat gtc tgt ggg gac aat atg gac ctc ata gat			1395
His Phe Gln Ala Gly His Val Cys Gly Asp Asn Met Asp Leu Ile Asp			
445	450	455	
ggg cag ccc aca gga tct gtg agg att tca ttt gga tac atg tcg acg			1443
Gly Gln Pro Thr Gly Ser Val Arg Ile Ser Phe Gly Tyr Met Ser Thr			
460	465	470	
ctg gat gat gtc cag gcc ttt ctt agg ttc atc ata gac act cgc ctg			1491
Leu Asp Asp Val Gln Ala Phe Leu Arg Phe Ile Ile Asp Thr Arg Leu			
475	480	485	490
cac tca tca ggg gac tgg cct gtc cct cag gcc cat gct gac acc ggg			1539
His Ser Ser Gly Asp Trp Pro Val Pro Gln Ala His Ala Asp Thr Gly			
495	500	505	

gag act gga gcc cca tca gca gac agc cag gct gat gtt ata cct gct	1587
Glu Thr Gly Ala Pro Ser Ala Asp Ser Gln Ala Asp Val Ile Pro Ala	
510 515 520	
gtc atg ggc aga cgt agc ctc tcg cct cag gaa gat gcc ctc aca ggc	1635
Val Met Gly Arg Arg Ser Leu Ser Pro Gln Glu Asp Ala Leu Thr Gly	
525 530 535	
tcc agg gtt tgg aac aac tcg tct act gtg aat gct gtg cct gtg gcc	1683
Ser Arg Val Trp Asn Asn Ser Ser Thr Val Asn Ala Val Pro Val Ala	
540 545 550	
cca cct gtg tgt gat gtc gcc aga acc cag ccg act cct tca gag aaa	1731
Pro Pro Val Cys Asp Val Ala Arg Thr Gln Pro Thr Pro Ser Glu Lys	
555 560 565 570	
gct gca gga gtc ctg gag ggg gcc ctt ggg cca cat gtt gtc act aac	1779
Ala Ala Gly Val Leu Glu Gly Ala Leu Gly Pro His Val Val Thr Asn	
575 580 585	
ctt tat ctc tat cca atc aaa tcc tgt gct gca ttt gag gtg acc agg	1827
Leu Tyr Leu Tyr Pro Ile Lys Ser Cys Ala Ala Phe Glu Val Thr Arg	
590 595 600	
tgg cct gta gga aac caa ggg ctg cta tat gac cgg agc tgg atg gtt	1875
Trp Pro Val Gly Asn Gln Gly Leu Leu Tyr Asp Arg Ser Trp Met Val	
605 610 615	
gtg aat cac aat ggt gtt tgc ctg agt cag aag cag gaa ccc cgg ctc	1923
Val Asn His Asn Gly Val Cys Leu Ser Gln Lys Gln Glu Pro Arg Leu	
620 625 630	
tgc ctg atc cag ccc ttc atc gac ttg cgg caa agg atc atg gtc atc	1971
Cys Leu Ile Gln Pro Phe Ile Asp Leu Arg Gln Arg Ile Met Val Ile	
635 640 645 650	
aaa gcc aaa ggg atg gag cct ata gag gtg cct ctt gag gaa aat agt	2019
Lys Ala Lys Gly Met Glu Pro Ile Glu Val Pro Leu Glu Glu Asn Ser	
655 660 665	
gaa cgg act cag att cgc caa agc agg gtc tgt gct gac aga gta agt	2067
Glu Arg Thr Gln Ile Arg Gln Ser Arg Val Cys Ala Asp Arg Val Ser	
670 675 680	
act tat gat tgt gga gaa aaa att tca agc tgg ttg tca aca ttt ttt	2115
Thr Tyr Asp Cys Gly Glu Lys Ile Ser Ser Trp Leu Ser Thr Phe Phe	
685 690 695	
ggc cgt cct tgt aat ttg atc aaa caa agt tca aac tct caa agg aat	2163
Gly Arg Pro Cys Asn Leu Ile Lys Gln Ser Ser Asn Ser Gln Arg Asn	
700 705 710	
gca aag aag aaa cat gga aaa gat caa ctt cct ggt aca atg gcc acc	2211
Ala Lys Lys Lys His Gly Lys Asp Gln Leu Pro Gly Thr Met Ala Thr	
715 720 725 730	

ctt tct ctg gtg aat gag gca cag tat ctg ctg atc aac aca tcc agt	2259
Leu Ser Leu Val Asn Glu Ala Gln Tyr Leu Leu Ile Asn Thr Ser Ser	
735 740 745	
att ttg gaa ctt cac cgg caa cta aac acc agt gat gag aat gga aag	2307
Ile Leu Glu Leu His Arg Gln Leu Asn Thr Ser Asp Glu Asn Gly Lys	
750 755 760	
gag gaa tta ttc tca ctg aag gat ctc agc ttg cgt ttt cgt gcc aat	2355
Glu Glu Leu Phe Ser Leu Lys Asp Leu Ser Leu Arg Phe Arg Ala Asn	
765 770 775	
att att atc aat gga aaa agg gct ttt gaa gaa gag aaa tgg gat gag	2403
Ile Ile Ile Asn Gly Lys Arg Ala Phe Glu Glu Glu Lys Trp Asp Glu	
780 785 790	
att tca att ggc tct ttg cgt ttc cag gtt ttg ggg cct tgt cac aga	2451
Ile Ser Ile Gly Ser Leu Arg Phe Gln Val Leu Gly Pro Cys His Arg	
795 800 805 810	
tgc cag atg att tgc atc gac cag caa act ggg caa cga aac cag cat	2499
Cys Gln Met Ile Cys Ile Asp Gln Gln Thr Gly Gln Arg Asn Gln His	
815 820 825	
gtt ttc caa aaa ctt tct gag agt cgt gaa aca aag gtg aac ttt ggc	2547
Val Phe Gln Lys Leu Ser Glu Ser Arg Glu Thr Lys Val Asn Phe Gly	
830 835 840	
atg tac ctg atg cat gca tca ttg gat tta tcc tcc cca tgt ttc ctg	2595
Met Tyr Leu Met His Ala Ser Leu Asp Leu Ser Ser Pro Cys Phe Leu	
845 850 855	
tct gta gga tct cag gtg ctc cct gtg ttg aaa gag aat gtg gaa ggt	2643
Ser Val Gly Ser Gln Val Leu Pro Val Leu Lys Glu Asn Val Glu Gly	
860 865 870	
cat gat tta cct gca tct gag aaa cac cag gat gtt acc tcc taa aaa	2691
His Asp Leu Pro Ala Ser Glu Lys His Gln Asp Val Thr Ser *	
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ctgtgaggtg tgcgaagccc cagccgagcg ggtgtgcgcg gcctgcacag tcacttatta 180
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ctgagatctg gcatgcatat ttgaacaatc actatcaagt cctctcacag gctcacatcc 540
aaciaa atg gat tta ctg ggc aaa cta ttt gag aat gac act ggc ttg 587
Met Asp Leu Leu Gly Lys Leu Phe Glu Asn Asp Thr Gly Leu
1 5 10
gat gaa gcc caa gaa gca gaa gcc att cgc atc ctg act tca atc ttg 635
Asp Glu Ala Gln Glu Ala Glu Ala Ile Arg Ile Leu Thr Ser Ile Leu
15 20 25 30
aac att cga gaa tct aca tct gac aaa gcc ccc caa aaa acc atc ttt 683
Asn Ile Arg Glu Ser Thr Ser Asp Lys Ala Pro Gln Lys Thr Ile Phe
35 40 45
gtt ctg aag atc ctg gtc atg ctt tac tac ctg atg atg aat tct tca 731
Val Leu Lys Ile Leu Val Met Leu Tyr Tyr Leu Met Met Asn Ser Ser
50 55 60
aag gca cag gaa tat ggc atg agg gcc ctc agt cta gcc aaa gaa caa 779
Lys Ala Gln Glu Tyr Gly Met Arg Ala Leu Ser Leu Ala Lys Glu Gln
65 70 75
cag ctt gat gtc cat gag caa agc acc att caa gag tta tta agt ctc 827
Gln Leu Asp Val His Glu Gln Ser Thr Ile Gln Glu Leu Leu Ser Leu
80 85 90
att tca act gaa gac cat ccc att act tag t gacccatgag ctctgcatca 878
Ile Ser Thr Glu Asp His Pro Ile Thr *
95 100
agggttattc caggggctac tgaagatcta atatattcca gccttgacaca actgctttga 938
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tttttttctt acacagcata ttaaggggaat ataaagcttt aggcatagaa atcactaaaa 1058
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gtagtcagat cactaatatg gtatttgtaa ttaaactaca aatagtttgt catttcccag 1178
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cccagtgaga gcggctttcc aggacggtgc gatgtgctgc gcagcgaaga ggcaggaggc      180
cggttctctg gggtagcggg acaggcgggc gcttactctg tgcgcttgct tccccaaccc      240
tgcaccggcc   atg cgc ccg gcc ttg gcg gtg ggc ctg gtg ttc gca ggc      289
              Met Arg Pro Ala Leu Ala Val Gly Leu Val Phe Ala Gly
              1               5               10

tgc tgc agt aac gtg atc ttc cta gag ctc ctg gcc cgg aag cat cca      337
Cys Cys Ser Asn Val Ile Phe Leu Glu Leu Leu Ala Arg Lys His Pro
              15               20               25

gga tgt ggg aac att gtg aca ttt gca caa ttt tta ttt att gct gtg      385
Gly Cys Gly Asn Ile Val Thr Phe Ala Gln Phe Leu Phe Ile Ala Val
              30               35               40               45

gaa ggc ttc ctc ttt gaa gct gat ttg gga agg aag cca cca gct atc      433
Glu Gly Phe Leu Phe Glu Ala Asp Leu Gly Arg Lys Pro Pro Ala Ile
              50               55               60

cca ata agg tac tat gcc ata atg gtg acc atg ttc ttc acc gtg agc      481
Pro Ile Arg Tyr Tyr Ala Ile Met Val Thr Met Phe Phe Thr Val Ser
              65               70               75

gtg gtg aac aac tat gcc ctg aat ctc aac att gcc atg ccc ctg cat      529
Val Val Asn Asn Tyr Ala Leu Asn Leu Asn Ile Ala Met Pro Leu His
              80               85               90

atg ata ttt aga tcc ggt tct cta att gcc aac acg att cta gga att      577
Met Ile Phe Arg Ser Gly Ser Leu Ile Ala Asn Thr Ile Leu Gly Ile
              95               100              105

atc att ttg aag aaa aga tac agt ata ttc aaa tat acc tcc att gcc      625
Ile Ile Leu Lys Lys Arg Tyr Ser Ile Phe Lys Tyr Thr Ser Ile Ala
              110              115              120              125

ctg gtg tct gtg ggg ata ttt att tgc act ttt atg tca gca aag cag      673
Leu Val Ser Val Gly Ile Phe Ile Cys Thr Phe Met Ser Ala Lys Gln
              130              135              140

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gtg act tcc cag tcc agc ttg agt gag aat gat gga ttc cag gca ttt	721
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gtg tgg tgg tta cta ggt att ggg gca ttg act ttt gct ctt ctg atg	769
Val Trp Trp Leu Leu Gly Ile Gly Ala Leu Thr Phe Ala Leu Leu Met	
160 165 170	
tca gca agg atg ggg ata ttc caa gag act ctc tac aaa cga ttt ggg	817
Ser Ala Arg Met Gly Ile Phe Gln Glu Thr Leu Tyr Lys Arg Phe Gly	
175 180 185	
aaa cac tcc aag gag gct ttg ttt tat aat cac gcc ctt cca ctt ccg	865
Lys His Ser Lys Glu Ala Leu Phe Tyr Asn His Ala Leu Pro Leu Pro	
190 195 200 205	
ggg ttc gtc ttc ttg gct tct gat att tat gac cat gca gtt cta ttc	913
Gly Phe Val Phe Leu Ala Ser Asp Ile Tyr Asp His Ala Val Leu Phe	
210 215 220	
aat aag tct gag tta tat gaa att ccc gtc atc gga gtg acc ctg ccc	961
Asn Lys Ser Glu Leu Tyr Glu Ile Pro Val Ile Gly Val Thr Leu Pro	
225 230 235	
atc atg tgg ttc tac ctc ctc atg aac atc atc act cag tac gtg tgc	1009
Ile Met Trp Phe Tyr Leu Leu Met Asn Ile Ile Thr Gln Tyr Val Cys	
240 245 250	
atc cgg ggt gtg ttt atc ctc acc aca gaa tgc gcc tcc ctc acc gtc	1057
Ile Arg Gly Val Phe Ile Leu Thr Thr Glu Cys Ala Ser Leu Thr Val	
255 260 265	
acg ctc gtc gtg acc cta cgc aaa ttt gtg agc ctc atc ttt tcc atc	1105
Thr Leu Val Val Thr Leu Arg Lys Phe Val Ser Leu Ile Phe Ser Ile	
270 275 280 285	
ttg tac ttc cag aac ccc ttc acc ctg tgg cac tgg ctg ggc acc ttg	1153
Leu Tyr Phe Gln Asn Pro Phe Thr Leu Trp His Trp Leu Gly Thr Leu	
290 295 300	
ttt gtc ttc att ggg acc tta atg tac aca gag gtg tgg aac aac cta	1201
Phe Val Phe Ile Gly Thr Leu Met Tyr Thr Glu Val Trp Asn Asn Leu	
305 310 315	
ggg acc aca aaa agt gag cct cag aag gac agc aag aag aac tga ggc	1249
Gly Thr Thr Lys Ser Glu Pro Gln Lys Asp Ser Lys Lys Asn *	
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aggaagaaga cgcagaagca ggacgaccct gaaagattca gcctcttcat cctcaaacag      180
gtcgcttctc gggagttctt ggtgttgaa tattttacag caaagcagtc gaccaggcct      240
cctcttccca cctgtccagc agcatgaaag cagcatgatt ggccgaccgc aggagaagcc      300
cccagaacca ggcccccaac tcagccatct gcggaggcca aggtgtgagc gacgtctcct      360
caccacagtg ctgtgtggtc tatacctcag ccaggagag gatgtgaaac cccccgcct      420
gcacatgagt ggtacaggcc aacaggaaca cctggctcca gccacgttca cagacatgtc      480
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atgggtgacc agcaactgta caagaccaac catgtggccc atggtagtga gaaccttttc      660
taccaacagc caccacttgg cgtccacagc gggctgagcc cactgatggc taccaatata      720
cctactccca ggccagcgag atccggaccc agaagcttac cagcgggtgtc ttacacaagc      780

tggaactcttt caccaggtg tttgccaaac aaaacctgcy aattcagggtc aacaat      836
atg gcc cag gtg ctg cac act cag tca gca gtg atg gat gga gcc cct      884
Met Ala Gln Val Leu His Thr Gln Ser Ala Val Met Asp Gly Ala Pro
   1             5             10            15

gac agt gct ctg cgc cag ctg ctg tct cag aag ccc atg gag ccc cca      932
Asp Ser Ala Leu Arg Gln Leu Leu Ser Gln Lys Pro Met Glu Pro Pro
           20             25             30

gca ccg gct atc cct tcc cgc tac cag cag gtg ccc cag cag cct cac      980
Ala Pro Ala Ile Pro Ser Arg Tyr Gln Gln Val Pro Gln Gln Pro His
           35             40             45

cct ggt ttc act ggt ggg ctg tcc aaa cca gct ctt cag gtc ggg cag      1028
Pro Gly Phe Thr Gly Gly Leu Ser Lys Pro Ala Leu Gln Val Gly Gln
           50             55             60

cac cct acc caa ggg cac ctg tat tat gac tac cag cag cct ctg gct      1076
His Pro Thr Gln Gly His Leu Tyr Tyr Asp Tyr Gln Gln Pro Leu Ala
           65             70             75             80

cag gtg cca gtg cag gga gga cag cca ctg cag gcc cca cag atg ctg      1124
Gln Val Pro Val Gln Gly Gly Gln Pro Leu Gln Ala Pro Gln Met Leu
           85             90             95
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tca Ser	cag Gln	cac His	atg Met 100	caa Gln	cag Gln	atg Met	cag Gln	cag Gln	cac His	cag Gln	tat Tyr	tac Tyr	cca Pro 110	ccg Pro	cag Gln	1172
caa Gln	cag Gln	cag Gln 115	caa Gln	gcc Ala	ggg Gly	caa Gln	cag Gln	cgt Arg	atc Ile	tcc Ser	atg Met	caa Gln 125	gaa Glu	ata Ile	cag Gln	1220
acg Thr	cag Gln 130	ccg Pro	caa Gln	caa Gln	att Ile	cgc Arg	cca Pro	tca Ser	cag Gln	cca Pro	cag Gln	ccg Pro	ccg Pro	cca Pro	cag Gln	1268
cag Gln 145	cag Gln	cag Gln	ccg Pro	cag Gln	cag Gln	cta Leu	cag Gln	ctg Leu	cag Gln	cag Gln	cgg Arg	cag Gln	ggt Gly	tca Ser	atg Met 160	1316
cag Gln	ata Ile	cct Pro	cag Gln	tat Tyr 165	tat Tyr	cag Gln	ccc Pro	caa Gln	ccc Pro	atg Met	atg Met	cag Gln	cac His 175	ttg Leu	caa Gln	1364
gag Glu	cag Gln	cag Gln	cag Gln 180	caa Gln	cag Gln	atg Met	cac His	ctg Leu	cag Gln	cct Pro	cct Pro	tct Ser	tat Tyr 190	cac His	agg Arg	1412
gac Asp	cct Pro	cac His 195	cag Gln	tat Tyr	acc Thr	cca Pro	gag Glu	cag Gln	gca Ala	cac His	act Thr	gtc Val	cag Gln	ctg Leu	att Ile	1460
ccc Pro	ctg Leu 210	ggc Gly	tcc Ser	atg Met	tcc Ser	cag Gln	tac Tyr	tac Tyr	tac Tyr	cag Gln	gag Glu	ccc Pro	cag Gln	cag Gln	ccc Pro	1508
tac Tyr 225	agc Ser	cac His	ccc Pro	ctc Leu	tac Tyr 230	cag Gln	cag Gln	agc Ser	cac His	ctg Leu	tcc Ser	cag Gln	cac His	cag Gln	cag Gln 240	1556
cgt Arg	gag Glu	gac Asp	agt Ser	cag Gln 245	ctg Leu	aag Lys	acc Thr	tac Tyr	tct Ser	agt Ser	gac Asp	aga Arg	cag Gln	gcc Ala 255	cag Gln	1604
gcc Ala	atg Met	ctg Leu	agc Ser	tcc Ser	cat His	ggg Gly	gac Asp	ctg Leu	ggg Gly	cct Pro	cct Pro	gac Asp	aca Thr	gga Gly	atg Met	1652
gga Gly	gac Asp	cca Pro	gcg Ala	agc Ser	tca Ser	gat Asp	ctg Leu	acc Thr	cgg Arg	gtc Val	agc Ser	agc Ser	acc Thr	ctc Leu	ccc Pro	1700
cat His	cgc Arg 290	ccc Pro	ctc Leu	cta Leu	tcc Ser	ccc Pro	agt Ser	ggg Gly	atc Ile	cac His	ctc Leu	aac Asn	aac Asn	atg Met	ggg Gly	1748
cct Pro 305	cag Gln	cat His	cag Gln	cag Gln	ctg Leu	tct Ser	ccc Pro	agt Ser	gcc Ala	atg Met	tgg Trp	ccc Pro	cag Gln	atg Met	cac His 320	1796

cta cct gat ggg aga gcc cag cca ggg tcc cct gag tca agt ggc caa	1844
Leu Pro Asp Gly Arg Ala Gln Pro Gly Ser Pro Glu Ser Ser Gly Gln	
325 330 335	
ccc aaa gga gcg ttt ggg gag cag ttt gat gcc aag aac aag ctg aca	1892
Pro Lys Gly Ala Phe Gly Glu Gln Phe Asp Ala Lys Asn Lys Leu Thr	
340 345 350	
tgc tcc atc tgc ctg aag gag ttc aag aac ctg cct gcc ctg aat ggc	1940
Cys Ser Ile Cys Leu Lys Glu Phe Lys Asn Leu Pro Ala Leu Asn Gly	
355 360 365	
cac atg cgg tcc cac ggg gga atg agg gcc tcc ccc aac ctc aaa cag	1988
His Met Arg Ser His Gly Gly Met Arg Ala Ser Pro Asn Leu Lys Gln	
370 375 380	
gaa atc ccc agg aag cat cag ccg agt gtg ccc aaa gcc gag gag ccc	2036
Glu Ile Pro Arg Lys His Gln Pro Ser Val Pro Lys Ala Glu Glu Pro	
385 390 395 400	
ctc aag acc gtg cag gag aag aaa aag ttc cgg cac cgg tcg gaa cct	2084
Leu Lys Thr Val Gln Glu Lys Lys Lys Phe Arg His Arg Ser Glu Pro	
405 410 415	
ctc ttc atc ccg ccg ccg ccc tcc tac aac ccg aac ccc gct gcc tcc	2132
Leu Phe Ile Pro Pro Pro Pro Ser Tyr Asn Pro Asn Pro Ala Ala Ser	
420 425 430	
tac tcg ggc gcc acc ctg tac cag agc cag ctg cgc tcc ccg cgc gtc	2180
Tyr Ser Gly Ala Thr Leu Tyr Gln Ser Gln Leu Arg Ser Pro Arg Val	
435 440 445	
ctc ggg gac cac ctg ctc ctg gac ccc acc cac gag ctg ccc cct tac	2228
Leu Gly Asp His Leu Leu Leu Asp Pro Thr His Glu Leu Pro Pro Tyr	
450 455 460	
acg ccc cca ccc atg ctg agc ccg gtg cgc cag ggc tcg ggg ctc ttc	2276
Thr Pro Pro Pro Met Leu Ser Pro Val Arg Gln Gly Ser Gly Leu Phe	
465 470 475 480	
agc aat gtc ctc atc tcc ggc cac ggc cct ggc gcc cac ccg cag ctg	2324
Ser Asn Val Leu Ile Ser Gly His Gly Pro Gly Ala His Pro Gln Leu	
485 490 495	
ccc ctg acg ccc ctg acg ccc aca cca cgg gtg ctg ctg tgt cgc tcc	2372
Pro Leu Thr Pro Leu Thr Pro Thr Pro Arg Val Leu Leu Cys Arg Ser	
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Asn Ser Ile Asp Gly Ser Asn Val Thr Val Thr Pro Gly Pro Gly Glu	
515 520 525	
cag act gta gat gtt gaa cca cgc atc aac att ggc ttg aga ttc caa	2468
Gln Thr Val Asp Val Glu Pro Arg Ile Asn Ile Gly Leu Arg Phe Gln	
530 535 540	
gca gaa atc cct gaa ctc caa gat atc tct gcc ctg gcc cag gac aca	2516

Ala Glu Ile Pro Glu Leu Gln Asp Ile Ser Ala Leu Ala Gln Asp Thr	545	550	555	560	
cac aag gcc aca ctg gta tgg aag ccc tgg cca gaa cta gaa aac cat	2564				
His Lys Ala Thr Leu Val Trp Lys Pro Trp Pro Glu Leu Glu Asn His		565	570	575	
gac ctc cag caa aga gtg gag aat ctt ctg aat ttg tgc tgt tcc agt	2612				
Asp Leu Gln Gln Arg Val Glu Asn Leu Leu Asn Leu Cys Cys Ser Ser		580	585	590	
gca ttg cca ggt gga ggg acc aat tct gaa ttt gct ttg cac tct ctg	2660				
Ala Leu Pro Gly Gly Gly Thr Asn Ser Glu Phe Ala Leu His Ser Leu		595	600	605	
ttt gag gcc aaa ggt gat gtg atg gtt gct ctg gaa atg ctg cta ctg	2708				
Phe Glu Ala Lys Gly Asp Val Met Val Ala Leu Glu Met Leu Leu Leu		610	615	620	
cgg aag cct gtc agg tta aaa tgt cat cct tta gca aat tac cac tat	2756				
Arg Lys Pro Val Arg Leu Lys Cys His Pro Leu Ala Asn Tyr His Tyr		625	630	635	640
gcc ggt tgc gac aag tgg acc tcc cta gaa aga aaa ctg ttt aac aaa	2804				
Ala Gly Ser Asp Lys Trp Thr Ser Leu Glu Arg Lys Leu Phe Asn Lys		645	650	655	
gca cta gcc act tac agc aaa gac ttt att ttt gta cag aag atg gtg	2852				
Ala Leu Ala Thr Tyr Ser Lys Asp Phe Ile Phe Val Gln Lys Met Val		660	665	670	
aag tcc aag acg gtg gct cag tgc gtg gag tac tac tac acg tgg aaa	2900				
Lys Ser Lys Thr Val Ala Gln Cys Val Glu Tyr Tyr Tyr Thr Trp Lys		675	680	685	
aag atc atg cgg ctg ggg cgg aaa cac cgg aca cgc ctg gca gaa atc	2948				
Lys Ile Met Arg Leu Gly Arg Lys His Arg Thr Arg Leu Ala Glu Ile		690	695	700	
atc gac gat tgt gtg aca agt gaa gaa gaa gaa gag tta gag gag gag	2996				
Ile Asp Asp Cys Val Thr Ser Glu Glu Glu Glu Glu Leu Glu Glu Glu		705	710	715	720
gag gag gag gac ccg gaa gaa gat agg aaa tcc aca aaa gaa gaa gag	3044				
Glu Glu Glu Asp Pro Glu Glu Asp Arg Lys Ser Thr Lys Glu Glu Glu		725	730	735	
agt gag gtg ccg aag tcc ccg gag cca cca ccc gtc ccc gtc ctg gct	3092				
Ser Glu Val Pro Lys Ser Pro Glu Pro Pro Pro Val Pro Val Leu Ala		740	745	750	
ccc acg gag ggg ccg ccc ctg cag gcc ctg ggc cag ccc tca ggc tcc	3140				
Pro Thr Glu Gly Pro Pro Leu Gln Ala Leu Gly Gln Pro Ser Gly Ser		755	760	765	
ttc atc tgt gaa atg ccc aac tgt ggg gct gac tgt aga tgt cat gtc	3188				
Phe Ile Cys Glu Met Pro Asn Cys Gly Ala Asp Cys Arg Cys His Val					

770	775	780	
act ccc ttt ctt ccc cag gtg ttc agc tcc cga cag gca ctg aat ggc			3236
Thr Pro Phe Leu Pro Gln Val Phe Ser Ser Arg Gln Ala Leu Asn Gly			
785	790	795 800	
cat gcc cgc atc cac ggg ggc acc aac cag gtg acc aag gcc cga ggt			3284
His Ala Arg Ile His Gly Gly Thr Asn Gln Val Thr Lys Ala Arg Gly			
	805	810 815	
gcc atc ccc tct ggg aag cag aag cct ggt ggc acc cag agt ggg tac			3332
Ala Ile Pro Ser Gly Lys Gln Lys Pro Gly Gly Thr Gln Ser Gly Tyr			
	820	825 830	
tgt tcg gta aag agc tca ccc tct cac agc acc acc agc ggc gag aca			3380
Cys Ser Val Lys Ser Ser Pro Ser His Ser Thr Thr Ser Gly Glu Thr			
	835	840 845	
gac ccc acc acc atc ttc ccc tgc aag gag tgt ggc aaa gtc ttc ttc			3428
Asp Pro Thr Thr Ile Phe Pro Cys Lys Glu Cys Gly Lys Val Phe Phe			
	850	855 860	
aag atc aaa agc cga aat gca cac atg aaa act cac atg cag cag gag			3476
Lys Ile Lys Ser Arg Asn Ala His Met Lys Thr His Met Gln Gln Glu			
	865	870 875 880	
gaa caa cag agg caa aag gct cag aag gcg gct ttt gca gct gag atg			3524
Glu Gln Gln Arg Gln Lys Ala Gln Lys Ala Ala Phe Ala Ala Glu Met			
	885	890 895	
gca gcc acg att gag agg act acg ggg ccc gtg ggg gcg ccg ggg ctg			3572
Ala Ala Thr Ile Glu Arg Thr Thr Gly Pro Val Gly Ala Pro Gly Leu			
	900	905 910	
ctg ccc ctg gac cag ctg agt ctg atc aaa ccc atc aag gat gtg gac			3620
Leu Pro Leu Asp Gln Leu Ser Leu Ile Lys Pro Ile Lys Asp Val Asp			
	915	920 925	
atc ctc gac gac gac gtc gtc cag cag ttg gga ggt gtc atg gaa gag			3668
Ile Leu Asp Asp Asp Val Val Gln Gln Leu Gly Gly Val Met Glu Glu			
	930	935 940	
gct gaa gtt gtg gac acc gat ctt ctc ttg gat gat caa gat tca gtc			3716
Ala Glu Val Val Asp Thr Asp Leu Leu Leu Asp Asp Gln Asp Ser Val			
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Leu Leu Gln Gly Asp Ala Glu Leu *			
	965		
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aacccttttta aactacctgt tttaaaagtg gtcattttat tcaggtttag aaaaaaaaaat			3888
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atg gcc cag gtg ctg cac act cag tca gca gtg atg gat gga gcc cct      884
Met Ala Gln Val Leu His Thr Gln Ser Ala Val Met Asp Gly Ala Pro
  1             5             10             15

gac agt gct ctc cgc cag ctg ctg tct cag aag ccc atg gag ccc cca      932
Asp Ser Ala Leu Arg Gln Leu Leu Ser Gln Lys Pro Met Glu Pro Pro
          20             25             30

gca ccg gct atc cct tcc cgc tac cag cag gtg ccc cag cag cct cac      980
Ala Pro Ala Ile Pro Ser Arg Tyr Gln Gln Val Pro Gln Gln Pro His
          35             40             45

cct ggt ttc act ggt ggg ctg tcc aaa cca gct ctt cag gtc ggg cag      1028
Pro Gly Phe Thr Gly Gly Leu Ser Lys Pro Ala Leu Gln Val Gly Gln
  50             55             60

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tca cag cac atg caa cag atg cag cag cac cag tat tac cca ccg cag Ser Gln His Met Gln Gln Met Gln Gln His Gln Tyr Tyr Pro Pro Gln 100 105 110	1172
caa cag cag caa gcc ggg caa cag cgt atc tcc atg caa gaa ata cag Gln Gln Gln Gln Ala Gly Gln Gln Arg Ile Ser Met Gln Glu Ile Gln 115 120 125	1220
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cta Leu	cct Pro	gat Asp	ggg Gly	aga Arg 325	gcc Ala	cag Gln	cca Pro	ggg Gly	tcc Ser 330	cct Pro	gag Glu	tca Ser	agt Ser	ggc Gly 335	caa Gln	1844
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Gln Ser Gly Tyr Cys Ser Val Lys Ser Ser Pro Ser His Ser Thr Thr	
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Gln Asp Ser Val Leu Leu Gln Gly Asp Ala Glu Leu *	
945 950 955	
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ccttgacgca ctgctggacc aggtttacaag atgttcacct aagattgaga cctagtgact 180
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tatgggtgcta aaagaactcc ttacctttct ctgactacaa tttatttgga catacttttg 300
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aggatc atg gac cat cct agt agg gaa aag gat gaa aga caa cgg aca 408
Met Asp His Pro Ser Arg Glu Lys Asp Glu Arg Gln Arg Thr
1 5 10
act aaa ccc atg gca caa agg agt gca cac tgc tct cga cca tct ggc 456
Thr Lys Pro Met Ala Gln Arg Ser Ala His Cys Ser Arg Pro Ser Gly

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ggc aag aag ata gga tgt ggg aac ttc gga gag ctc aga tta ggt gaa	Gly Lys Lys Ile Gly Cys Gly Asn Phe Gly Glu Leu Arg Leu Gly Glu	552		
	50 55 60			
ggt ctc cca cag gtg tat tac ttt gga cca tgt ggg aaa tat aat gcc	Gly Leu Pro Gln Val Tyr Tyr Phe Gly Pro Cys Gly Lys Tyr Asn Ala	600		
	65 70 75			
atg gtg ctg gag ctc ctt ggc cct agc ttg gag gac ttg ttt gac ctc	Met Val Leu Glu Leu Leu Gly Pro Ser Leu Glu Asp Leu Phe Asp Leu	648		
	80 85 90			
tgt gac cga aca ttt act ttg aag acg gtg tta atg ata gcc atc cag	Cys Asp Arg Thr Phe Thr Leu Lys Thr Val Leu Met Ile Ala Ile Gln	696		
	95 100 105 110			
ctg ctt tct cga atg gaa tac gtg cac tca aag aac ctc att tac cga	Leu Leu Ser Arg Met Glu Tyr Val His Ser Lys Asn Leu Ile Tyr Arg	744		
	115 120 125			
gat gtc aag cca gag aac ttc ctg att ggt cga caa ggc aat aag aaa	Asp Val Lys Pro Glu Asn Phe Leu Ile Gly Arg Gln Gly Asn Lys Lys	792		
	130 135 140			
gag cat gtt ata cac att ata gac ttt gga ctg gcc aag gaa tac att	Glu His Val Ile His Ile Ile Asp Phe Gly Leu Ala Lys Glu Tyr Ile	840		
	145 150 155			
gac ccc gaa acc aaa aaa cac ata cct tat agg gaa cac aaa agt tta	Asp Pro Glu Thr Lys Lys His Ile Pro Tyr Arg Glu His Lys Ser Leu	888		
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	175 180 185 190			
caa agc cgg aga gat gat ttg gaa gcc cta ggc cat atg ttc atg tat	Gln Ser Arg Arg Asp Asp Leu Glu Ala Leu Gly His Met Phe Met Tyr	984		
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Tyr Val Arg Arg Leu Asp Phe Phe Glu Lys Pro Asp Tyr Glu Tyr Leu	
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cgg acc ctc ttc aca gac ctc ttt gaa aag aaa ggc tac acc ttt gac	1224
Arg Thr Leu Phe Thr Asp Leu Phe Glu Lys Lys Gly Tyr Thr Phe Asp	
275 280 285	
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Tyr Ala Tyr Asp Trp Val Gly Arg Pro Ile Pro Thr Pro Val Gly Ser	
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Val His Val Asp Ser Gly Ala Ser Ala Ile Thr Arg Glu Ser His Thr	
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His Arg Asp Arg Pro Ser Gln Gln Gln Pro Leu Arg Asn Gln Val Val	
320 325 330	
agc tca acc aat gga gag ctg aat gtt gat gat ccc acg gga gcc cac	1416
Ser Ser Thr Asn Gly Glu Leu Asn Val Asp Asp Pro Thr Gly Ala His	
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Ser Asn Ala Pro Ile Thr Ala His Ala Glu Val Glu Val Val Glu Glu	
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gct aag tgc tgc tgt ttc ttt aag agg aaa agg aag aag act gct cag	1512
Ala Lys Cys Cys Cys Phe Phe Lys Arg Lys Arg Lys Lys Thr Ala Gln	
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Arg His Lys *	
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ttaattcca ccagcttgc agcc atg gcc cct gag cac gaa atc ccc aag 531
Met Ala Pro Glu His Glu Ile Pro Lys
1 5
att ggc tgg tac agc cgc ttt gct agg cat cct ttc tat ggc tct gca 579
Ile Gly Trp Tyr Ser Arg Phe Ala Arg His Pro Phe Tyr Gly Ser Ala
10 15 20 25
gga gtt aat tca gga gtc atg tta atg aat tta act cgg ata aga agt 627
Gly Val Asn Ser Gly Val Met Leu Met Asn Leu Thr Arg Ile Arg Ser
30 35 40
acc cag ttc aag aac agc atg att cca aca ggc ctg gct tgg gag gac 675
Thr Gln Phe Lys Asn Ser Met Ile Pro Thr Gly Leu Ala Trp Glu Asp
45 50 55
atg ttg tac cct ctg tac cag aag tac aag aat gcc atc acg tgg gga 723
Met Leu Tyr Pro Leu Tyr Gln Lys Tyr Lys Asn Ala Ile Thr Trp Gly
60 65 70
gac cag gat tta tta aat att att ttt tat ttc aac cca gag tgt ctc 771
Asp Gln Asp Leu Leu Asn Ile Ile Phe Tyr Phe Asn Pro Glu Cys Leu

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Tyr Val Phe Pro Cys Gln Trp Asn Tyr Arg Pro Asp His Cys Met Tyr			
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Gly Ser Asn Cys Arg Glu Ala Glu His Glu Gly Val Ser Val Leu His			
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Gly Asn Arg Gly Val Tyr His Asp Asp Lys Gln Pro Thr Phe Arg Ala			
125	130		135
ctc tat gaa gca ata cgg gat ttt ccc ttt caa gac aat ctc ttt caa			963
Leu Tyr Glu Ala Ile Arg Asp Phe Pro Phe Gln Asp Asn Leu Phe Gln			
140	145		150
tcc atg tat tac ccc ctt cag ctg aag ttt ttg gag act gtg cac act			1011
Ser Met Tyr Tyr Pro Leu Gln Leu Lys Phe Leu Glu Thr Val His Thr			
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Leu Cys Gly Arg Ile Pro Gln Val Phe Leu Lys Gln Ile Glu Lys Thr			
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Met Lys Arg Ala Tyr Glu Lys His Val Ile Ile His Val Gly Pro Asn			
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Gln Met His *			
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Gly Ile Ser Gly Lys Ser Gln Ile Leu Phe Ala Leu Val Phe Thr Thr		
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Arg Tyr Leu Asp Leu Phe Thr Asn Phe Ile Ser Ile Tyr Asn Thr Val		
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Met Lys Val Val Phe Leu Leu Cys Ala Tyr Val Thr Val Tyr Met Ile		
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Tyr Gly Lys Phe Arg Lys Thr Phe Asp Ser Glu Asn Asp Thr Phe Arg		
80 85 90		
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Glu Ser Val Ala Ile Leu Pro Gln Leu Phe Met Ile Ser Lys Thr Gly		
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Phe Tyr Asp Gln Ile Ala Val Val Ser Gly Val Val Gln Thr Ile Phe		
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Tyr Cys Asp Phe Phe Tyr Leu Tyr Val Thr Lys Val Leu Lys Gly Lys		
195 200 205		
aag tta agt ctt cca atg cca atc tga ggacc ttcagagaca gtctacgcct	795	
Lys Leu Ser Leu Pro Met Pro Ile *		
210 215		
taacaagcac atgaaggaaa ctattctgaa tgttctcttt ggcaacttat ccataatttg	855	

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ggatcaaatg ttaaaaccag aaaagtgttt agtgtggatt tcagcaaaac ctgatcatcc 915
caccagaag accttctcat caatagatcg cccttaaaga cccattgtaa ggtcataaaa 975
aacctcggcc aactgcacaa agatgggtgcc tctactgcaac aagaaacctt aaggtgtctt 1035
accgacgaaa taaaaaacat aaatgattgt tctccaaggc ctgagggcaa gactcatgat 1095
gagcaagtca accccaatct ggaacaatgt ccctcctctt agaatgtccc aactaaagac 1155
cagttaaaat attagggtag gttcttgtga atttcactt tccaggtaga tgaccaaatt 1215
taggtgggtca agatataaag gtgtcagcta gttttaagtg tgaaacttat ttcactttca 1275
cactgccttc aggccagaag caaaccaaat ttaccaggtt tggctggagg agttttgtga 1335
ctcatctttt actggtttga attttttcaa accagtggct gatacctgcc ttgtacttag 1395
taccttaata ccaataacct aatgggtactt aggcgagtac catttgcaca atcactgttt 1455
tacttatgag cagatacaga tatatccaaa cccttaccta ctaggtatcc tgctagggtt 1515
ttcaattcca attcttgtat taagtttttt cctttcagtt ttaggtgcga aagtaatcag 1575
tcaatccaat atcccccatc tttgtcttga aacaaaaact gttttaagac gtctacgttg 1635
aattattcag agaattaagc aataaaagct cacaccttat tgtcaaaaaa 1685

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<210> 190
<211> 716
<212> DNA
<213> Homo sapiens

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<220>
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<222> (151)..(636)

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accgggggcg gagacgtggc agccgcctcg cccgccagaa agtttcctag aagtttgctg 120
ggcgcggggcg cacgactgac tggctggacc          atg aac gtg ttc cga atc ctc 171
                                         Met Asn Val Phe Arg Ile Leu
                                         1                      5

ggc gac ctg agc cac ctc ctg gcc atg atc ttg ctg ctg ggg aag atc 219
Gly Asp Leu Ser His Leu Leu Ala Met Ile Leu Leu Leu Gly Lys Ile
      10                      15                      20

tgg agg tcc aag tgc tgc aag ggc atc tct ggg aag agc cag atc ctg 267
Trp Arg Ser Lys Cys Cys Lys Gly Ile Ser Gly Lys Ser Gln Ile Leu
      25                      30                      35

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ttt gct ctc gtc ttc acc acc agg tac ctg gac ctg ttc acc aac ttc      315
Phe Ala Leu Val Phe Thr Thr Arg Tyr Leu Asp Leu Phe Thr Asn Phe
 40                      45                      50                      55

atc tcc atc tac aac aca gta atg aag atc ctc tgg act ttc tct atc      363
Ile Ser Ile Tyr Asn Thr Val Met Lys Ile Leu Trp Thr Phe Ser Ile
                      60                      65                      70

tat ctg gaa tca gtg gct atc ctg ccc cag ctc ttc atg atc agc aag      411
Tyr Leu Glu Ser Val Ala Ile Leu Pro Gln Leu Phe Met Ile Ser Lys
                      75                      80                      85

act gga gag gct gag acc ata act act cac tac ctg ttc ttt ctg ggt      459
Thr Gly Glu Ala Glu Thr Ile Thr Thr His Tyr Leu Phe Phe Leu Gly
                      90                      95                      100

ctg tac cgg gca ctc tac ctg gct aac tgg atc aag cgg tac cag act      507
Leu Tyr Arg Ala Leu Tyr Leu Ala Asn Trp Ile Lys Arg Tyr Gln Thr
                      105                      110                      115

gag aat ttc tat gac caa att gca gtc ggg tct gga gta gta caa acc      555
Glu Asn Phe Tyr Asp Gln Ile Ala Val Gly Ser Gly Val Val Gln Thr
                      120                      125                      130                      135

atc ttc tac tgt gac ttc ttc tac ttg tat gtg acc aaa gtc ctt aag      603
Ile Phe Tyr Cys Asp Phe Phe Tyr Leu Tyr Val Thr Lys Val Leu Lys
                      140                      145                      150

gga aag aag tta agt ctt cca atg cca atc tga ggaccttc agagacagtc      654
Gly Lys Lys Leu Ser Leu Pro Met Pro Ile *
                      155                      160

tacgccttaa caagcacatg aaggaaacta ttttgaatgt tctctttggc aacttatcca      714

ta                                                                    716

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<210> 191
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (380)..(706)

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ttacaggcac ctgccaccat gccagctaa tttttatatt tttaagagat ggggggttcac      180
catgttggcc aggctggtct caaactcctg acctcaggcg atccgcccac cttggcctcc      240

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cag ttc atg cgt att cag aat gta ggc caa aag aaa gct gaa gag agt Gln Phe Met Arg Ile Gln Asn Val Gly Gln Lys Lys Ala Glu Glu Ser 215 220 225	727
cca gca gaa att atc atc cag gct att cct cag tat gct att cct tgt Pro Ala Glu Ile Ile Ile Gln Ala Ile Pro Gln Tyr Ala Ile Pro Cys 230 235 240	775
cac tcc agc tcc aat gtg gtg gtg gag ccc agt ggg ctt ctt gag cta His Ser Ser Ser Asn Val Val Val Glu Pro Ser Gly Leu Leu Glu Leu 245 250 255	823
aac aac ttc act agt caa cag ctg gat gat gag gag aca gca atg gag Asn Asn Phe Thr Ser Gln Gln Leu Asp Asp Glu Glu Thr Ala Met Glu 260 265 270 275	871
cag gac ata gac agt agc acg gag gat gga act gaa ccc agc cct tct Gln Asp Ile Asp Ser Ser Thr Glu Asp Gly Thr Glu Pro Ser Pro Ser 280 285 290	919
cag agc tct gct gaa cgg tcc tag tggtttggaca caatagtgca ctttaaaacc Gln Ser Ser Ala Glu Arg Ser *	973
295	
tgcttggtta ccaagtgtcc agggaaaccc ttgtattttg atgactaaaa agagcacttt	1033
gccccgtactt aggctgtgga ccctaaaaca gcagtgtttc aacaagatgt tgctgcagga	1093
gcagctttttt aaaacaagat aaaactcaca ggggaatgta ctttttttaa aaaaaaaaa	1152
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gagctcccat taggagccgc tggctgcggc agcaggggac tagcgtgaga gttggctaaa	180
aaaaagaaaa gaac atg gag gca gat ata atc aca aat ctt cga tgc agg Met Glu Ala Asp Ile Ile Thr Asn Leu Arg Cys Arg 1 5 10	230
ctc aaa gag gct gaa gaa gag cga cta aaa gct gca cag tat ggt tta Leu Lys Glu Ala Glu Glu Glu Arg Leu Lys Ala Ala Gln Tyr Gly Leu 15 20 25	278

caa cta gta gag agt caa aat gaa tta cag aat caa ttg gat aaa tgt	326
Gln Leu Val Glu Ser Gln Asn Glu Leu Gln Asn Gln Leu Asp Lys Cys	
30 35 40	
cg t aat gaa atg atg acc atg act gag agt tat gaa caa gaa aaa tat	374
Arg Asn Glu Met Met Thr Met Thr Glu Ser Tyr Glu Gln Glu Lys Tyr	
45 50 55 60	
acc ctt caa aga gaa gtt gaa ctc aag agt cga atg tta gaa agt ttg	422
Thr Leu Gln Arg Glu Val Glu Leu Lys Ser Arg Met Leu Glu Ser Leu	
65 70 75	
agc tgc gaa tgt gaa gct att aaa caa caa caa aaa atg cac ctg gag	470
Ser Cys Glu Cys Glu Ala Ile Lys Gln Gln Gln Lys Met His Leu Glu	
80 85 90	
aaa ttg gaa gaa caa cta agc aga agc cat gga cag gaa gtg aat gaa	518
Lys Leu Glu Glu Gln Leu Ser Arg Ser His Gly Gln Glu Val Asn Glu	
95 100 105	
cta aaa act aag ata gaa aaa ctg aaa gtg gaa tta gat gaa gcc agg	566
Leu Lys Thr Lys Ile Glu Lys Leu Lys Val Glu Leu Asp Glu Ala Arg	
110 115 120	
ctt agt gaa aag cag ctg aag cac caa gta gat cat cag aag gaa ctc	614
Leu Ser Glu Lys Gln Leu Lys His Gln Val Asp His Gln Lys Glu Leu	
125 130 135 140	
ctc tct tgt aaa tca gag gaa ctg cgc gta atg tct gaa cgt gtg cag	662
Leu Ser Cys Lys Ser Glu Glu Leu Arg Val Met Ser Glu Arg Val Gln	
145 150 155	
gaa agc atg tct tca gag atg ctg gct ctt caa att gag ctg aca gaa	710
Glu Ser Met Ser Ser Glu Met Leu Ala Leu Gln Ile Glu Leu Thr Glu	
160 165 170	
atg gag agt atg aag acc acc ctc aaa gaa gaa gtg aat gaa cta caa	758
Met Glu Ser Met Lys Thr Thr Leu Lys Glu Glu Val Asn Glu Leu Gln	
175 180 185	
tac aga caa gaa cag cta gaa ctt ctt att act aac cta atg cgc cag	806
Tyr Arg Gln Glu Gln Leu Glu Leu Leu Ile Thr Asn Leu Met Arg Gln	
190 195 200	
gta gac cgg ctt aaa gag gaa aaa gaa gag cga gag aaa gaa gca gtt	854
Val Asp Arg Leu Lys Glu Glu Lys Glu Glu Arg Glu Lys Glu Ala Val	
205 210 215 220	
tct tac tat aat gcc cta gag aaa gct cgt gta gca aat caa gat ctt	902
Ser Tyr Tyr Asn Ala Leu Glu Lys Ala Arg Val Ala Asn Gln Asp Leu	
225 230 235	
cag gta cag ttg gac cag gca ctc cag caa gcc ttg gat ccc aat agt	950
Gln Val Gln Leu Asp Gln Ala Leu Gln Gln Ala Leu Asp Pro Asn Ser	
240 245 250	
aaa ggc aac tct ttg ttt gca gag gtg gaa gat cga agg gca gca atg	998

Lys	Gly	Asn	Ser	Leu	Phe	Ala	Glu	Val	Glu	Asp	Arg	Arg	Ala	Ala	Met	
		255					260						265			
gaa	cgt	cag	ctt	atc	agt	atg	aaa	gtc	aag	tat	cag	tca	cta	aag	aag	1046
Glu	Arg	Gln	Leu	Ile	Ser	Met	Lys	Val	Lys	Tyr	Gln	Ser	Leu	Lys	Lys	
		270					275									
caa	aat	gta	ttt	aac	aga	gaa	cag	atg	cag	aga	atg	aag	tta	caa	att	1094
Gln	Asn	Val	Phe	Asn	Arg	Glu	Gln	Met	Gln	Arg	Met	Lys	Leu	Gln	Ile	
		285					290								300	
gcc	acg	ttg	cta	cag	atg	aaa	ggg	tct	caa	act	gaa	ttt	gag	cag	cag	1142
Ala	Thr	Leu	Leu	Gln	Met	Lys	Gly	Ser	Gln	Thr	Glu	Phe	Glu	Gln	Gln	
				305					310					315		
gaa	cgg	ttg	ctt	gcc	atg	ttg	gag	cag	aag	aat	ggt	gaa	ata	aaa	cat	1190
Glu	Arg	Leu	Leu	Ala	Met	Leu	Glu	Gln	Lys	Asn	Gly	Glu	Ile	Lys	His	
			320					325					330			
ctt	tta	ggt	gaa	att	aga	aat	ctg	gag	aaa	ttt	aag	aat	tta	tat	gac	1238
Leu	Leu	Gly	Glu	Ile	Arg	Asn	Leu	Glu	Lys	Phe	Lys	Asn	Leu	Tyr	Asp	
		335					340						345			
agt	atg	gaa	tcc	aag	cct	tca	gtc	gac	tct	ggt	act	ctg	gaa	gat	aac	1286
Ser	Met	Glu	Ser	Lys	Pro	Ser	Val	Asp	Ser	Gly	Thr	Leu	Glu	Asp	Asn	
		350					355					360				
acc	tat	tat	aca	gat	tta	ctt	cag	atg	aag	ctg	gat	aac	tta	aac	aaa	1334
Thr	Tyr	Tyr	Thr	Asp	Leu	Leu	Gln	Met	Lys	Leu	Asp	Asn	Leu	Asn	Lys	
		365				370				375					380	
gaa	att	gaa	agc	act	aaa	ggt	gaa	ttg	tcc	ata	cag	cga	atg	aaa	gca	1382
Glu	Ile	Glu	Ser	Thr	Lys	Gly	Glu	Leu	Ser	Ile	Gln	Arg	Met	Lys	Ala	
				385					390					395		
tta	ttt	gag	agc	cag	cgg	gct	cta	gat	att	gag	cga	aaa	ctt	ttt	tgc	1430
Leu	Phe	Glu	Ser	Gln	Arg	Ala	Leu	Asp	Ile	Glu	Arg	Lys	Leu	Phe	Cys	
			400					405						410		
aaa	tga	aagatgcctc	cagcttttcag	aaagtgaaaa	tatgaaactg	agagctaaac										1486
Lys	*															
tagatgaatt	gaaactaaaa	tatgaacctg	aagagacagt	tgaagtgcct	gtactgaaaa											1546
agaggcgtga	ggtgctccct	gtggatataa	ccaccgctaa	agatgcatgt	gtcaacaaca											1606
gtgctctcgg	gggagaagtt	tatcgattac	cgcctcagaa	agaggagaca	cagtctctgcc											1666
ctaacagttt	agaagataac	aacttgcaat	tagaaaaatc	agtttctata	cacacaccag											1726
tagtcagtct	ctctcctcac	aaaaatctgc	ccgtggatat	gcagctgaag	aaggaaaaga											1786
aatgtgtgaa	actcatagga	gttcccgtcg	acgctgaggc	cttaagtga	agaagtggaa											1846
acaccccaaa	ctctcccagg	ttagctgctg	aatcaaagct	tcaaacagaa	gttaaagaag											1906

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<210> 194
<211> 1042
<212> DNA
<213> Homo sapiens
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<221> CDS
<222> (528) .. (953)
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ttatggtata	tgcaaagcaa	ttaaaacagc	tcttgccaaa	gagtaaacac	catataaata		180
ttcattaaat	aacatacaaa	cataccaggt	tgggaaaaat	cagtaagcat	aggagtcagg		240
aaattccaag	ttggttatca	caactcttgg	cccacagggc	tttaatccag	gtgcccttgt		300
ctcctaccct	tgttgccatc	ccagtgtctc	cagggagtaa	gtagaaataa	agatcctatc		360
tcacctcttg	ggcattttcc	cctgccctga	aagcgtataa	tcgcttagca	cagtcggtgc		420
ttaagggggc	aggctccaaa	gaagattaaa	ggaacagttt	gtgggggtgca	ctgggcagca		480
gtactctcct	ctgagttcaa	tcatcttgca	ctctaagaat	caccacc	atg gcc ctt		536
					Met Ala Leu		

Met Ala Leu
1

gtg cca ggg aga agc aag gag gat ggg ctt tgg act aga aat agc cca	584
Val Pro Gly Arg Ser Lys Glu Asp Gly Leu Trp Thr Arg Asn Ser Pro	
5 10 15	
ggc tcc tcc cag cat cca gaa agt ccc agg ctg ccc aac cct ctc tgg	632
Gly Ser Ser Gln His Pro Glu Ser Pro Arg Leu Pro Asn Pro Leu Trp	
20 25 30 35	
gac aga gga aaa att ggc aag gtt gaa ggt cac cag cac att cag gtt	680
Asp Arg Gly Lys Ile Gly Lys Val Glu Gly His Gln His Ile Gln Val	
40 45 50	
agt act tcc tca gcc tgt gtc tgg cag ctg gct tac cct cca gtt tgg	728
Ser Thr Ser Ser Ala Cys Val Trp Gln Leu Ala Tyr Pro Pro Val Trp	
55 60 65	
ccc aac ctc cct gct gtc cct att cag gat ttc tct caa aag tcc cat	776
Pro Asn Leu Pro Ala Val Pro Ile Gln Asp Phe Ser Gln Lys Ser His	
70 75 80	
ctg ccg tct att gtg gtg gaa tcc agt gag gtg aat gaa gag agt ggg	824
Leu Pro Ser Ile Val Val Glu Ser Ser Glu Val Asn Glu Glu Ser Gly	
85 90 95	
gat ctc cat ttg ccc cat gag gag ctg ctg ctg ctc act gat ggt gag	872
Asp Leu His Leu Pro His Glu Glu Leu Leu Leu Leu Thr Asp Gly Glu	
100 105 110 115	
gaa gag gat gct gag gcc ttc ttc caa gac caa agt gaa gag cca ggt	920
Glu Glu Asp Ala Glu Ala Phe Phe Gln Asp Gln Ser Glu Glu Pro Gly	
120 125 130	
gag gga ggt ggc tca ttc agg ggg cca ctg tga gctgaatg ttctgggcag	971
Glu Gly Gly Gly Ser Phe Arg Gly Pro Leu *	
135 140	
agccaagatg gaagtcagtt acggcccctg cattcagcag taaaaggcac acagcaggtg	1031
ctcaataaat g	1042

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 <212> DNA
 <213> Homo sapiens

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 <222> (17)..(739)

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	1 5 10	

gtt ctg aat cta gtg acg tct gcc agg agc cag aag aca gaa cct cta	97
Val Leu Asn Leu Val Thr Ser Ala Arg Ser Gln Lys Thr Glu Pro Leu	
15 20 25	
agt ggc tct ggg gac cag cca ctc ttc cgt gga gct gat cga tat gac	145
Ser Gly Ser Gly Asp Gln Pro Leu Phe Arg Gly Ala Asp Arg Tyr Asp	
30 35 40	
ttt gcc atc atg ata cct cca gga ggc acg gaa tgc ttt tgg caa ttt	193
Phe Ala Ile Met Ile Pro Pro Gly Gly Thr Glu Cys Phe Trp Gln Phe	
45 50 55	
gcc cac cag act gga tac ttc tat ttc agt tac gag gtt cag cgg aca	241
Ala His Gln Thr Gly Tyr Phe Tyr Phe Ser Tyr Glu Val Gln Arg Thr	
60 65 70 75	
gtg ggg atg tca cat gac cgg cat gtt gct gcc acg gca cat aac cca	289
Val Gly Met Ser His Asp Arg His Val Ala Ala Thr Ala His Asn Pro	
80 85 90	
cag gga ttt ctc ata gac acc tcc cag ggt gtt cgg ggc cag att aac	337
Gln Gly Phe Leu Ile Asp Thr Ser Gln Gly Val Arg Gly Gln Ile Asn	
95 100 105	
ttc tct acc caa gag aca ggt ttt tat cag ctt tgt cta agt aat cag	385
Phe Ser Thr Gln Glu Thr Gly Phe Tyr Gln Leu Cys Leu Ser Asn Gln	
110 115 120	
cat aat cac ttc ggt tct gtg caa gtg tac ctc aac ttt ggg gtc ttc	433
His Asn His Phe Gly Ser Val Gln Val Tyr Leu Asn Phe Gly Val Phe	
125 130 135	
tat gag ggg cct gag act gat cac aaa cag aag gaa aga aaa caa ctg	481
Tyr Glu Gly Pro Glu Thr Asp His Lys Gln Lys Glu Arg Lys Gln Leu	
140 145 150 155	
aat gat act ctg gat gca att gag gac ggc aca caa aag gtg cag aac	529
Asn Asp Thr Leu Asp Ala Ile Glu Asp Gly Thr Gln Lys Val Gln Asn	
160 165 170	
aat atc ttt cac atg tgg cga tac tac aac ttt gcc cgg atg agg aaa	577
Asn Ile Phe His Met Trp Arg Tyr Tyr Asn Phe Ala Arg Met Arg Lys	
175 180 185	
atg gct gac ttt ttc ctt atc caa tca aac tat aac tac gtg aac tgg	625
Met Ala Asp Phe Phe Leu Ile Gln Ser Asn Tyr Asn Tyr Val Asn Trp	
190 195 200	
tgg tgg aca gcc cag agc ctt gtt att att ctt tct ggg atc ctg caa	673
Trp Ser Thr Ala Gln Ser Leu Val Ile Ile Leu Ser Gly Ile Leu Gln	
205 210 215	
ctg tat ttc ttg aag cgt ctc ttc aat gtt cca aca act aca gat aca	721
Leu Tyr Phe Leu Lys Arg Leu Phe Asn Val Pro Thr Thr Thr Asp Thr	
220 225 230 235	
aag aag cca aga tgc taa gctaag gtgactatag caccctggct gttttcttct	775

Lys Lys Pro Arg Cys *
240

ggggcttagt cgaatcagct ttgtaatggt atgggacaaa aatcaattat ctcattaatg 835
tttttagtctg ctgcacacat ctaaaaaagc aaaatggcaa taaaatcata acagtgtaaaa 895
aaaaaaaaa 903

<210> 196
<211> 649
<212> DNA
<213> Homo sapiens

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<222> (19)..(312)

<400> 196

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Met Ala Thr Pro Ser Leu Arg Gly Arg Leu Ala
1 5 10

cgg ttt ggg aac ccg cgg aag cct gtg ctg aag ccc aat aaa cct ctc 99
Arg Phe Gly Asn Pro Arg Lys Pro Val Leu Lys Pro Asn Lys Pro Leu
15 20 25

att cta gct aac cgc gtc ggg gag cgg cgc cgg gag aag ggc gag gcg 147
Ile Leu Ala Asn Arg Val Gly Glu Arg Arg Arg Glu Lys Gly Glu Ala
30 35 40

act tgc atc acg gag atg tcg gtg atg atg gct tgc tgg aag cag aat 195
Thr Cys Ile Thr Glu Met Ser Val Met Met Ala Cys Trp Lys Gln Asn
45 50 55

gaa ttc cgc gac gat gcg tgc aga aaa gag atc cag ggc ttc ctc gat 243
Glu Phe Arg Asp Asp Ala Cys Arg Lys Glu Ile Gln Gly Phe Leu Asp
60 65 70 75

tgt gcc gcg agg gct cag gtg acc gat gcc tcc tgg ggt gct ttc tca 291
Cys Ala Ala Arg Ala Gln Val Thr Asp Gly Ser Trp Gly Ala Phe Ser
80 85 90

gga aaa gaa tgg ggg aga tag aa gtaatgattc tccctgcctt ttgctaggaa 344
Gly Lys Glu Trp Gly Arg *
95

aggccctttc attcatttgg gaggtatatt attcacgcca aagtgggaaa ggttacagtt 404

ttgaaggctg tgtgatcttg acggatttat tcattgctct gaactttcga gttactgtac 464

gtaaaatgag gctaaccaat accaccttaa agaatgttgt gagtgtcaga tgaagtaatg 524

aatgggaaaa tcattttgaa aaatgtaaat tgctgctcaa gtagacatta ttgtgtgaaa 584

tagaactaaa gagactaaac taaataatga caatagtttg gttcctgtct aggctaattg	644
ctagg	649

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<212> DNA
<213> Homo sapiens

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	1 5	
ccc tac gga cag tcc cag cca agc tgc ttc tac cgt gta aaa atg ggc		101
Pro Tyr Gly Gln Ser Gln Pro Ser Cys Phe Tyr Arg Val Lys Met Gly		
	10 15 20	
ttc gtg atg ggt tgc gcc gtg ggc atg gcg gcc gag gcg ctc ttc ggc		149
Phe Val Met Gly Cys Ala Val Gly Met Ala Ala Glu Ala Leu Phe Gly		
	25 30 35	
acc ttt tcc tgt ctc agg atc gga atg cgg ggt cga gag ctg atg ggc		197
Thr Phe Ser Cys Leu Arg Ile Gly Met Arg Gly Arg Glu Leu Met Gly		
	40 45 50	
ggc att ggg aaa acc atg atg cag agt ggc ggc acc ttt ggc aca ttc		245
Gly Ile Gly Lys Thr Met Met Gln Ser Gly Gly Thr Phe Gly Thr Phe		
	55 60 65 70	
atg gcc att ggg atg ggc atc cga tgc taa c catggttgcc aactacatct		296
Met Ala Ile Gly Met Gly Ile Arg Cys *		
	75 80	
gtcccttccc atcaatccca gcccatgtac taataaaaga aagtctttga gtaaaaaaaaa		356
aaaa		360

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<210> 198
<211> 1280
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (206)..(535)

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 gattctgggg cgcactcagg gtttaggtgc cccctggtgt ggcctaaatg tccccacctg 120
 ggccatcttt ctggggagga ctctcccagg tagggaaggc cagaggtggc ccagtgcctg 180
 gagggttagg gtctctgcct gggat atg caa gag gaa gta gga aag gga ggt 232
 Met Gln Glu Glu Val Gly Lys Gly Gly
 1 5
 ctc atg gat gat cct agg ctg cta gaa gtc ctt aag gcc cca tct agt 280
 Leu Met Asp Asp Pro Arg Leu Leu Glu Val Leu Lys Ala Pro Ser Ser
 10 15 20 25
 cca ttc cac tcc cta ccc cca ttc cag agc cga gta gta agt tta cag 328
 Pro Phe His Ser Leu Pro Pro Phe Gln Ser Arg Val Val Ser Leu Gln
 30 35 40
 atg ttt ccc cca tta cgt acc ccc acc cat ccc tgc tgc agc gag cct 376
 Met Phe Pro Pro Leu Arg Thr Pro Thr His Pro Cys Cys Ser Glu Pro
 45 50 55
 gag agc cag gca gag cca ggc aca gct cct cag tct tct cac aca gtc 424
 Glu Ser Gln Ala Glu Pro Gly Thr Ala Pro Gln Ser Ser His Thr Val
 60 65 70
 ctg ccg gtg gcc ttc cct cat gac cct tgc ttg gga ggg tgg agc act 472
 Leu Pro Val Ala Phe Pro His Asp Pro Cys Leu Gly Gly Trp Ser Thr
 75 80 85
 ggc tcc ttg acc cta aaa ggt agc tgg cag ggg caa gat ggg ggc cag 520
 Gly Ser Leu Thr Leu Lys Gly Ser Trp Gln Gly Gln Asp Gly Gly Gln
 90 95 100 105
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 Leu Pro Asn Gly *
 110
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 ctgtttctgg ggcaccttcg aggaggcgtt gtggagggca tcgccccctg tttattcaca 695
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 agtgtgaata cctctgcaca tatgggtgta tctgtgtgtg ctctgtgtata tgggggtggg 1055
 aacatgagac ttctgtgac cagtccacc tggctcccag ctgtctgtat cctcctgccc 1115

His Gly Glu Lys Leu Lys Met Phe Cys Lys Glu Asp Val Leu Ile Met	
105 110 115	
tgt gag gcc tgc agc cag tcc cca gag cat gag gcc cac agt gtt gtg	679
Cys Glu Ala Cys Ser Gln Ser Pro Glu His Glu Ala His Ser Val Val	
120 125 130	
cca atg gag gat gtt gcc tgg gag tac aag tgg gaa ctt cat gag gcc	727
Pro Met Glu Asp Val Ala Trp Glu Tyr Lys Trp Glu Leu His Glu Ala	
135 140 145	
ctc gaa cat ctg aag aaa gag caa gaa gag gcc tgg aag ctt gaa gtt	775
Leu Glu His Leu Lys Lys Glu Gln Glu Glu Ala Trp Lys Leu Glu Val	
150 155 160	
ggt gaa agg aaa cga act gcc acc tgg aag ata cag gtg gaa acc cga	823
Gly Glu Arg Lys Arg Thr Ala Thr Trp Lys Ile Gln Val Glu Thr Arg	
165 170 175 180	
aaa cag agt att gta tgg gag ttt gaa aaa tac cag cga tta cta gag	871
Lys Gln Ser Ile Val Trp Glu Phe Glu Lys Tyr Gln Arg Leu Leu Glu	
185 190 195	
aaa aag cag cca cca cat cgg cag ctg ggg gca gag gta gca gca gct	919
Lys Lys Gln Pro Pro His Arg Gln Leu Gly Ala Glu Val Ala Ala Ala	
200 205 210	
ctg gcc agc cta cag cgg gag gca gcg gag acc atg cag aaa ctg gag	967
Leu Ala Ser Leu Gln Arg Glu Ala Ala Glu Thr Met Gln Lys Leu Glu	
215 220 225	
ttg aac cat agc gag ctc atc cag cag agc cag gtc ctg tgg agg atg	1015
Leu Asn His Ser Glu Leu Ile Gln Gln Ser Gln Val Leu Trp Arg Met	
230 235 240	
att gca gag ttg aaa gag agg tcg cag agg cct gtc cgc tgg atg ttg	1063
Ile Ala Glu Leu Lys Glu Arg Ser Gln Arg Pro Val Arg Trp Met Leu	
245 250 255 260	
cag gat att cag gaa gtg tta aac agg agc aaa tct tgg agc ttg cag	1111
Gln Asp Ile Gln Glu Val Leu Asn Arg Ser Lys Ser Trp Ser Leu Gln	
265 270 275	
cag cca gaa cca atc tcc ctg gag ttg aag aca gat tgc cgt gtg ctg	1159
Gln Pro Glu Pro Ile Ser Leu Glu Leu Lys Thr Asp Cys Arg Val Leu	
280 285 290	
ggg cta aga gag atc ctg aag act tat gca gct gat gtg cgc ttg gat	1207
Gly Leu Arg Glu Ile Leu Lys Thr Tyr Ala Ala Asp Val Arg Leu Asp	
295 300 305	
cca gat act gct tac tcc cgt ctc atc gtg tct gag gac aga aaa cgt	1255
Pro Asp Thr Ala Tyr Ser Arg Leu Ile Val Ser Glu Asp Arg Lys Arg	
310 315 320	
gtg cac tat gga gac acc aac cag aaa ctg cca gac aat cct gag aga	1303
Val His Tyr Gly Asp Thr Asn Gln Lys Leu Pro Asp Asn Pro Glu Arg	

325	330	335	340	
ttt tac cgc tat aat atc gtc ctg gga agc cag tgc atc tcc tca ggc				1351
Phe Tyr Arg Tyr Asn Ile Val Leu Gly Ser Gln Cys Ile Ser Ser Gly	345	350	355	
cgg cac tac tgg gag gtg gag gtg gga gac agg tct gag tgg ggc ctg				1399
Arg His Tyr Trp Glu Val Glu Val Gly Asp Arg Ser Glu Trp Gly Leu	360	365	370	
gga gta tgt aag caa aat gta gac cgg aag gag gtg gtc tac tta tcc				1447
Gly Val Cys Lys Gln Asn Val Asp Arg Lys Glu Val Val Tyr Leu Ser	375	380	385	
ccc cac tat gga ttc tgg gtg ata agg ctg agg aag gga aat gag tac				1495
Pro His Tyr Gly Phe Trp Val Ile Arg Leu Arg Lys Gly Asn Glu Tyr	390	395	400	
cga gca ggc acc gat gag tac cca atc ctg tcc ttg ccg gtc cct cct				1543
Arg Ala Gly Thr Asp Glu Tyr Pro Ile Leu Ser Leu Pro Val Pro Pro	405	410	415	420
cgc cgg gtg gga atc ttc gtg gat tat gag gcc cat gac att tct ttc				1591
Arg Arg Val Gly Ile Phe Val Asp Tyr Glu Ala His Asp Ile Ser Phe	425	430	435	
tac aat gtg act gac tgt ggc tcc cac atc ttc act ttc ccc cgc tat				1639
Tyr Asn Val Thr Asp Cys Gly Ser His Ile Phe Thr Phe Pro Arg Tyr	440	445	450	
ccc ttc cct ggg cgc ctc ctg ccc tat ttt agt cct tgc tac agc att				1687
Pro Phe Pro Gly Arg Leu Leu Pro Tyr Phe Ser Pro Cys Tyr Ser Ile	455	460	465	
gga acc aac aac act gct cct ctg gcc atc tgc tcc ctg gat ggg gag				1735
Gly Thr Asn Asn Thr Ala Pro Leu Ala Ile Cys Ser Leu Asp Gly Glu	470	475	480	
gac taa gaaagctacc accctaacca cagaggcttg gaattgggcc tggcccccat				1791
Asp *				
485				
ggggcttggga ggaccgagcc actgacaggt atcccctgaa actgagctga gcccagtatc				1851
caaggattcc tctgtctgat cctttggtct ttgctaccag gctgaagtct gtcatgaaac				1911
cacttatttt aaaaagcaga ggcccagtca aatgagcatt gcatcccatg agggaagcac				1971
gacagggctg atggtgagga tcagagcagt tctaaggatga ctcggtgggg taaggatcag				2031
gactttgtcc atgtagtagc caaccacct cttccctgat tcccgtccgg tgtcacagtt				2091
cagtcagtga ggatgatgaa gtagatacag tcttcaggac accattagat gggctttccc				2151
aataggccaa aaaaatgctg cgcataacca gagctggttg ttgtgctgag gccagtcaga				2211
ggatgcttcc cctgaggttt gctataacta agcaaccttt atgtgactct caccttctga				2271

cctcctggca agagaaattc agtgcagcag ggggacacag acctgcccac gccaccccac 2331
 tgccgttccc tctctgagca caagctgggc aaatcactgt cccttggact ccagtagacc 2391
 agtgcctag tcttgccctt tttctctaag tggcaggatc agaaaacctg cgagcttttag 2451
 tttgtatatt cactttatga atgaggaaac tgaaatggcc ttaagggagc aagttatttc 2511
 tttttttttg agactcctca aaaaagaaaa aaaaaaaa 2549

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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (331)..(1047)

<400> 200

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 tctcaccagc agagaacagc tgacggtctt tccataagtg cttctaagag agatgtgtgg 180
 taccctgggc taagtagaca gcaactgagc cctccctccc accccagggc tcccagagca 240
 acagggagca gggagcatag gacctggccg cagccaggaa tctacactga ccggtctcagc 300
 ccatgaagta tcttgggctg aagtcacagg atg aga ctg ttt gta tct gta 351
 Met Arg Leu Phe Val Ser Val
 1 5
 act gtc ctt gtc atc tgt ctt gca gat tta gaa gag gaa tca gaa agc 399
 Thr Val Leu Val Ile Cys Leu Ala Asp Leu Glu Glu Glu Ser Glu Ser
 10 15 20
 tgg gac aac tct gag gct gaa gag gag gag aaa gcc cct gtg ttg cca 447
 Trp Asp Asn Ser Glu Ala Glu Glu Glu Glu Lys Ala Pro Val Leu Pro
 25 30 35
 gag agt aca gaa ggg cgg gag ctg acc cag ggc ccg gca gag tcc tcc 495
 Glu Ser Thr Glu Gly Arg Glu Leu Thr Gln Gly Pro Ala Glu Ser Ser
 40 45 50 55
 tct ctc tca ggc tgt ggg agc tgg cag ccc cgg aag ctg cca gtc ttc 543
 Ser Leu Ser Gly Cys Gly Ser Trp Gln Pro Arg Lys Leu Pro Val Phe
 60 65 70
 aag tcc ctc cgg cac atg agg cag gtc ctg ggt gcc cct tct ttc cgc 591
 Lys Ser Leu Arg His Met Arg Gln Val Leu Gly Ala Pro Ser Phe Arg
 75 80 85

atg ctg gcc tgg cac gtt ctc atg ggg aac cag gtg atc tgg aaa agc	639
Met Leu Ala Trp His Val Leu Met Gly Asn Gln Val Ile Trp Lys Ser	
90 95 100	
aga gac gtg gac ctc gtc cag tca gct ttt gaa gta ctt cgg acc atg	687
Arg Asp Val Asp Leu Val Gln Ser Ala Phe Glu Val Leu Arg Thr Met	
105 110 115	
ctt ccc gtg ggc tgc gtc cgc atc atc cca tac agc agc cag tac gag	735
Leu Pro Val Gly Cys Val Arg Ile Ile Pro Tyr Ser Ser Gln Tyr Glu	
120 125 130 135	
gag gcc tat cgg tgc aac ttc ctg ggg ctc agc ccg cac gtg cag atc	783
Glu Ala Tyr Arg Cys Asn Phe Leu Gly Leu Ser Pro His Val Gln Ile	
140 145 150	
ccc ccc cac gtg ctc tcc tca gag ttt gct gtc atc gtg gag gtc cac	831
Pro Pro His Val Leu Ser Ser Glu Phe Ala Val Ile Val Glu Val His	
155 160 165	
gca gcc gca cgt tcc acc ctc cac cct gtg ggg tgt gag gat gac cag	879
Ala Ala Ala Arg Ser Thr Leu His Pro Val Gly Cys Glu Asp Asp Gln	
170 175 180	
tct ctc agc aag tac gag ttt gtg gtg acc agt ggg agc cct gta gct	927
Ser Leu Ser Lys Tyr Glu Phe Val Val Thr Ser Gly Ser Pro Val Ala	
185 190 195	
gca gac cga gtg ggc ccc acc atc ctg aat aag att gaa gcg gct ctg	975
Ala Asp Arg Val Gly Pro Thr Ile Leu Asn Lys Ile Glu Ala Ala Leu	
200 205 210 215	
acc aac cag aac ctg tct gtg gat gtg gtg gac cag tgc ctc gtc tgc	1023
Thr Asn Gln Asn Leu Ser Val Asp Val Val Asp Gln Cys Leu Val Cys	
220 225 230	
ctc aag gag gag tgg atg aag taa gcaacagtgt ggggtgaggcc cctttgcttg	1077
Leu Lys Glu Glu Trp Met Lys *	
235	
cgaccctgga gaaaacctgg agctgtttcc aaaagaggag ctgggccgtg gccactgagg	1137
gaggagctga gagaagaggt tgggggcggg gttccaactc cacgtccgcc actgcaaagc	1197
tcaggtggcc tcgggaggcg gtcattcatgt ctgcctccgg ctccctgcatg gggaggtggg	1257
gggtctatcat gactagtgt gctgtgaaca ttcttgatcc ggtctctgac aaacacgcct	1317
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 <211> 441
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (90)..(416)

<400> 201

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accactgaag ctgatcatga gatgactgt atg ctg aca cac ccc ctt cag ggg 113
Met Leu Thr His Pro Leu Gln Gly
1 5

cct ggc ctt gac tta ggg ctg cac tgt atc ctc agc aac ggc ctt gca 161
Pro Gly Leu Asp Leu Gly Leu His Cys Ile Leu Ser Asn Gly Leu Ala
10 15 20

gga gcc cct ttt gga ctg ctt tcc cta ttc agc cca aag ttg ggg tgg 209
Gly Ala Pro Phe Gly Leu Leu Ser Leu Phe Ser Pro Lys Leu Gly Trp
25 30 35 40

tgg gag aag agg ggt tgg agt gaa tcc atc tct att caa att cca gct 257
Trp Glu Lys Arg Gly Trp Ser Glu Ser Ile Ser Ile Gln Ile Pro Ala
45 50 55

ggg att act cta gga gtc ttc ctg gct tgt ttt ggg ctc aaa ctt agc 305
Gly Ile Thr Leu Gly Val Phe Leu Ala Cys Phe Gly Leu Lys Leu Ser
60 65 70

tac att gtt tat tgg ctc cca aag tcg gga ttg aag agt gaa aag atg 353
Tyr Ile Val Tyr Trp Leu Pro Lys Ser Gly Leu Lys Ser Glu Lys Met
75 80 85

cag gca atg aat cct tct gca cac tcc tcc ccc cac att cct gac act 401
Gln Ala Met Asn Pro Ser Ala His Ser Ser Pro His Ile Pro Asp Thr
90 95 100

agt aag aac caa taa acacttggtg acggaaaaaa aaaaa 441
Ser Lys Asn Gln *
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<210> 202

<211> 732

<212> DNA

<213> Homo sapiens

<220>

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<222> (72)..(296)

<400> 202

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act ctg gag gca gaa ttc aac agc ccg tcc ccc cca aca cct gag cca			212
Thr Leu Glu Ala Glu Phe Asn Ser Pro Ser Pro Pro Thr Pro Glu Pro			
20	25	30	
ggt gaa ggg ccc cgt aaa ttg gaa gga tgc aca agt tcc aag gtt acg			260
Gly Glu Gly Pro Arg Lys Leu Glu Gly Cys Thr Ser Ser Lys Val Thr			
35	40	45	50
ttt cag cct ccc agt agc att gga tgc agg aaa aaa tac att gac ggt			308
Phe Gln Pro Pro Ser Ser Ile Gly Cys Arg Lys Lys Tyr Ile Asp Gly			
55	60	65	
gaa aaa caa gcc gaa cca gtt gta gtt tta gat cct gtt tct aca cat			356
Glu Lys Gln Ala Glu Pro Val Val Val Leu Asp Pro Val Ser Thr His			
70	75	80	
gaa ccc caa acc aaa gac cag gtt gct gaa aaa gat cca act caa cac			404
Glu Pro Gln Thr Lys Asp Gln Val Ala Glu Lys Asp Pro Thr Gln His			
85	90	95	
aag gag gat gaa ggc gaa att caa cca gaa aac aaa gaa gac agc att			452
Lys Glu Asp Glu Gly Glu Ile Gln Pro Glu Asn Lys Glu Asp Ser Ile			
100	105	110	
gaa aac gtg aga gag aca gac agc tcc aac tgc tga tcca taaaccagaa			502
Glu Asn Val Arg Glu Thr Asp Ser Ser Asn Cys *			
115	120	125	
gcctgacatg tttggaagtc cttttcaata agcacatgat tagtgttggt atattggcaa			562
gggctgtaga cattctgctc tggctactgt attcagaata caggttcttt tctgggtgtca			622
cttttgtaag tagcaactat aaacataagt aagctgttta gcaaaacaca cattcctagt			682
aggttttggt tttttgatct ttataaagat gaggtttttt tcctagttac tgtattaagt			742
atgacttctt ttagaagggt acaaaaaaat tcagatgttg ataccttttt aggaaatgtg			802
cataccactc atcaaaggtg atgctgaaag tttgaggtgc ttgtatataa tcggataaac			862
aaaactgac aacccaatgt gattttaaaa gcccccaaag aagcttctgt tttgggtctg			922
atcctcttga tggagaaact gcagcagcat ggaaattggt gggtagctgt gcatacaagt			982
tattttctac agtagactga gataaactga aaactcagga gctggcatca aactcgtagt			1042
cccatagtca gtgttaatta cacacattgt taactattgg atgaaaaata catgctattg			1102
atttgtgtcca aagcctcccg aggacctccg tggggatgct ctggtagcct gaatacagaa			1162
ctgaggtgaa agtccaaacc ttgaatttta cagtagtaag ttggtaaacc atgtgctctg			1222
tgctatgagt taattatggt ttcccaaata ctaatgtggc acaagtacca tattttatca			1282
gagttcttat gtacagtatg gtgaagataa gtgacaagca cacatttttc ttgcttcact			1342

gctgttctat attacacagg tttgttgttg ttttttttaa aaaagaaatt aagcagtagt 1402
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gattaaaaaaa aaaa 1476

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<213> Homo sapiens

<220>
<221> CDS
<222> (193)..(564)

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cctggggcaca cacttccgga cacacatgca cacacagggtg cagatatgct gcctggacac 120
acgcagactg acgtgctttt gggaggggtgt gccgtgaagc ctgcagtacg tgtgccgtga 180
ggctcatagt tg atg agg gac ttt ccc tgc tcc acc gtc act ccc cca 228
Met Arg Asp Phe Pro Cys Ser Thr Val Thr Pro Pro
1 5 10
act ctg ccc gcc tct gtc ccc gcc tca gtc ccc gcc tcc atc ccc gcc 276
Thr Leu Pro Ala Ser Val Pro Ala Ser Val Pro Ala Ser Ile Pro Ala
15 20 25
tct gtc ccc tgg cct tgg cgg cta ttt ttg cca cct gcc ttg ggt gcc 324
Ser Val Pro Trp Pro Trp Arg Leu Phe Leu Pro Pro Ala Leu Gly Ala
30 35 40
cag gag tcc cct act gct gtg ggc tgg ggt tgg ggg cac agc agc ccc 372
Gln Glu Ser Pro Thr Ala Val Gly Trp Gly Trp Gly His Ser Ser Pro
45 50 55 60
aag cct gag agg ctg gag ccc atg gct agt ggc tca tcc cca ctg cat 420
Lys Pro Glu Arg Leu Glu Pro Met Ala Ser Gly Ser Ser Pro Leu His
65 70 75
tct ccc cct gac aca gag aag ggg cct tgg tat tta tat tta aga aat 468
Ser Pro Pro Asp Thr Glu Lys Gly Pro Trp Tyr Leu Tyr Leu Arg Asn
80 85 90
gaa gat aat att aat aat gat gga agg aag act ggg ttg cag gga ctg 516
Glu Asp Asn Ile Asn Asn Asp Gly Arg Lys Thr Gly Leu Gln Gly Leu
95 100 105
tgg tct ctc ctg ggg ccc ggg acc cgc ctg gtc ttt cag cca tgc tga 564
Trp Ser Leu Leu Gly Pro Gly Thr Arg Leu Val Phe Gln Pro Cys *
110 115 120

cta aag cat cag tcc aat cag aag aca gga gtc att gtc caa cag cgg	541
Leu Lys His Gln Ser Asn Gln Lys Thr Gly Val Ile Val Gln Gln Arg	
145 150 155	
tac aaa gat gtg aat gtt tat gta aac ccc aaa aag cta act gtt atc	589
Tyr Lys Asp Val Asn Val Tyr Val Asn Pro Lys Lys Leu Thr Val Ile	
160 165 170	
aaa gcc aaa gag cag ctc aag ctt ctg gaa gtg ctg gtt gga att att	637
Lys Ala Lys Glu Gln Leu Lys Leu Leu Glu Val Leu Val Gly Ile Ile	
175 180 185	
cat cag acc aag tgg agc tgg aga aga acc gga aag cag ggt gat gga	685
His Gln Thr Lys Trp Ser Trp Arg Arg Thr Gly Lys Gln Gly Asp Gly	
190 195 200 205	
gag agg ctt gtg gtt cat ggc ctg ctg cca ggg gga tct gct atg aag	733
Glu Arg Leu Val Val His Gly Leu Leu Pro Gly Gly Ser Ala Met Lys	
210 215 220	
agc ggt cag gta ctc att ggt gat gtc ctt gtt gct gtg aat gat gtc	781
Ser Gly Gln Val Leu Ile Gly Asp Val Leu Val Ala Val Asn Asp Val	
225 230 235	
gat gtt act act gaa aac atc gag aga gtt ctg tct tgc att cct gga	829
Asp Val Thr Thr Glu Asn Ile Glu Arg Val Leu Ser Cys Ile Pro Gly	
240 245 250	
cct atg cag gtg aaa ctg aca ttt gaa aat gca tat gat gtg aaa agg	877
Pro Met Gln Val Lys Leu Thr Phe Glu Asn Ala Tyr Asp Val Lys Arg	
255 260 265	
gag aca tcc cat cca aga cag aaa aag aca cag tcc aac aca agt gat	925
Glu Thr Ser His Pro Arg Gln Lys Lys Thr Gln Ser Asn Thr Ser Asp	
270 275 280 285	
tta gtc aag ctt ctc tgg gga gaa gag gtt gaa ggt atc cag cag agt	973
Leu Val Lys Leu Leu Trp Gly Glu Glu Val Glu Gly Ile Gln Gln Ser	
290 295 300	
ggc cta aac act cct cat atc att atg tat ctc aca cta cag ctc gac	1021
Gly Leu Asn Thr Pro His Ile Ile Met Tyr Leu Thr Leu Gln Leu Asp	
305 310 315	
tca gaa acc tca aag gaa gag cag gaa att ctt tat cat tat cca atg	1069
Ser Glu Thr Ser Lys Glu Glu Gln Glu Ile Leu Tyr His Tyr Pro Met	
320 325 330	
tct gaa gca tct cag aaa ctt aaa agt gtg aga ggg att ttt ctc aca	1117
Ser Glu Ala Ser Gln Lys Leu Lys Ser Val Arg Gly Ile Phe Leu Thr	
335 340 345	
ctc tgt gac atg ctg gaa aac gta act ggg aca caa gtt act agt tca	1165
Leu Cys Asp Met Leu Glu Asn Val Thr Gly Thr Gln Val Thr Ser Ser	
350 355 360 365	

tcc ctc ctt tta aat gga aaa caa att cat gtg gct tat tgg aaa gaa	1213
Ser Leu Leu Leu Asn Gly Lys Gln Ile His Val Ala Tyr Trp Lys Glu	
370 375 380	
tct gac aag ttg ttg cta att ggc ctg cct gct gaa gaa gtt cct ctt	1261
Ser Asp Lys Leu Leu Leu Ile Gly Leu Pro Ala Glu Glu Val Pro Leu	
385 390 395	
cct cgt cta agg aac atg ata gaa aat gtc atc caa acc tta aaa ttt	1309
Pro Arg Leu Arg Asn Met Ile Glu Asn Val Ile Gln Thr Leu Lys Phe	
400 405 410	
atg tat ggt tct tta gat agt gcc ttt tgc cag att gag aat gtt cct	1357
Met Tyr Gly Ser Leu Asp Ser Ala Phe Cys Gln Ile Glu Asn Val Pro	
415 420 425	
cgt ttg gat cat ttt ttt aac ttg ttc ttt caa aga gca ctt cag cct	1405
Arg Leu Asp His Phe Phe Asn Leu Phe Phe Gln Arg Ala Leu Gln Pro	
430 435 440 445	
gcg aaa ctg cat tcc agc gcc agt ccc agt gct cag cag tac gat gct	1453
Ala Lys Leu His Ser Ser Ala Ser Pro Ser Ala Gln Gln Tyr Asp Ala	
450 455 460	
tcc agt gca gta ctt tta gac aac ctc cct gga gtc cgg tgg ctc aca	1501
Ser Ser Ala Val Leu Leu Asp Asn Leu Pro Gly Val Arg Trp Leu Thr	
465 470 475	
ctt cca ctg gaa atc aag atg gaa tta gac atg gca tta agt gac ttg	1549
Leu Pro Leu Glu Ile Lys Met Glu Leu Asp Met Ala Leu Ser Asp Leu	
480 485 490	
gag gct gca gat ttt gca gaa ctg tcc gag gat tac tat gac atg agg	1597
Glu Ala Ala Asp Phe Ala Glu Leu Ser Glu Asp Tyr Tyr Asp Met Arg	
495 500 505	
cgg ctg tat aca att ttg ggg tct tct cta ttt tac aag ggt tat ttg	1645
Arg Leu Tyr Thr Ile Leu Gly Ser Ser Leu Phe Tyr Lys Gly Tyr Leu	
510 515 520 525	
ata tgc agt cat ttg ccc aag gat gat ctt att gat att gcc gta tac	1693
Ile Cys Ser His Leu Pro Lys Asp Asp Leu Ile Asp Ile Ala Val Tyr	
530 535 540	
tgt cgc cac tat tgc ctg ctg cct tta gca gca aaa caa aga att ggt	1741
Cys Arg His Tyr Cys Leu Leu Pro Leu Ala Ala Lys Gln Arg Ile Gly	
545 550 555	
cag ttg atc ata tgg aga gaa gtg ttt cct cag cat cac ctc cga cct	1789
Gln Leu Ile Ile Trp Arg Glu Val Phe Pro Gln His His Leu Arg Pro	
560 565 570	
ttg gca gac tca agc act gaa gtc ttt ccg gaa cct gaa gga aga tat	1837
Leu Ala Asp Ser Ser Thr Glu Val Phe Pro Glu Pro Glu Gly Arg Tyr	
575 580 585	
ttt ttg cta gtt gtt ggc ttg aaa cat tat atg cta tgt gta cta tta	1885

Phe	Leu	Leu	Val	Val	Gly	Leu	Lys	His	Tyr	Met	Leu	Cys	Val	Leu	Leu	
590					595					600					605	
gaa	gct	gga	ggt	tgc	gca	tcc	aaa	gct	att	ggg	agt	cct	gga	cca	gac	1933
Glu	Ala	Gly	Gly	Cys	Ala	Ser	Lys	Ala	Ile	Gly	Ser	Pro	Gly	Pro	Asp	
				610					615					620		
tgt	gta	tat	gtg	gat	caa	gtc	aaa	aca	act	ctt	cac	cag	ctg	gat	gga	1981
Cys	Val	Tyr	Val	Asp	Gln	Val	Lys	Thr	Thr	Leu	His	Gln	Leu	Asp	Gly	
			625					630					635			
gta	gat	tct	cgc	ata	gat	gaa	cgg	cta	gca	tct	tct	cca	gtc	ccc	tgt	2029
Val	Asp	Ser	Arg	Ile	Asp	Glu	Arg	Leu	Ala	Ser	Ser	Pro	Val	Pro	Cys	
		640					645					650				
ttg	tct	tgt	gct	gac	tgg	ttc	ctt	act	gga	tca	cgt	gaa	aaa	aca	gat	2077
Leu	Ser	Cys	Ala	Asp	Trp	Phe	Leu	Thr	Gly	Ser	Arg	Glu	Lys	Thr	Asp	
	655					660					665					
agc	ttg	acc	act	tgc	cct	att	ctc	agt	agg	cta	caa	ggt	act	tcc	aaa	2125
Ser	Leu	Thr	Thr	Ser	Pro	Ile	Leu	Ser	Arg	Leu	Gln	Gly	Thr	Ser	Lys	
670					675					680					685	
gta	gca	act	tct	cca	aca	tgc	aga	aga	acg	ctt	ttt	ggt	gac	tat	tcc	2173
Val	Ala	Thr	Ser	Pro	Thr	Cys	Arg	Arg	Thr	Leu	Phe	Gly	Asp	Tyr	Ser	
				690					695					700		
tta	aag	aca	cgc	aag	cct	agt	cct	tcc	tgt	agt	agt	gga	gga	tct	gac	2221
Leu	Lys	Thr	Arg	Lys	Pro	Ser	Pro	Ser	Cys	Ser	Ser	Gly	Gly	Ser	Asp	
			705					710					715			
aat	ggt	tgt	gaa	ggt	gga	gaa	gat	gat	ggc	ttt	agc	ccc	cat	act	aca	2269
Asn	Gly	Cys	Glu	Gly	Gly	Glu	Asp	Asp	Gly	Phe	Ser	Pro	His	Thr	Thr	
		720					725					730				
ccg	gat	gca	gta	cgg	aag	caa	aga	gaa	tct	cag	ggc	tct	gat	ggt	tta	2317
Pro	Asp	Ala	Val	Arg	Lys	Gln	Arg	Glu	Ser	Gln	Gly	Ser	Asp	Gly	Leu	
	735					740					745					
gaa	gaa	agt	ggg	acc	ttg	ctt	aag	gtc	act	aaa	aag	aag	tct	act	ctt	2365
Glu	Glu	Ser	Gly	Thr	Leu	Leu	Lys	Val	Thr	Lys	Lys	Lys	Ser	Thr	Leu	
750					755				760						765	
cca	aat	cca	ttt	cat	ttg	gga	aac	ttg	aaa	aag	gac	ctt	cca	gaa	aaa	2413
Pro	Asn	Pro	Phe	His	Leu	Gly	Asn	Leu	Lys	Lys	Asp	Leu	Pro	Glu	Lys	
				770					775					780		
gaa	tta	gaa	ata	tat	aac	aca	gtg	aaa	ctg	aca	tct	ggt	cct	gag	aac	2461
Glu	Leu	Glu	Ile	Tyr	Asn	Thr	Val	Lys	Leu	Thr	Ser	Gly	Pro	Glu	Asn	
			785					790					795			
aca	ctt	ttc	cac	tac	gtt	gcc	tta	gaa	aca	gtg	caa	gga	atc	ttt	att	2509
Thr	Leu	Phe	His	Tyr	Val	Ala	Leu	Glu	Thr	Val	Gln	Gly	Ile	Phe	Ile	
		800					805					810				
act	cct	acc	ctt	gaa	gag	gtg	gca	cag	cta	agt	ggc	tct	atc	cac	cct	2557
Thr	Pro	Thr	Leu	Glu	Glu	Val	Ala	Gln	Leu	Ser	Gly	Ser	Ile	His	Pro	

815	820	825	
cag cta ata aag aat ttc cat cag tgt tgt ctt tcc att cgt gca gtt			2605
Gln Leu Ile Lys Asn Phe His Gln Cys Cys Leu Ser Ile Arg Ala Val			
830	835	840	845
ttc caa cag aca ttg gtg gaa gag aaa aag aaa gga cta aat agt gga			2653
Phe Gln Gln Thr Leu Val Glu Glu Lys Lys Lys Gly Leu Asn Ser Gly			
	850	855	860
gac cat tca gat tct gca aag tca gtg tct tct ctt aac cct gtt aaa			2701
Asp His Ser Asp Ser Ala Lys Ser Val Ser Ser Leu Asn Pro Val Lys			
	865	870	875
gaa cat ggt gtg ttg ttt gaa tgt tca cct gga aac tgg act gat cag			2749
Glu His Gly Val Leu Phe Glu Cys Ser Pro Gly Asn Trp Thr Asp Gln			
	880	885	890
aaa aaa gca cca cca gtt atg gct tac tgg gta gta ggg aga ctt ttt			2797
Lys Lys Ala Pro Pro Val Met Ala Tyr Trp Val Val Gly Arg Leu Phe			
	895	900	905
ctt cat cca aaa cct caa gaa ctt tat gtc tgt ttt cat gac tca gtc			2845
Leu His Pro Lys Pro Gln Glu Leu Tyr Val Cys Phe His Asp Ser Val			
	910	915	920
aca gaa att gcc att gaa ata gct ttt aaa ttg ttc ttt ggg tta acc			2893
Thr Glu Ile Ala Ile Glu Ile Ala Phe Lys Leu Phe Phe Gly Leu Thr			
	930	935	940
ttg tag ctgtgctttc ttgatgcgta gaaacacgtg catggaggat caaacactgt			2949
Leu *			
cagaattgct gaaatcaata cacaaagaga taaagtttag cttcttttta ctattcaata			3009
ttgaacataa tattgttaaa tattgagatg aaatgctgtt ggatttgata cattaaatct			3069
taatgtaata ttgtaagact tttgagaata tacttgatta aaatgtgaaa gaagggattg			3129
ttaacttatt gctatTTTTGG tatataatgt taatttattg actagtttga aataatgtga			3189
agtgtttttt atatcagatt aatataggaa atgtttattc ttgaaaaata aaaaaaaaaa			3249

<210> 206
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 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (71)..(2836)

 <400> 206

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Ser Gly Gln Val Leu Ile Gly Asp Val Leu Val Ala Val Asn Asp Val	
225 230 235	
gat gtt act act gaa aac atc gag aga gtt ctg tct tgc att cct gga	829
Asp Val Thr Thr Glu Asn Ile Glu Arg Val Leu Ser Cys Ile Pro Gly	
240 245 250	
cct atg cag gtg aaa ctg aca ttt gaa aat gca tat gat gtg aaa agg	877
Pro Met Gln Val Lys Leu Thr Phe Glu Asn Ala Tyr Asp Val Lys Arg	
255 260 265	
gag aca tcc cat cca aga cag aaa aag aca cag tcc aac aca agt gat	925
Glu Thr Ser His Pro Arg Gln Lys Lys Thr Gln Ser Asn Thr Ser Asp	
270 275 280 285	
tta gtc aag ctt ctc tgg gga gaa gag gtt gaa ggt atc cag cag agt	973
Leu Val Lys Leu Leu Trp Gly Glu Glu Val Glu Gly Ile Gln Gln Ser	
290 295 300	
ggc cta aac act cct cat atc att atg tat ctc aca cta cag ctc gac	1021
Gly Leu Asn Thr Pro His Ile Ile Met Tyr Leu Thr Leu Gln Leu Asp	
305 310 315	
tca gaa acc tca aag gaa gag cag gaa att ctt tat cat tat cca atg	1069
Ser Glu Thr Ser Lys Glu Glu Gln Glu Ile Leu Tyr His Tyr Pro Met	
320 325 330	
tct gaa gca tct cag aaa ctt aaa agt gtg aga ggg att ttt ctc aca	1117
Ser Glu Ala Ser Gln Lys Leu Lys Ser Val Arg Gly Ile Phe Leu Thr	
335 340 345	
ctc tgt gac atg ctg gaa aac gta act ggg aca caa gtt act agt tca	1165
Leu Cys Asp Met Leu Glu Asn Val Thr Gly Thr Gln Val Thr Ser Ser	
350 355 360 365	
tcc ctc ctt tta aat gga aaa caa att cat gtg gct tat tgg aaa gaa	1213
Ser Leu Leu Leu Asn Gly Lys Gln Ile His Val Ala Tyr Trp Lys Glu	
370 375 380	
tct gac aag ttg ttg cta att ggc ctg cct gct gaa gaa gtt cct ctt	1261
Ser Asp Lys Leu Leu Leu Ile Gly Leu Pro Ala Glu Glu Val Pro Leu	
385 390 395	
cct cgt cta agg aac atg ata gaa aat gtc atc caa acc tta aaa ttt	1309
Pro Arg Leu Arg Asn Met Ile Glu Asn Val Ile Gln Thr Leu Lys Phe	
400 405 410	
atg tat ggt tct tta gat agt gcc ttt tgc cag att gag aat gtt cct	1357
Met Tyr Gly Ser Leu Asp Ser Ala Phe Cys Gln Ile Glu Asn Val Pro	
415 420 425	
cgt ttg gat cat ttt ttt aac ttg ttc ttt caa aga gca ctt cag cct	1405
Arg Leu Asp His Phe Phe Asn Leu Phe Phe Gln Arg Ala Leu Gln Pro	
430 435 440 445	

Thr Cys Arg Arg Thr Leu Phe Gly Asp Tyr Ser Leu Lys Thr Arg Lys	
670 675 680 685	
cct agt cct tcc tgt agt agt gga gga tct gac aat ggt tgt gaa ggt	2173
Pro Ser Pro Ser Cys Ser Ser Gly Gly Ser Asp Asn Gly Cys Glu Gly	
690 695 700	
gga gaa gat gat ggc ttt agc ccc cat act aca ccg gat gca gta cgg	2221
Gly Glu Asp Asp Gly Phe Ser Pro His Thr Thr Pro Asp Ala Val Arg	
705 710 715	
aag caa aga gaa tct cag ggc tct gat ggt tta gaa gaa agt ggg acc	2269
Lys Gln Arg Glu Ser Gln Gly Ser Asp Gly Leu Glu Glu Ser Gly Thr	
720 725 730	
ttg ctt aag gtc act aaa aag aag tct act ctt cca aat cca ttt cat	2317
Leu Leu Lys Val Thr Lys Lys Lys Ser Thr Leu Pro Asn Pro Phe His	
735 740 745	
ttg gga aac ttg aaa aag gac ctt cca gaa aaa gaa tta gaa ata tat	2365
Leu Gly Asn Leu Lys Lys Asp Leu Pro Glu Lys Glu Leu Glu Ile Tyr	
750 755 760 765	
aac aca gtg aaa ctg aca tct ggt cct gag aac aca ctt ttc cac tac	2413
Asn Thr Val Lys Leu Thr Ser Gly Pro Glu Asn Thr Leu Phe His Tyr	
770 775 780	
gtt gcc tta gaa aca gtg caa gga atc ttt att act cct acc ctt gaa	2461
Val Ala Leu Glu Thr Val Gln Gly Ile Phe Ile Thr Pro Thr Leu Glu	
785 790 795	
gag gtg gca cag cta agt ggc tct atc cac cct cag cta ata aag aat	2509
Glu Val Ala Gln Leu Ser Gly Ser Ile His Pro Gln Leu Ile Lys Asn	
800 805 810	
ttc cat cag tgt tgt ctt tcc att cgt gca gtt ttc caa cag aca ttg	2557
Phe His Gln Cys Cys Leu Ser Ile Arg Ala Val Phe Gln Gln Thr Leu	
815 820 825	
gtg gaa gag aaa aag aaa gga cta aat agt gga gac cat tca gat tct	2605
Val Glu Glu Lys Lys Lys Gly Leu Asn Ser Gly Asp His Ser Asp Ser	
830 835 840 845	
gca aag tca gtg tct tct ctt aac cct gtt aaa gaa cat ggt gtg ttg	2653
Ala Lys Ser Val Ser Ser Leu Asn Pro Val Lys Glu His Gly Val Leu	
850 855 860	
ttt gaa tgt tca cct gga aac tgg act gat cag aaa aaa gca cca cca	2701
Phe Glu Cys Ser Pro Gly Asn Trp Thr Asp Gln Lys Lys Ala Pro Pro	
865 870 875	
gtt atg gct tac tgg gta gta ggg aga ctt ttt ctt cat cca aaa cct	2749
Val Met Ala Tyr Trp Val Val Gly Arg Leu Phe Leu His Pro Lys Pro	
880 885 890	
caa gaa ctt tat gtc tgt ttt cat gac tca gtc aca gaa att gcc att	2797
Gln Glu Leu Tyr Val Cys Phe His Asp Ser Val Thr Glu Ile Ala Ile	

895	900	905	
gaa ata gct ttt aaa ttg ttc ttt ggg tta acc ttg tag ctgtgctttc			2846
Glu Ile Ala Phe Lys Leu Phe Phe Gly Leu Thr Leu *			
910	915	920	
ttgatgcgta gaaacacgtg catggaggat caaacactgt cagaattgct gaaatcaata			2906
cacaaagaga taaagtttag cttcttttta ctattcaata ttgaacataa tattgttaaa			2966
tattgagatg aaatgctggt ggatttgata cattaaatct taatgtaata ttgtaagact			3026
tttgagaata tacttgatta aaatgtgaaa gaagggttg ttaacttatt gctattttgg			3086
tatataatgt taatttattg actagtttga aataatgtga agtgtttttt atatcagatt			3146
aatataggaa atgtttattc ttgaaaaata aaaaaaaaaa			3186

<210> 207
 <211> 1595
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (306)..(1496)

 <220>
 <221> misc_feature
 <222> (1)...(1595)
 <223> n = a,t,c or g

<400> 207			
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gtggaaacat gtcttgcgac acccaccagc gactgctaca acccagcggc ggcgntgntg			120
gtcacggagc tggggccggg ggcagcccg gagctggctg gggccctgc aaggaccgtc			180
tggggcctgc ccagccaaga gtgtgtgcaa cacatcgggtg ctgagcagca gcctgcagtc			240
actggagtat ctcatcaacg acatccggcc gccctgcatc aaggagcaga tgctgggcaa			300
gggct atg aga cgg tgg ccg tgc ccc ggc tac tcg acc acc agc atg			347
Met Arg Arg Trp Pro Cys Pro Gly Tyr Ser Thr Thr Ser Met			
1 5 10			
ccc aca tcc gcc tac ccg tct aca gat aag gcc tgc ctg cgg aca tac			395
Pro Thr Ser Ala Tyr Pro Ser Thr Asp Lys Ala Cys Leu Arg Thr Tyr			
15 20 25 30			
gga cat gcg gac agg gcg cag agc cgg gag gca ggc cgc aga aca ggg			443
Gly His Ala Asp Arg Ala Gln Ser Arg Glu Ala Gly Arg Arg Thr Gly			
35 40 45			

tgg gcg gct cgc agg ggc gct cag ccc cac cct gtg cct gct gat gcc	491
Trp Ala Ala Arg Gly Ala Gln Pro His Pro Val Pro Ala Asp Ala	
50 55 60	
cac agg gga gcc agg ctg gct gcc gcc tcg ctg tgg ccg gat gga ggg	539
His Arg Gly Ala Arg Leu Ala Ala Ala Ser Leu Trp Pro Asp Gly Gly	
65 70 75	
tgg cag ggc aac ctc aca tac caa ggc ccc tcc cca cca tcg gtt gcc	587
Trp Gln Gly Asn Leu Thr Tyr Gln Gly Pro Ser Pro Pro Ser Val Ala	
80 85 90	
cca gga cac agt gag ggc ctg ggg gca gcc act gac gcc cat gcc ttc	635
Pro Gly His Ser Glu Gly Leu Gly Ala Ala Thr Asp Ala His Ala Phe	
95 100 105 110	
ctt tat cta agc tgg cag agg cag gga gag aga aac cac tca aaa aca	683
Leu Tyr Leu Ser Trp Gln Arg Gln Gly Glu Arg Asn His Ser Lys Thr	
115 120 125	
gga atg gtt ctt tct ggg cct cct ggg aca ggg gcc cag gcc aag gtg	731
Gly Met Val Leu Ser Gly Pro Pro Gly Thr Gly Ala Gln Ala Lys Val	
130 135 140	
ggg tgc agg agg aaa cag gcg cac cag agt cag ggt ggg ggc agg gca	779
Gly Cys Arg Arg Lys Gln Ala His Gln Ser Gln Gly Gly Gly Arg Ala	
145 150 155	
gcc ccc cca ggg gtc agg cag ctg tgt ctc ccc aca ctg gct ccc cag	827
Ala Pro Pro Gly Val Arg Gln Leu Cys Leu Pro Thr Leu Ala Pro Gln	
160 165 170	
tat tct gga aaa ggg gta cag gag gcc gat agg aag tca ctg ggc cca	875
Tyr Ser Gly Lys Gly Val Gln Glu Ala Asp Arg Lys Ser Leu Gly Pro	
175 180 185 190	
aag tgt ctc ccc acc agc cag gtg aag acc act ctg aca gag gct cca	923
Lys Cys Leu Pro Thr Ser Gln Val Lys Thr Thr Leu Thr Glu Ala Pro	
195 200 205	
ggg act ata cca gtc ccc ctg ttc ctc ctt ccc cta ccc cca cca ttc	971
Gly Thr Ile Pro Val Pro Leu Phe Leu Leu Pro Leu Pro Pro Pro Phe	
210 215 220	
ctt cct aac aca gag ttg cac ccc cat ccc cat tct cca aac cct gga	1019
Leu Pro Asn Thr Glu Leu His Pro His Pro His Ser Pro Asn Pro Gly	
225 230 235	
cta cca tat tcc ccc ttc cct cca ata cat ctt ata ggg ctg ctg ggt	1067
Leu Pro Tyr Ser Pro Phe Pro Pro Ile His Leu Ile Gly Leu Leu Gly	
240 245 250	
aca gtt gtt cag gct gtg cac tgc aca agg gca cct tgt cca agg aga	1115
Thr Val Val Gln Ala Val His Cys Thr Arg Ala Pro Cys Pro Arg Arg	
255 260 265 270	

cac cac ttt cac cca aac ttg tat att tat tac aat ttt ctg cat ctt	1163
His His Phe His Pro Asn Leu Tyr Ile Tyr Tyr Asn Phe Leu His Leu	
275 280 285	
gag gaa ggg gcg tca ttt tcc tgt tcg cac aaa ggc acc aca ggg gct	1211
Glu Glu Gly Ala Ser Phe Ser Cys Ser His Lys Gly Thr Thr Gly Ala	
290 295 300	
aac agt ggg cct gca atc tta gat ccc atc ctt gcc ttc ttc gag gga	1259
Asn Ser Gly Pro Ala Ile Leu Asp Pro Ile Leu Ala Phe Phe Glu Gly	
305 310 315	
tct ctt ggg acc ctc ctg gtt tta act ggg agg ccc aga cca act cct	1307
Ser Leu Gly Thr Leu Leu Val Leu Thr Gly Arg Pro Arg Pro Thr Pro	
320 325 330	
ttc ctg caa acc acc ctc caa ggc ctg tcc cac acg atc aag gca ggg	1355
Phe Leu Gln Thr Thr Leu Gln Gly Leu Ser His Thr Ile Lys Ala Gly	
335 340 345 350	
aaa gat agg cag gag tcc cct cac gaa gtc ctc aag tcc tgg ccc ctc	1403
Lys Asp Arg Gln Glu Ser Pro His Glu Val Leu Lys Ser Trp Pro Leu	
355 360 365	
tgg cgc tct gga agc ggt act gta tct ctc tcc aag gcc tgg tca agc	1451
Trp Arg Ser Gly Ser Gly Thr Val Ser Leu Ser Lys Ala Trp Ser Ser	
370 375 380	
act aag tgc att tac aaa tct ctg aga atg ttt ttt tta tac taa aat	1499
Thr Lys Cys Ile Tyr Lys Ser Leu Arg Met Phe Phe Leu Tyr *	
385 390 395	
tgaccattat attctactgt gagaagtgc gctctgcacta tattgtttta aaaacgaaga	1559
gaaagaagaa aaaggaaaac acagaaaaaa aaaaaa	1595

<210> 208
 <211> 1463
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (288)..(1235)

<400> 208	
aaaataaccc tactaaagg gaataagctt gcggccgccc ggggagccgc gggagaggcg	60
gcggcggggg gaggaggag aggagggcc agccggcggc acgggaggcc cggttttgaa	120
gccgcttctc tgcccagatt aggtttcgcc cagcgcaatt tctttctcta tgtactttgc	180
gaataagttt cggagcatcg gttaacagcc tatgggtgaa atttggtttt cattcatgaa	240

tgagaaatta ttcttgacag aagtatttta aaagaaaaat ctttacg	atg gcc tca	296
	Met Ala Ser	
	1	
gca gta ctt agt tct gtt ccc acc acc gct tct cgt ttt gcc ctg tta		344
Ala Val Leu Ser Ser Val Pro Thr Thr Ala Ser Arg Phe Ala Leu Leu		
5 10 15		
caa gtg gat agt ggc agt ggc tct gat tct gaa cct gga aaa ggt aaa		392
Gln Val Asp Ser Gly Ser Gly Ser Asp Ser Glu Pro Gly Lys Gly Lys		
20 25 30 35		
ggt cga aat act gga aag tct caa act tta gga agc aag tca act aca		440
Gly Arg Asn Thr Gly Lys Ser Gln Thr Leu Gly Ser Lys Ser Thr Thr		
40 45 50		
aat gag aaa aaa aga gag aaa aga aga aaa aag aag gaa cag caa cag		488
Asn Glu Lys Lys Arg Glu Lys Arg Arg Lys Lys Lys Glu Gln Gln Gln		
55 60 65		
agt gaa gca aat gag ctc agg aat ctt gct ttt aag aaa att ccc cag		536
Ser Glu Ala Asn Glu Leu Arg Asn Leu Ala Phe Lys Lys Ile Pro Gln		
70 75 80		
aaa tcc tcc cat gct gtt tgt aac gct caa cat gat ctt cca ttg tca		584
Lys Ser Ser His Ala Val Cys Asn Ala Gln His Asp Leu Pro Leu Ser		
85 90 95		
aac cca gta cag aag gat tca cga gaa gaa aat tgg caa gag tgg aga		632
Asn Pro Val Gln Lys Asp Ser Arg Glu Glu Asn Trp Gln Glu Trp Arg		
100 105 110 115		
caa aga gat gag cag ctg aca tct gaa atg ttt gaa gca gat ctt gag		680
Gln Arg Asp Glu Gln Leu Thr Ser Glu Met Phe Glu Ala Asp Leu Glu		
120 125 130		
aag gca ttg tta cta agt aaa cta gaa tat gaa gag cac aaa aag gag		728
Lys Ala Leu Leu Ser Lys Leu Glu Tyr Glu Glu His Lys Lys Glu		
135 140 145		
tat gaa gat gct gaa aat act tca act cag tcc aaa gtt atg aat aaa		776
Tyr Glu Asp Ala Glu Asn Thr Ser Thr Gln Ser Lys Val Met Asn Lys		
150 155 160		
aaa gat aaa aga aag aat cat cag gga aaa gac aga cct ctc aca gta		824
Lys Asp Lys Arg Lys Asn His Gln Gly Lys Asp Arg Pro Leu Thr Val		
165 170 175		
tca cta aaa gat ttt cat tcg gaa gat cac att agt aaa aag act gag		872
Ser Leu Lys Asp Phe His Ser Glu Asp His Ile Ser Lys Lys Thr Glu		
180 185 190 195		
gaa gtg gtt ctg aaa gat gga aga att gaa aga cta aag tta gag ctt		920
Glu Val Val Leu Lys Asp Gly Arg Ile Glu Arg Leu Lys Leu Glu Leu		
200 205 210		
gaa agg aaa gat gct gaa atc cag aag ctg aaa aat gta atc act caa		968

Glu Arg Lys Asp Ala Glu Ile Gln Lys Leu Lys Asn Val Ile Thr Gln	
215 220 225	
tgg gag gca aag tat aag gaa gta aag gca aga aat gca caa tta ttg	1016
Trp Glu Ala Lys Tyr Lys Glu Val Lys Ala Arg Asn Ala Gln Leu Leu	
230 235 240	
aaa atg ctt cag gaa ggt gaa atg aaa gat aag gca gaa ata ctt ctg	1064
Lys Met Leu Gln Glu Gly Glu Met Lys Asp Lys Ala Glu Ile Leu Leu	
245 250 255	
caa gtt gat gaa tca caa agt atc aag aat gag ctc act att cag gtg	1112
Gln Val Asp Glu Ser Gln Ser Ile Lys Asn Glu Leu Thr Ile Gln Val	
260 265 270 275	
act tca ctt cat gct gca tta gaa caa gaa aga tct aaa gtg aaa gta	1160
Thr Ser Leu His Ala Ala Leu Glu Gln Glu Arg Ser Lys Val Lys Val	
280 285 290	
tta caa gca gag tta gcc aaa tac cag ggt ggc aga aaa ggg aaa aga	1208
Leu Gln Ala Glu Leu Ala Lys Tyr Gln Gly Gly Arg Lys Gly Lys Arg	
295 300 305	
aac tct gaa tcc gac cag tgt agg tga ttaca ttagcctttg aagtcaacac	1260
Asn Ser Glu Ser Asp Gln Cys Arg *	
310 315	
aaagtttaaa acttcacagga ttttgcaaag ttgtatatat ttaatgctgt gcaactgcta	1320
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acaaatacca gttcatacat tcttgttcca ataggagtt atg gga gga aaa att	174
Met Gly Gly Lys Ile	
1 5	
att cca agc aat cac aca gga tca act ttt tct cct tgt aga ata tgt	222

cctaacaagc acgcagttcc tgatgattgg cctcaggtcc cagagagctc cagcaggtgt 480

aggagtccat gggcctgaca cctttgctgg tctctgctgg atccccgacga agtcaggtcc 540

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actccccaaag atgaggggcag taaggtgctg aggaccctgg aagtaacttg cttttctcaa 720

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ctctgccagg ggcctgggaa gctgtcaagg ag atg gcc agc cta caa aac act 833
Met Ala Ser Leu Gln Asn Thr
1 5

gac gtc ttc atc tgc aca agc ccc atc aag atg ttc aag tac tgt ccc 881
Asp Val Phe Ile Cys Thr Ser Pro Ile Lys Met Phe Lys Tyr Cys Pro
10 15 20

tat gag aag tat gcc tgg gtg gag aag tac ttt ggc cct gac ttt ctg 929
Tyr Glu Lys Tyr Ala Trp Val Glu Lys Tyr Phe Gly Pro Asp Phe Leu
25 30 35

gag cag att gtg ctg acc aga gac aag acc gtg gtc tct gct gac ctt 977
Glu Gln Ile Val Leu Thr Arg Asp Lys Thr Val Val Ser Ala Asp Leu
40 45 50 55

ctc ata gac gac cgg ccg gac atc aca ggg gcc gag cca acc ccc agc 1025
Leu Ile Asp Asp Arg Pro Asp Ile Thr Gly Ala Glu Pro Thr Pro Ser
60 65 70

tgg gag cat gtc ctc ttc acc gcc tgc cac aac cag cac ctg cag ctg 1073
Trp Glu His Val Leu Phe Thr Ala Cys His Asn Gln His Leu Gln Leu
75 80 85

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Gln Pro Pro Arg Arg Arg Leu His Ser Trp Ala Asp Asp Trp Lys Ala
90 95 100

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105 110

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 aaccaggggt gctaaaaata accaggccca aatggaccag aagcaactcc catggacttt 180
 ggcttgcagt catggtcaga agagatacag gcacagatcc cactattacg aaggagccaa 240
 aatatctgcc aagataaaaa tggaagtaac tcctctggat ttatgtgtcc aggggtggat 300
 atggaaagac ttgtgaagta ttaatcaaaa atcaccgag gctttttcag actattattc 360
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 tcagcacagt gaaagccagt acctaaagat tctaacaagc cttgctgaag ttgctacaac 480
 aaatggtcat aaactgctta gcctctctag caattatgat gctcaa atg aag agc 535
 Met Lys Ser
 1
 ctt tta agg att gtg aga atg ttt tgt cac gtc ttt cga att ggt cca 583
 Leu Leu Arg Ile Val Arg Met Phe Cys His Val Phe Arg Ile Gly Pro
 5 10 15
 tcc tcc ccc agt aat gga att gat atg ggc tac aat ggg aat aaa act 631
 Ser Ser Pro Ser Asn Gly Ile Asp Met Gly Tyr Asn Gly Asn Lys Thr
 20 25 30 35
 cca aaa agc cag gtg ttc aag cct ctg gaa ttg ctt tgg cac tcg tta 679
 Pro Lys Ser Gln Val Phe Lys Pro Leu Glu Leu Leu Trp His Ser Leu
 40 45 50

gat gaa tgg cta gtt tta ata gcc cca gaa ttg atg aaa aac aaa aga Asp Glu Trp Leu Val Leu Ile Ala Pro Glu Leu Met Lys Asn Lys Arg 55 60 65	727
gac tca aca gag atc act tct att tta ctg aaa caa aaa ggc caa gat Asp Ser Thr Glu Ile Thr Ser Ile Leu Leu Lys Gln Lys Gly Gln Asp 70 75 80	775
caa gat gct gct tcc att cct cca ttt gaa cct cca gga cct ggg agc Gln Asp Ala Ala Ser Ile Pro Pro Phe Glu Pro Pro Gly Pro Gly Ser 85 90 95	823
tat gaa aat ctg tcc act ggc aca agg gaa tct aaa cca gat gct ctt Tyr Glu Asn Leu Ser Thr Gly Thr Arg Glu Ser Lys Pro Asp Ala Leu 100 105 110 115	871
gca ggg aga cag gaa gcc agt gca gat tgt cag gat gtt att tct atg Ala Gly Arg Gln Glu Ala Ser Ala Asp Cys Gln Asp Val Ile Ser Met 120 125 130	919
aca gct aac cgg cta agt gct gtc att caa gct ttt tac atg tgc tgt Thr Ala Asn Arg Leu Ser Ala Val Ile Gln Ala Phe Tyr Met Cys Cys 135 140 145	967
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gtc tgc aaa cat gat gaa gtt tta aaa tgc ttt gtt aat aga aat ccc Val Cys Lys His Asp Glu Val Leu Lys Cys Phe Val Asn Arg Asn Pro 165 170 175	1063
aaa att ata ttt gac cac ttt cac ttt ctc ctt gaa tgt cct gag ttg Lys Ile Ile Phe Asp His Phe His Phe Leu Leu Glu Cys Pro Glu Leu 180 185 190 195	1111
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gat tct att ttt agg agt agc tgt gaa gtt gtg tca aaa gca aat tgt Asp Ser Ile Phe Arg Ser Ser Cys Glu Val Val Ser Lys Ala Asn Cys 245 250 255	1303
gca aag cta aag caa ggg att gct gta cgg ttc cat gga gaa gaa ggc Ala Lys Leu Lys Gln Gly Ile Ala Val Arg Phe His Gly Glu Glu Gly 260 265 270 275	1351
atg ggt caa ggt gtt gtg cgt gag tgg ttt gat att ctg tcc aat gag	1399

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Ile	Val	Asn	Pro	Asp	Tyr	Ala	Leu	Phe	Thr	Gln	Ser	Ala	Asp	Gly	Thr	
295				300				305								
act	ttt	cag	cct	aat	agc	aac	tct	tat	gta	aat	cct	gat	cac	ttg	aac	1495
Thr	Phe	Gln	Pro	Asn	Ser	Asn	Ser	Tyr	Val	Asn	Pro	Asp	His	Leu	Asn	
310				315				320								
tat	ttt	cgg	ttt	gct	ggg	cag	atc	ttg	gga	tta	gcg	ttg	aac	cac	agg	1543
Tyr	Phe	Arg	Phe	Ala	Gly	Gln	Ile	Leu	Gly	Leu	Ala	Leu	Asn	His	Arg	
325				330				335								
cag	ctg	gtc	aat	att	tac	ttc	aca	cga	tcc	ttc	tac	aag	cac	att	ctt	1591
Gln	Leu	Val	Asn	Ile	Tyr	Phe	Thr	Arg	Ser	Phe	Tyr	Lys	His	Ile	Leu	
340				345				350				355				
ggt	att	cct	gta	aat	tac	caa	gat	gtg	gca	tcc	att	gat	cca	gaa	tat	1639
Gly	Ile	Pro	Val	Asn	Tyr	Gln	Asp	Val	Ala	Ser	Ile	Asp	Pro	Glu	Tyr	
360				365				370								
gcg	aaa	aat	ttg	caa	tgg	att	tta	gat	aat	gat	ata	agt	gat	ctg	ggt	1687
Ala	Lys	Asn	Leu	Gln	Trp	Ile	Leu	Asp	Asn	Asp	Ile	Ser	Asp	Leu	Gly	
375				380				385								
cta	gaa	cta	act	ttt	tct	gtt	gag	act	gat	gtg	ttt	gga	gca	atg	gaa	1735
Leu	Glu	Leu	Thr	Phe	Ser	Val	Glu	Thr	Asp	Val	Phe	Gly	Ala	Met	Glu	
390				395				400								
gag	gtg	cct	ttg	aaa	cct	ggg	ggt	ggg	agt	att	ctt	gtg	aca	caa	aat	1783
Glu	Val	Pro	Leu	Lys	Pro	Gly	Gly	Gly	Ser	Ile	Leu	Val	Thr	Gln	Asn	
405				410				415								
aat	aaa	gcg	gag	tac	gtc	cag	ctt	gtt	act	gaa	ctt	cga	atg	aca	aga	1831
Asn	Lys	Ala	Glu	Tyr	Val	Gln	Leu	Val	Thr	Glu	Leu	Arg	Met	Thr	Arg	
420				425				430				435				
gcc	att	cag	cct	cag	atc	aat	gct	ttt	tta	cag	ggc	ttt	cat	atg	ttc	1879
Ala	Ile	Gln	Pro	Gln	Ile	Asn	Ala	Phe	Leu	Gln	Gly	Phe	His	Met	Phe	
440				445				450								
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Ile	Pro	Pro	Ser	Leu	Ile	Gln	Leu	Phe	Asp	Glu	Tyr	Glu	Leu	Glu	Leu	
455				460				465								
ctg	ctt	tct	ggc	atg	cca	gaa	att	gat	gtg	agt	gat	tgg	ata	aaa	aat	1975
Leu	Leu	Ser	Gly	Met	Pro	Glu	Ile	Asp	Val	Ser	Asp	Trp	Ile	Lys	Asn	
470				475				480								
aca	gaa	tac	aca	agt	ggc	tat	gaa	aga	gaa	gat	cca	gtt	att	cag	tgg	2023
Thr	Glu	Tyr	Thr	Ser	Gly	Tyr	Glu	Arg	Glu	Asp	Pro	Val	Ile	Gln	Trp	
485				490				495								
ttc	tgg	gaa	gtt	gta	gaa	gac	att	act	caa	gag	gag	aga	gtt	ctt	ctc	2071
Phe	Trp	Glu	Val	Val	Glu	Asp	Ile	Thr	Gln	Glu	Glu	Arg	Val	Leu	Leu	

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Leu Gln Phe Val Thr Gly Ser Ser Arg Val Pro His Gly Gly Phe Ala				
	520	525	530	
aat atc atg ggt gga agt gga ttg caa aac ttt aca atc gct gct gtg				2167
Asn Ile Met Gly Gly Ser Gly Leu Gln Asn Phe Thr Ile Ala Ala Val				
	535	540	545	
cca tat act cca aat ctt tta cca act tca agc aca tgc atc aac atg				2215
Pro Tyr Thr Pro Asn Leu Leu Pro Thr Ser Ser Thr Cys Ile Asn Met				
	550	555	560	
ctc aag tta cct gaa tac cca agt aaa gaa ata ctc aag gac aga ctt				2263
Leu Lys Leu Pro Glu Tyr Pro Ser Lys Glu Ile Leu Lys Asp Arg Leu				
	565	570	575	
ctt gtg gca cta cat tgt ggc agc tat ggt tac aca atg gca taa tga				2311
Leu Val Ala Leu His Cys Gly Ser Tyr Gly Thr Met Ala *				
	580	585	590	
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aaatgtcaac aaaaaagcag cctaaatgca acccataggc agggctgatg cttccaattt				2431
ataaaggatc atcaggtttt ctgtttctct cttttccctt ttatgttttc tctgtttgta				2491
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ccaggcagca acagtgtacg gcgacattgg agcggacctc acggcgacct caatttccac	300
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Met Asn Asp Gly Val Thr Phe	
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Ile Gly Leu Ser Trp Ser Pro Arg Arg Arg Gly Leu Gly Ile Gln Arg	
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Thr Ile His Pro His Ile Asp Ala Ala Glu Thr Leu Arg Gly Leu Thr	
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Asn Ala Pro Val Gln Lys Val Ser Thr Trp Thr Asn Thr Gly Arg Glu	
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Thr Pro Met Ser Pro Cys Ala Thr Cys Ser Glu Gly Thr Leu Val Ala	
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Glu Ser Gly Arg Gly Trp Ala Gly Gly Ser Ile Asp Phe His Arg Val	
90 95 100	

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Cys Leu Gln Ile Phe Ala Gly Ser Ala Gly Lys Gly Gln Gly Leu Asp	
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Thr Ser Val Ala Val Pro Pro Gly Trp Ala Asp Pro Phe Leu Phe Pro	
120 125 130 135	
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Ser His Arg Ser Leu Phe Pro Glu Ile Leu Gly Lys Cys Gly Glu Val	
140 145 150	
gcc ccg tgc cgt cga atc ccc atc ctg gtt tac tga agtg cagaagtgac	1136
Ala Pro Cys Arg Arg Ile Pro Ile Leu Val Tyr *	
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agatcatttt gatcatcttc agctgtcttc tcttcacata caggaaaggc cttggaaagc	360
agtcgttgcg ccagacagcc cagggaagag cggcagcctg aggacctagg gccacctgct	420
gttccctggg attcatgtcc ttctggggag gagggaggac ccaggaca atg gct gct	477
Met Ala Ala	

gtt cat gat ctg gag atg gag agc atg aat ctg aat atg ggg aga gag	525
Val His Asp Leu Glu Met Glu Ser Met Asn Leu Asn Met Gly Arg Glu	
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Met Lys Glu Glu Leu Glu Glu Glu Glu Lys Met Arg Glu Asp Gly Gly	
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ggt aaa gat cgg gcc aag agt aaa aag gtc cac agg att gtc tca aaa	621
Gly Lys Asp Arg Ala Lys Ser Lys Lys Val His Arg Ile Val Ser Lys	
40 45 50	
tgg atg ctg ccc gaa aag tcc cga gga aca tac ttg gag aga gct aac	669
Trp Met Leu Pro Glu Lys Ser Arg Gly Thr Tyr Leu Glu Arg Ala Asn	
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Cys Phe Pro Pro Pro Val Phe Ile Ile Ser Ile Ser Leu Ala Glu Leu	
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Ala Val Phe Ile Tyr Tyr Ala Val Trp Lys Pro Gln Lys Gln Trp Ile	
85 90 95	
acg ttg gac aca ggc atc ttg gag agt ccc ttt atc tac agt cct gag	813
Thr Leu Asp Thr Gly Ile Leu Glu Ser Pro Phe Ile Tyr Ser Pro Glu	
100 105 110 115	
aag agg gag gaa gcc tgg agg ttt atc tca tac atg ctg gta cat gct	861
Lys Arg Glu Glu Ala Trp Arg Phe Ile Ser Tyr Met Leu Val His Ala	
120 125 130	
gga gtt cag cac atc ttg ggg aat ctt tgt atg cag ctt gtt ttg ggt	909
Gly Val Gln His Ile Leu Gly Asn Leu Cys Met Gln Leu Val Leu Gly	
135 140 145	
att ccc ttg gaa atg gtc cac aaa ggc ctc cgt gtg ggg ctg gtg tac	957
Ile Pro Leu Glu Met Val His Lys Gly Leu Arg Val Gly Leu Val Tyr	
150 155 160	
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Leu Ala Gly Val Ile Ala Gly Ser Leu Ala Ser Ser Ile Phe Asp Pro	
165 170 175	
ctc aga tat ctt gtg gga gct tca gga gga gtc tat gct ctg atg gga	1053
Leu Arg Tyr Leu Val Gly Ala Ser Gly Gly Val Tyr Ala Leu Met Gly	
180 185 190 195	
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Gly Tyr Phe Met Asn Val Leu Val Asn Phe Gln Glu Met Ile Pro Ala	
200 205 210	
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Phe Gly Ile Phe Arg Leu Leu Ile Ile Ile Leu Ile Ile Val Leu Asp	
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Met Gly Phe Ala Leu Tyr Arg Arg Phe Phe Val Pro Glu Asp Gly Ser
230 235 240

ccg gtg tct ttt gca gct cac att gca ggt gga ttt gct gga atg tcc 1245
Pro Val Ser Phe Ala Ala His Ile Ala Gly Gly Phe Ala Gly Met Ser
245 250 255

att ggc tac acg gtg ttt agc tgc ttt gat aaa gca ctg atg aaa gat 1293
Ile Gly Tyr Thr Val Phe Ser Cys Phe Asp Lys Ala Leu Met Lys Asp
260 265 270 275

cca agg ttt tgg ata gca att gct gca tat tta gct tgt gtc tta ttt 1341
Pro Arg Phe Trp Ile Ala Ile Ala Ala Tyr Leu Ala Cys Val Leu Phe
280 285 290

gct gtg ttt ttc aac att ttc cta tct cca gca aac tga cctgccccta 1390
Ala Val Phe Phe Asn Ile Phe Leu Ser Pro Ala Asn *

295 300

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ttttggagtt gacatgcatg tggattggag gaaaaataat caacatatat tctcctttcg 180

tactgttttaa atcacaggaa gaagcggctt taagacaaag atcaaacc aa a atg aca 237
Met Thr
1

act gct cac ttt tac tgt caa tac tgc aca gca tca ctt ctt ggg aag 285
Thr Ala His Phe Tyr Cys Gln Tyr Cys Thr Ala Ser Leu Leu Gly Lys
5 10 15

aaa tat gta cta aag gat gac agt cca tac tgt gtt aca tgt tat gat 333
Lys Tyr Val Leu Lys Asp Asp Ser Pro Tyr Cys Val Thr Cys Tyr Asp
20 25 30

cgt gta ttt tct aac tat tgc gag gaa tgc aaa aaa cca att gaa tct	381
Arg Val Phe Ser Asn Tyr Cys Glu Glu Cys Lys Lys Pro Ile Glu Ser	
35 40 45 50	
gat tct aag gat ctt tgt tac aaa gac cgg cac tgg cat gaa gga tgc	429
Asp Ser Lys Asp Leu Cys Tyr Lys Asp Arg His Trp His Glu Gly Cys	
55 60 65	
ttc aag tgc acc aaa tgc aat cac tct ttg gtg gaa aag cct ttt gct	477
Phe Lys Cys Thr Lys Cys Asn His Ser Leu Val Glu Lys Pro Phe Ala	
70 75 80	
gcc aag gat gag cgc ctg ctg tgc acg gag tgc tat tct aac gag tgc	525
Ala Lys Asp Glu Arg Leu Leu Cys Thr Glu Cys Tyr Ser Asn Glu Cys	
85 90 95	
tcc tcc aag tgc ttc cac tgc aag agg acc atc atg cct ggt tcc cgc	573
Ser Ser Lys Cys Phe His Cys Lys Arg Thr Ile Met Pro Gly Ser Arg	
100 105 110	
aaa atg gaa ttt aag gga aac tac tgg cat gaa acc tgt ttt gtg tgt	621
Lys Met Glu Phe Lys Gly Asn Tyr Trp His Glu Thr Cys Phe Val Cys	
115 120 125 130	
gag aat tgc cga caa cct ata ggg aca aag cct ttg atc tcc aaa gag	669
Glu Asn Cys Arg Gln Pro Ile Gly Thr Lys Pro Leu Ile Ser Lys Glu	
135 140 145	
agt ggc aat tat tgt gtg cca tgt ttt gag aag gag ttt gct cac tac	717
Ser Gly Asn Tyr Cys Val Pro Cys Phe Glu Lys Glu Phe Ala His Tyr	
150 155 160	
tgc aac ttt tgt aag aag gtg ata act tca ggt ggg ata aca ttt tgt	765
Cys Asn Phe Cys Lys Lys Val Ile Thr Ser Gly Gly Ile Thr Phe Cys	
165 170 175	
gac cag cta tgg cat aaa gag tgt ttt ctg tgt agt ggc tgt agg aaa	813
Asp Gln Leu Trp His Lys Glu Cys Phe Leu Cys Ser Gly Cys Arg Lys	
180 185 190	
gat ctc tgt gaa gaa cag ttc atg tcc aga gac gac tat cca ttc tgc	861
Asp Leu Cys Glu Glu Gln Phe Met Ser Arg Asp Asp Tyr Pro Phe Cys	
195 200 205 210	
atg gac tgc tac aac cat ctt tat gcc aac aag tgt gta gcc tgt tcc	909
Met Asp Cys Tyr Asn His Leu Tyr Ala Asn Lys Cys Val Ala Cys Ser	
215 220 225	
aaa ccc att agt ggt ctc aca ggt gcc aag ttt atc tgc ttt caa gac	957
Lys Pro Ile Ser Gly Leu Thr Gly Ala Lys Phe Ile Cys Phe Gln Asp	
230 235 240	
agc cag tgg cat agc gaa tgc ttt aac tgc ggg aaa tgc tct gtc tcc	1005
Ser Gln Trp His Ser Glu Cys Phe Asn Cys Gly Lys Cys Ser Val Ser	
245 250 255	

ttg gtg ggt aaa ggc ttc ctg acc cag aac aag gaa atc ttc tgc caa 1053
 Leu Val Gly Lys Gly Phe Leu Thr Gln Asn Lys Glu Ile Phe Cys Gln
 260 265 270
 aaa tgt ggc tcc gga atg gac act gac atc tag gagacagt ccttgcccac 1104
 Lys Cys Gly Ser Gly Met Asp Thr Asp Ile *
 275 280 285
 ctaaaatcca ttttgccttc gttgtcacta aagccagaac tcaaaaaaaaa aaaa 1158

<210> 215
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 <213> Homo sapiens

<220>
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 <222> (1)..(1920)

<400> 215

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 Met Leu Leu Arg Lys Arg Tyr Arg His Arg Pro Cys Arg Leu Gln Phe
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ctc ctg ctg ctc ctg atg ctg gga tgc gtc ctg atg atg gtg gcg atg 96
 Leu Leu Leu Leu Leu Met Leu Gly Cys Val Leu Met Met Val Ala Met
 20 25 30

ttg cac cct ccc cac cac acc ctg cac cag act gtc aca gcc caa gcc 144
 Leu His Pro Pro His His Thr Leu His Gln Thr Val Thr Ala Gln Ala
 35 40 45

agc aag cac agc cct gaa gcc agg tac cgc ctg gac ttt ggg gaa tcc 192
 Ser Lys His Ser Pro Glu Ala Arg Tyr Arg Leu Asp Phe Gly Glu Ser
 50 55 60

cag gat tgg gta ctg gaa gct gag gat gag ggt gaa gag tac agc cct 240
 Gln Asp Trp Val Leu Glu Ala Glu Asp Glu Gly Glu Glu Tyr Ser Pro
 65 70 75 80

ctg gag ggc ctg cca ccc ttt atc tca ctg cgg gag gat cag ctg ctg 288
 Leu Glu Gly Leu Pro Pro Phe Ile Ser Leu Arg Glu Asp Gln Leu Leu
 85 90 95

gtg gcc gtg gcc tta ccc cag gcc aga agg aac cag agc cag ggc agg 336
 Val Ala Val Ala Leu Pro Gln Ala Arg Arg Asn Gln Ser Gln Gly Arg
 100 105 110

aga ggt ggg agc tac cgc ctc atc aag cag cca agg agg cag gat aag 384
 Arg Gly Gly Ser Tyr Arg Leu Ile Lys Gln Pro Arg Arg Gln Asp Lys
 115 120 125

gaa gcc cca aag agg gac tgg ggg gct gat gag gac ggg gag gtg tct 432
 Glu Ala Pro Lys Arg Asp Trp Gly Ala Asp Glu Asp Gly Glu Val Ser

130					135					140										
gaa	gaa	gag	gag	ttg	acc	ccg	ttc	agc	ctg	gac	cca	cgt	ggc	ctc	cag	480				
Glu	Glu	Glu	Glu	Leu	Thr	Pro	Phe	Ser	Leu	Asp	Pro	Arg	Gly	Leu	Gln	160				
145					150					155										
gag	gca	ctc	agt	gcc	cgc	atc	ccc	ctc	cag	agg	gct	ctg	ccc	gag	gtg	528				
Glu	Ala	Leu	Ser	Ala	Arg	Ile	Pro	Leu	Gln	Arg	Ala	Leu	Pro	Glu	Val	175				
				165					170											
cgg	cac	cca	ctg	tgt	ctg	cag	cag	cac	cct	cag	gac	agc	ctg	ccc	aca	576				
Arg	His	Pro	Leu	Cys	Leu	Gln	Gln	His	Pro	Gln	Asp	Ser	Leu	Pro	Thr	190				
			180					185					190							
gcc	agc	gtc	atc	ctc	tgt	ttc	cat	gat	gag	gcc	tgg	tcc	act	ctc	ctg	624				
Ala	Ser	Val	Ile	Leu	Cys	Phe	His	Asp	Glu	Ala	Trp	Ser	Thr	Leu	Leu	205				
		195					200					205								
cgg	act	gta	cac	agc	atc	ctc	gac	aca	gtg	ccc	agg	gcc	ttc	ctg	aag	672				
Arg	Thr	Val	His	Ser	Ile	Leu	Asp	Thr	Val	Pro	Arg	Ala	Phe	Leu	Lys	220				
	210					215					220									
gag	atc	atc	ctc	gtg	gac	gac	ctc	agc	cag	caa	gga	caa	ctc	aag	tct	720				
Glu	Ile	Ile	Leu	Val	Asp	Asp	Leu	Ser	Gln	Gln	Gly	Gln	Leu	Lys	Ser	240				
225					230					235										
gct	ctc	agc	gaa	tat	gtg	gcc	agg	ctg	gag	ggg	gtg	aag	tta	ctc	agg	768				
Ala	Leu	Ser	Glu	Tyr	Val	Ala	Arg	Leu	Glu	Gly	Val	Lys	Leu	Leu	Arg	255				
			245						250											
agc	aac	aag	agg	ctg	ggt	gcc	atc	agg	gcc	cgg	atg	ctg	ggg	gcc	acc	816				
Ser	Asn	Lys	Arg	Leu	Gly	Ala	Ile	Arg	Ala	Arg	Met	Leu	Gly	Ala	Thr	270				
			260					265					270							
aga	gcc	acc	ggg	gat	gtg	ctc	gtc	ttc	atg	gat	gcc	cac	tgc	gag	tgc	864				
Arg	Ala	Thr	Gly	Asp	Val	Leu	Val	Phe	Met	Asp	Ala	His	Cys	Glu	Cys	285				
		275					280													
cac	cca	ggc	tgg	ctg	gag	ccc	ctc	ctc	agc	aga	ata	gct	ggt	gac	agg	912				
His	Pro	Gly	Trp	Leu	Glu	Pro	Leu	Leu	Ser	Arg	Ile	Ala	Gly	Asp	Arg	300				
	290					295														
agc	cga	gtg	gta	tct	ccg	gtg	ata	gat	gtg	att	gac	tgg	aag	act	ttc	960				
Ser	Arg	Val	Val	Ser	Pro	Val	Ile	Asp	Val	Ile	Asp	Trp	Lys	Thr	Phe	320				
305					310					315										
cag	tat	tac	ccc	tca	aag	gac	ctg	cag	cgt	ggg	gtg	ttg	gac	tgg	aag	1008				
Gln	Tyr	Tyr	Pro	Ser	Lys	Asp	Leu	Gln	Arg	Gly	Val	Leu	Asp	Trp	Lys	335				
			325						330											
ctg	gat	ttc	cac	tgg	gaa	cct	ttg	cca	gag	cat	gtg	agg	aag	gcc	ctc	1056				
Leu	Asp	Phe	His	Trp	Glu	Pro	Leu	Pro	Glu	His	Val	Arg	Lys	Ala	Leu	345				
			340					345					350							
cag	tcc	ccc	ata	agc	ccc	atc	agg	agc	cct	gtg	gtg	ccc	gga	gag	gtg	1104				
Gln	Ser	Pro	Ile	Ser	Pro	Ile	Arg	Ser	Pro	Val	Val	Pro	Gly	Glu	Val	355				
		355					360					365								

gtg gcc atg gac aga cat tac ttc caa aac act gga gcg tat gac tct	1152
Val Ala Met Asp Arg His Tyr Phe Gln Asn Thr Gly Ala Tyr Asp Ser	
370 375 380	
ctt atg tcg ctg cga ggt ggt gaa aac ctc gaa ctg tct ttc aag gcc	1200
Leu Met Ser Leu Arg Gly Gly Glu Asn Leu Glu Leu Ser Phe Lys Ala	
385 390 395 400	
tgg ctc tgt ggt ggc tct gtt gaa atc ctt ccc tgc tct cgg gta gga	1248
Trp Leu Cys Gly Gly Ser Val Glu Ile Leu Pro Cys Ser Arg Val Gly	
405 410 415	
cac atc tac caa aat cag gat tcc cat tcc ccc ctc gac cag gag gcc	1296
His Ile Tyr Gln Asn Gln Asp Ser His Ser Pro Leu Asp Gln Glu Ala	
420 425 430	
acc ctg agg aac agg gtt cgc att gct gag acc tgg ctg ggg tca ttc	1344
Thr Leu Arg Asn Arg Val Arg Ile Ala Glu Thr Trp Leu Gly Ser Phe	
435 440 445	
aaa gaa acc ttc tac aag cat agc cca gag gcc ttc tcc ttg agc aag	1392
Lys Glu Thr Phe Tyr Lys His Ser Pro Glu Ala Phe Ser Leu Ser Lys	
450 455 460	
gct gag aag cca gac tgc atg gaa cgc ttg cag ctg caa agg aga ctg	1440
Ala Glu Lys Pro Asp Cys Met Glu Arg Leu Gln Leu Gln Arg Arg Leu	
465 470 475 480	
ggt tgt cgg aca ttc cac tgg ttt ctg gct aat gtc tac cct gag ctg	1488
Gly Cys Arg Thr Phe His Trp Phe Leu Ala Asn Val Tyr Pro Glu Leu	
485 490 495	
tac cca tct gaa ccc agg ccc agt ttc tct gga aag ctc cac aac act	1536
Tyr Pro Ser Glu Pro Arg Pro Ser Phe Ser Gly Lys Leu His Asn Thr	
500 505 510	
gga ctt ggg ctc tgt gca gac tgc cag gca gaa ggg gac atc ctg ggc	1584
Gly Leu Gly Leu Cys Ala Asp Cys Gln Ala Glu Gly Asp Ile Leu Gly	
515 520 525	
tgt ccc atg gtg ttg gct cct tgc agt gac agc cgg cag caa cag tac	1632
Cys Pro Met Val Leu Ala Pro Cys Ser Asp Ser Arg Gln Gln Gln Tyr	
530 535 540	
ctg cag cac acc agc agg aag gag att cac ttt ggc agc cca cag cac	1680
Leu Gln His Thr Ser Arg Lys Glu Ile His Phe Gly Ser Pro Gln His	
545 550 555 560	
ctg tgc ttt gct gtc agg cag gag cag gtg att ctt cag aac tgc acg	1728
Leu Cys Phe Ala Val Arg Gln Glu Gln Val Ile Leu Gln Asn Cys Thr	
565 570 575	
gag gaa ggc ctg gcc atc cac cag cag cac tgg gac ttc cag gag aat	1776
Glu Glu Gly Leu Ala Ile His Gln Gln His Trp Asp Phe Gln Glu Asn	
580 585 590	

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ggg atg att gtc cac att ctt tct ggg aaa tgc atg gaa gct gtg gtg      1824
Gly Met Ile Val His Ile Leu Ser Gly Lys Cys Met Glu Ala Val Val
      595                      600                      605

caa gaa aac aat aaa gat ttg tac ctg cgt ccg tgt gat gga aaa gcc      1872
Gln Glu Asn Asn Lys Asp Leu Tyr Leu Arg Pro Cys Asp Gly Lys Ala
      610                      615                      620

cgc cag cag tgg cgt ttt gac cag atc aat gct gtg gat gaa cga tga      1920
Arg Gln Gln Trp Arg Phe Asp Gln Ile Asn Ala Val Asp Glu Arg *
      625                      630                      635                      640

atgtcaatgt cagaaggaaa agagaatttt ggccatcaaa atccagctcc aagtgaactt      1980

aaagagctta tataatttcat gaagctgata cttttgtgtg tgtgctcctg gtgttaggag      2040

agaaaaaagc tctatgaaag aatataggaa gtttctcctt ttcacacctt aaaaaaaaaa      2100

aa                                                                    2102

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<210> 216
<211> 4675
<212> DNA
<213> Homo sapiens

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<222> (187)..(4599)

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ccccactga agggcaaagt ccagcggatt ctacactgga ggtggacgga gccccctgcc      180

cccttc      atg gtg ggg ctg ccg ggg cct gac gtg gag ccc agc ctc cct      228
      Met Val Gly Leu Pro Gly Pro Asp Val Glu Pro Ser Leu Pro
      1                      5                      10

cca cct aag ccc ctg gag ggc atc cct gag aga gag ttc ttt gtc aag      276
Pro Pro Lys Pro Leu Glu Gly Ile Pro Glu Arg Glu Phe Phe Val Lys
      15                      20                      25                      30

tgg gca ggg ctg tcc tac tgg cat tgc tcc tgg gtg aag gag cta cag      324
Trp Ala Gly Leu Ser Tyr Trp His Cys Ser Trp Val Lys Glu Leu Gln
      35                      40                      45

ctg gag ctg tac cac acg gtg atg tat cgc aac tac caa aga aag aac      372
Leu Glu Leu Tyr His Thr Val Met Tyr Arg Asn Tyr Gln Arg Lys Asn
      50                      55                      60

gac atg gat gag ccg ccc ccc ttt gac tac ggc tct ggg gat gaa gac      420
Asp Met Asp Glu Pro Pro Pro Phe Asp Tyr Gly Ser Gly Asp Glu Asp

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65	70	75	
ggc aag agc gag aag agg aag aac aag gac ccc ctc tat gcc aag atg Gly Lys Ser Glu Lys Arg Lys Asn Lys Asp Pro Leu Tyr Ala Lys Met 80 85 90			468
gag gag cgc ttc tac cgc tat ggc atc aag cca gag tgg atg atg att Glu Glu Arg Phe Tyr Arg Tyr Gly Ile Lys Pro Glu Trp Met Met Ile 95 100 105 110			516
cac cga atc ctg aac cat agc ttt gac aag aag ggg gat gtg cac tac His Arg Ile Leu Asn His Ser Phe Asp Lys Lys Gly Asp Val His Tyr 115 120 125			564
ctg atc aag tgg aaa gac ctg ccc tat gac cag tgc acc tgg gag atc Leu Ile Lys Trp Lys Asp Leu Pro Tyr Asp Gln Cys Thr Trp Glu Ile 130 135 140			612
gat gac atc gac atc ccc tac tac gac aac ctc aag cag gcc tac tgg Asp Asp Ile Asp Ile Pro Tyr Tyr Asp Asn Leu Lys Gln Ala Tyr Trp 145 150 155			660
ggc cac agg gag ctg atg ctg gga gaa gac acc agg ctg ccc aag agg Gly His Arg Glu Leu Met Leu Gly Glu Asp Thr Arg Leu Pro Lys Arg 160 165 170			708
ctg ctc aag aag ggc aag aag ctg agg gac gac aag cag gag aag ccg Leu Leu Lys Lys Gly Lys Lys Leu Arg Asp Asp Lys Gln Glu Lys Pro 175 180 185 190			756
ccg gac acg ccc att gtg gac ccc acg gtc aag ttc gac aag cag cca Pro Asp Thr Pro Ile Val Asp Pro Thr Val Lys Phe Asp Lys Gln Pro 195 200 205			804
tgg tac atc gac tcc aca ggc ggc aca ctg cac ccg tac cag ctg gag Trp Tyr Ile Asp Ser Thr Gly Gly Thr Leu His Pro Tyr Gln Leu Glu 210 215 220			852
ggc ctc aac tgg ctg cgc ttc tct tgg gcc cag ggc act gac acc atc Gly Leu Asn Trp Leu Arg Phe Ser Trp Ala Gln Gly Thr Asp Thr Ile 225 230 235			900
ctg gcc gat gag atg ggt ctg ggc aag acg gtg cag acc atc gtg ttc Leu Ala Asp Glu Met Gly Leu Gly Lys Thr Val Gln Thr Ile Val Phe 240 245 250			948
ctt tac tcc ctc tac aag gag ggc cac tcc aaa ggg ccc tac ctg gtt Leu Tyr Ser Leu Tyr Lys Glu Gly His Ser Lys Gly Pro Tyr Leu Val 255 260 265 270			996
agc gcg ccc ctc tcc acc atc atc aac tgg gaa cgc gag ttt gag atg Ser Ala Pro Leu Ser Thr Ile Ile Asn Trp Glu Arg Glu Phe Glu Met 275 280 285			1044
tgg gcg ccc gac ttc tac gtg gtc acc tac acg ggg gac aag gag agc Trp Ala Pro Asp Phe Tyr Val Val Thr Tyr Thr Gly Asp Lys Glu Ser 290 295 300			1092

cgc tcg gtg att cgg gag aac gag ttt tcc ttt gag gac aac gcc att	1140
Arg Ser Val Ile Arg Glu Asn Glu Phe Ser Phe Glu Asp Asn Ala Ile	
305 310 315	
cgg agt ggg aag aag gta ttc cgt atg aag aaa gaa gtg cag atc aaa	1188
Arg Ser Gly Lys Lys Val Phe Arg Met Lys Lys Glu Val Gln Ile Lys	
320 325 330	
ttc cac gtg ctg ctc acc tcc tat gag ctc atc acc atc gac cag gcc	1236
Phe His Val Leu Leu Thr Ser Tyr Glu Leu Ile Thr Ile Asp Gln Ala	
335 340 345 350	
atc ctg ggc tcc atc gag tgg gcc tgc ctg gtg gta gat gag gcc cac	1284
Ile Leu Gly Ser Ile Glu Trp Ala Cys Leu Val Val Asp Glu Ala His	
355 360 365	
cgc ctc aag aac aac cag tcc aag ttt ttt agg gtc tta aac agc tac	1332
Arg Leu Lys Asn Asn Gln Ser Lys Phe Phe Arg Val Leu Asn Ser Tyr	
370 375 380	
aag att gat tac aag ctg ctg ctg aca ggg acc ccc ctt cag aac aac	1380
Lys Ile Asp Tyr Lys Leu Leu Thr Gly Thr Pro Leu Gln Asn Asn	
385 390 395	
ctg gag gag ctg ttc cat ctc ctc aac ttc ctg act cca gag agg ttc	1428
Leu Glu Glu Leu Phe His Leu Leu Asn Phe Leu Thr Pro Glu Arg Phe	
400 405 410	
aac aac ctg gag ggc ttc ctg gag gag ttt gct gac atc tcc aag gaa	1476
Asn Asn Leu Glu Gly Phe Leu Glu Glu Phe Ala Asp Ile Ser Lys Glu	
415 420 425 430	
gac cag atc aag aag ctg cat gac ctg ctg ggg ccg cac atg ctc agg	1524
Asp Gln Ile Lys Lys Leu His Asp Leu Leu Gly Pro His Met Leu Arg	
435 440 445	
cgg ctc aag gct gac gtg ttc aag aac atg ccg gcc aag acc gag ctc	1572
Arg Leu Lys Ala Asp Val Phe Lys Asn Met Pro Ala Lys Thr Glu Leu	
450 455 460	
att gtc cgg gtg gag ctg agc cag atg cag aag aag tac tac aag ttc	1620
Ile Val Arg Val Glu Leu Ser Gln Met Gln Lys Lys Tyr Tyr Lys Phe	
465 470 475	
atc ctc aca cgg aac ttt gag gca ctg aac tcc aag ggg ggc ggc aac	1668
Ile Leu Thr Arg Asn Phe Glu Ala Leu Asn Ser Lys Gly Gly Gly Asn	
480 485 490	
caa gta tcg ctg ctc aac atc atg atg gac ctg aaa aag tgc tgc aac	1716
Gln Val Ser Leu Leu Asn Ile Met Met Asp Leu Lys Lys Cys Cys Asn	
495 500 505 510	
cac ccc tac ctc ttc cct gtg gct gcc gtg gag gcc cct gtc ttg ccc	1764
His Pro Tyr Leu Phe Pro Val Ala Ala Val Glu Ala Pro Val Leu Pro	
515 520 525	

aat ggc tcc tac gat gga agc tcc ctg gtc aag tct tca ggg aag ctc	1812
Asn Gly Ser Tyr Asp Gly Ser Ser Leu Val Lys Ser Ser Gly Lys Leu	
530 535 540	
atg ctg cta cag aag atg ctg aag aaa ctg cgg gat gag ggg cac cgt	1860
Met Leu Leu Gln Lys Met Leu Lys Lys Leu Arg Asp Glu Gly His Arg	
545 550 555	
gtg ctc atc ttc tcc cag atg acc aag atg ctg gac ctc ctg gag gac	1908
Val Leu Ile Phe Ser Gln Met Thr Lys Met Leu Asp Leu Leu Glu Asp	
560 565 570	
ttc ctg gag tac gaa ggc tac aag tat gag cgg att gat ggt ggc atc	1956
Phe Leu Glu Tyr Glu Gly Tyr Lys Tyr Glu Arg Ile Asp Gly Gly Ile	
575 580 585 590	
acc ggg ggc ctc cgg cag gag gca atc gac aga ttc aat gcc ccc ggg	2004
Thr Gly Gly Leu Arg Gln Glu Ala Ile Asp Arg Phe Asn Ala Pro Gly	
595 600 605	
gcc cag cag ttc tgc ttc ctc ctc tca acc cgg gca ggt ggt ctg ggc	2052
Ala Gln Gln Phe Cys Phe Leu Leu Ser Thr Arg Ala Gly Leu Gly	
610 615 620	
atc aac ctg gcc acg gcg gac act gtc atc atc tac gac tcg gac tgg	2100
Ile Asn Leu Ala Thr Ala Asp Thr Val Ile Ile Tyr Asp Ser Asp Trp	
625 630 635	
aac ccg cac aat gac atc cag gcc ttc agc cgc gcc cac cgc atc ggc	2148
Asn Pro His Asn Asp Ile Gln Ala Phe Ser Arg Ala His Arg Ile Gly	
640 645 650	
cag aac aag aag gtg atg atc tac cgc ttc gtg act cgg gcc tcg gtg	2196
Gln Asn Lys Lys Val Met Ile Tyr Arg Phe Val Thr Arg Ala Ser Val	
655 660 665 670	
gag gag cgc atc acg cag gtg gcc aag cgc aag atg atg ctc acc cac	2244
Glu Glu Arg Ile Thr Gln Val Ala Lys Arg Lys Met Met Leu Thr His	
675 680 685	
ctg gtg gtg cgg ccc ggc ctc ggc tcc aag tcg ggg tcc atg acc aag	2292
Leu Val Val Arg Pro Gly Leu Gly Ser Lys Ser Gly Ser Met Thr Lys	
690 695 700	
cag gag ctg gac gac atc ctc aag ttc ggc acg gag gaa ctc ttc aag	2340
Gln Glu Leu Asp Asp Ile Leu Lys Phe Gly Thr Glu Glu Leu Phe Lys	
705 710 715	
gac gac gtg gag ggc atg atg tct cag ggc cag agg ccg gtc aca ccc	2388
Asp Asp Val Glu Gly Met Met Ser Gln Gly Gln Arg Pro Val Thr Pro	
720 725 730	
atc cct gat gtc cag tcc tcc aaa ggg ggg aac ttg gcc gcc agt gca	2436
Ile Pro Asp Val Gln Ser Ser Lys Gly Gly Asn Leu Ala Ala Ser Ala	
735 740 745 750	
aag aag aag cac ggt agc acc ccg cca ggt gac aac aag gac gtg gag	2484

Lys	Lys	Lys	His	Gly	Ser	Thr	Pro	Pro	Gly	Asp	Asn	Lys	Asp	Val	Glu	
				755					760					765		
gac	agc	agt	gtg	atc	cac	tat	gac	gat	gcg	gcc	atc	tcc	aag	ctg	ctg	2532
Asp	Ser	Ser	Val	Ile	His	Tyr	Asp	Asp	Ala	Ala	Ile	Ser	Lys	Leu	Leu	
			770					775					780			
gac	cgg	aac	cag	gac	gct	aca	gat	gac	acg	gag	cta	cag	aac	atg	aac	2580
Asp	Arg	Asn	Gln	Asp	Ala	Thr	Asp	Asp	Thr	Glu	Leu	Gln	Asn	Met	Asn	
		785					790					795				
gag	tac	ctg	agc	tcc	ttc	aag	gtg	gcg	cag	tac	gtg	gtg	cgc	gag	gag	2628
Glu	Tyr	Leu	Ser	Ser	Phe	Lys	Val	Ala	Gln	Tyr	Val	Val	Arg	Glu	Glu	
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gac	ggc	gtg	gag	gag	gtg	gag	cgg	gaa	atc	atc	aag	cag	gag	gag	aac	2676
Asp	Gly	Val	Glu	Glu	Val	Glu	Arg	Glu	Ile	Ile	Lys	Gln	Glu	Glu	Asn	
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gtg	gac	ccc	gac	tac	tgg	gag	aag	ctg	ctg	cgg	cac	cac	tat	gag	cag	2724
Val	Asp	Pro	Asp	Tyr	Trp	Glu	Lys	Leu	Leu	Arg	His	His	Tyr	Glu	Gln	
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cag	cag	gag	gac	ctg	gcc	cgc	aac	ctg	ggc	aag	ggc	aag	cgc	atc	cgc	2772
Gln	Gln	Glu	Asp	Leu	Ala	Arg	Asn	Leu	Gly	Lys	Gly	Lys	Arg	Ile	Arg	
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aag	cag	gtc	aac	tac	aac	gat	gcc	tcc	cag	gag	gac	cag	gag	tgg	cag	2820
Lys	Gln	Val	Asn	Tyr	Asn	Asp	Ala	Ser	Gln	Glu	Asp	Gln	Glu	Trp	Gln	
		865					870					875				
gat	gag	ctc	tct	gat	aac	cag	tca	gaa	tat	tcc	att	ggc	tct	gag	gat	2868
Asp	Glu	Leu	Ser	Asp	Asn	Gln	Ser	Glu	Tyr	Ser	Ile	Gly	Ser	Glu	Asp	
	880					885					890					
gag	gat	gag	gac	ttt	gaa	gag	agg	ccg	gaa	ggg	cag	agt	gga	cga	cga	2916
Glu	Asp	Glu	Asp	Phe	Glu	Glu	Arg	Pro	Glu	Gly	Gln	Ser	Gly	Arg	Arg	
895					900					905					910	
caa	tcc	cgg	agg	cag	ctg	aag	agt	gac	agg	gac	aag	ccc	ctg	ccc	ccg	2964
Gln	Ser	Arg	Arg	Gln	Leu	Lys	Ser	Asp	Arg	Asp	Lys	Pro	Leu	Pro	Pro	
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ctt	ctc	gcc	cga	gtt	ggt	ggc	aac	atc	gag	gtg	ctg	ggc	ttc	aat	gcc	3012
Leu	Leu	Ala	Arg	Val	Gly	Gly	Asn	Ile	Glu	Val	Leu	Gly	Phe	Asn	Ala	
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Arg	Gln	Arg	Lys	Ala	Phe	Leu	Asn	Ala	Ile	Met	Arg	Trp	Gly	Met	Pro	
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ccg	cag	gac	gcc	ttc	aac	tcc	cac	tgg	ctg	gtg	cgg	gac	ctt	cga	ggg	3108
Pro	Gln	Asp	Ala	Phe	Asn	Ser	His	Trp	Leu	Val	Arg	Asp	Leu	Arg	Gly	
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Lys	Ser	Glu	Lys	Glu	Phe	Arg	Ala	Tyr	Val	Ser	Leu	Phe	Met	Arg	His	

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Leu Cys Glu Pro Gly Ala Asp Gly Ala Glu Thr Phe Ala Asp Gly Val				
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ccc cgg gag ggc ctc tcc agg cag cac gtg ctg acc cgc atc ggg gtc				3252
Pro Arg Glu Gly Leu Ser Arg Gln His Val Leu Thr Arg Ile Gly Val				
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atg tca cta gtt agg aag aag gtt cag gag ttt gag cat gtc aac ggg				3300
Met Ser Leu Val Arg Lys Lys Val Gln Glu Phe Glu His Val Asn Gly				
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Lys Tyr Ser Thr Pro Asp Leu Ile Pro Glu Gly Pro Glu Gly Lys Lys				
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ccg ggc gag gtg atc tcc tcg gac ccc aac aca cca gtg ccc gcc agc				3396
Pro Gly Glu Val Ile Ser Ser Asp Pro Asn Thr Pro Val Pro Ala Ser				
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cct gcc cac ctc ctg cca gcc ccg ctg ggc ctg cca gac aaa atg gaa				3444
Pro Ala His Leu Leu Pro Ala Pro Leu Gly Leu Pro Asp Lys Met Glu				
	1075	1080	1085	
gcc cag ctg ggc tac atg gat gag aaa gac ccc ggg gca cag aag cca				3492
Ala Gln Leu Gly Tyr Met Asp Glu Lys Asp Pro Gly Ala Gln Lys Pro				
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agg cag ccc ctg gaa gtc cag gcc ctt cca gcc gcc ttg gat aga gtg				3540
Arg Gln Pro Leu Glu Val Gln Ala Leu Pro Ala Ala Leu Asp Arg Val				
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gag agt gag gac aag cac gag agc cca gcc agc aag gag aga gcc cga				3588
Glu Ser Glu Asp Lys His Glu Ser Pro Ala Ser Lys Glu Arg Ala Arg				
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gag gag cgg cca gag gag acg gag aag gcc ccg ccc tcc ccg gag cag				3636
Glu Glu Arg Pro Glu Glu Thr Glu Lys Ala Pro Pro Ser Pro Glu Gln				
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ctg ccg aga gag gag gtg ctt cct gag aag gag aag atc ctg gac aag				3684
Leu Pro Arg Glu Glu Val Leu Pro Glu Lys Glu Lys Ile Leu Asp Lys				
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ctg gag ctg agc ttg atc cac agc aga ggg gac agt tcc gaa ctc agg				3732
Leu Glu Leu Ser Leu Ile His Ser Arg Gly Asp Ser Ser Glu Leu Arg				
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cca gat gac acc aag gct gag gag aag gag ccc att gaa aca cag caa				3780
Pro Asp Asp Thr Lys Ala Glu Glu Lys Glu Pro Ile Glu Thr Gln Gln				
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Asn Gly Asp Lys Glu Glu Asp Asp Glu Gly Lys Lys Glu Asp Lys Lys				
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ggg Gly	aaa Lys	ttc Phe	aag Lys	ttc Phe	atg Met	ttc Phe	aac Asn	atc Ile	gcg Ala	gac Asp	ggg Gly	ggc Gly	ttc Phe	acg Thr	gag Glu	3876
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			1235					1240					1245			
aaa Lys	atc Ile	tac Tyr	gac Asp	atc Ile	tgg Trp	cac His	cgg Arg	cgc Arg	cat His	gac Asp	tac Tyr	tgg Trp	ctg Leu	ctg Leu	gcg Ala	3972
		1250					1255					1260				
ggc Gly	atc Ile	gtg Val	acg Thr	cac His	ggc Gly	tac Tyr	gcc Ala	cgc Arg	tgg Trp	cag Gln	gac Asp	atc Ile	cag Gln	aat Asn	gac Asp	4020
		1265					1270				1275					
cca Pro	cgg Arg	tac Tyr	atg Met	atc Ile	ctc Leu	aac Asn	gag Glu	ccc Pro	ttc Phe	aag Lys	tct Ser	gag Glu	gtc Val	cac His	aag Lys	4068
	1280				1285					1290						
ggc Gly	aac Asn	tac Tyr	ctg Leu	gag Glu	atg Met	aag Lys	aac Asn	aag Lys	ttc Phe	ctg Leu	gcc Ala	cgc Arg	agg Arg	ttt Phe	aag Lys	4116
1295			1300					1305							1310	
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		1330					1335				1340					
gcc Ala	cgc Arg	ctg Leu	gct Ala	gaa Glu	gtg Val	gag Glu	tgc Cys	ctc Leu	gcc Ala	gag Glu	agc Ser	cac His	cag Gln	cac His	ctg Leu	4260
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tcc Ser	aag Lys	gag Glu	tcc Ser	ctt Leu	gct Ala	ggg Gly	aac Asn	aag Lys	cct Pro	gcc Ala	aat Asn	gcc Ala	gtc Val	ctg Leu	cac His	4308
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aag Lys	gtc Val	ctg Leu	aac Asn	cag Gln	ctg Leu	gag Glu	gag Glu	ctg Leu	ctg Leu	agc Ser	gac Asp	atg Met	aag Lys	gcc Ala	gac Asp	4356
1375			1380					1385					1390			
gtg Val	acc Thr	cgg Arg	ctg Leu	cca Pro	tcc Ser	atg Met	ctg Leu	tcc Ser	cgc Arg	atc Ile	ccc Pro	ccg Pro	gtg Val	gcc Ala	gcc Ala	4404
			1395				1400						1405			
cgg Arg	ctg Leu	cag Gln	atg Met	tcg Ser	gag Glu	cgc Arg	agc Ser	atc Ile	ctg Leu	agc Ser	cgc Arg	ctg Leu	acc Thr	aac Asn	cgc Arg	4452
		1410				1415					1420					
gcc Ala	ggg Gly	gac Asp	ccc Pro	acc Thr	atc Ile	cag Gln	cag Gln	ggc Gly	gct Ala	ttc Phe	ggc Gly	tcc Ser	tcc Ser	cag Gln	atg Met	4500
	1425					1430					1435					

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Tyr Ser Asn Asn Phe Gly Pro Asn Phe Arg Gly Pro Gly Pro Gly Gly	
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att gtc aac tac aac cag atg ccc ctg ggg ccc tat gtg acc gat atc	4596
Ile Val Asn Tyr Asn Gln Met Pro Leu Gly Pro Tyr Val Thr Asp Ile	
1455 1460 1465 1470	
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Met Ala Ser Pro Asp Pro Pro Ala Thr Ser Tyr Ala Pro Ser Asp	
1 5 10 15	
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Val Pro Ser Gly Val Ala Leu Phe Leu Thr Ile Pro Phe Ala Phe Phe	
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ctg ccc gag ctg ata ttt ggg ttc ttg gtc tgg acc atg gta gcc gcc	203
Leu Pro Glu Leu Ile Phe Gly Phe Leu Val Trp Thr Met Val Ala Ala	
35 40 45	
acc cac ata gta tac ccc ttg ctg caa gga tgg gtg atg tat gtc tcg	251
Thr His Ile Val Tyr Pro Leu Leu Gln Gly Trp Val Met Tyr Val Ser	
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ctc acc tcg ttt ctc atc tcc ttg atg ttc ctg ttg tct tac ttg ttt	299
Leu Thr Ser Phe Leu Ile Ser Leu Met Phe Leu Leu Ser Tyr Leu Phe	
65 70 75	
gga ttt tac aaa aga ttt gaa tcc tgg aga gtt ctg gac agc ctg tac	347
Gly Phe Tyr Lys Arg Phe Glu Ser Trp Arg Val Leu Asp Ser Leu Tyr	
80 85 90 95	
cac ggg acc act ggc atc ctg tac atg agc gct gcc gtc cta caa gta	395
His Gly Thr Thr Gly Ile Leu Tyr Met Ser Ala Ala Val Leu Gln Val	
100 105 110	

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cat gcc acg att gtt tct gag aaa ctg ctg gac cca aga att tac tac      443
His Ala Thr Ile Val Ser Glu Lys Leu Leu Asp Pro Arg Ile Tyr Tyr
      115                      120                      125

att aat tcg gca gcc tcg ttc ttc gcc ttc atc gcc acg ctg ctc tac      491
Ile Asn Ser Ala Ala Ser Phe Phe Ala Phe Ile Ala Thr Leu Leu Tyr
      130                      135                      140

att ctc cat gcc ttc agc atc tat tac cac tga tgcacagg cgccaggcca      542
Ile Leu His Ala Phe Ser Ile Tyr Tyr His *
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gccatctgga tgacaaacgg aagatccact aaaacgtcca cgggattaac agaacgtcct      662

tgcagactga gcgatgacac cacactttgt ttggacattt aaattcactc tgctgaatag      722

gaggaagctt ttctttttcc tgggaaaaca actgtctctt ggaattatct gaccatgaac      782

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aggggaatac tcagtctgat cttttttttg tttgttttat tttgtttttt ttgagacgga      962

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ccaggcgcgc ccgctgctcg gtggcaggag ggccggcgga gcgcc      atg gcc tgc      174
                                     Met Ala Cys
                                     1

atc ctg aag aga aag tct gtg att gct gtg agc ttc ata gca gcg ttc      222
Ile Leu Lys Arg Lys Ser Val Ile Ala Val Ser Phe Ile Ala Ala Phe
      5                      10                      15

ctt ttc ctg ctg gtt gtg cgt ctt gta aat gaa gtg aat ttc cca ttg      270
Leu Phe Leu Leu Val Val Arg Leu Val Asn Glu Val Asn Phe Pro Leu

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cta cta aac tgc ttt gga caa cct ggt aca aag tgg ata cca ttc tcc				318
Leu Leu Asn Cys Phe Gly Gln Pro Gly Thr Lys Trp Ile Pro Phe Ser	40	45	50	
tac aca tac agg cgg ccc ctt cga act cac tat gga tac ata aat gtg				366
Tyr Thr Tyr Arg Arg Pro Leu Arg Thr His Tyr Gly Tyr Ile Asn Val	55	60	65	
aag aca caa gag cct ttg caa ctg gac tgt gac ctt tgt gcc ata gtg				414
Lys Thr Gln Glu Pro Leu Gln Leu Asp Cys Asp Leu Cys Ala Ile Val	70	75	80	
tca aac tca ggt cag atg gtt ggc cag aag gtg gga aat gag ata gat				462
Ser Asn Ser Gly Gln Met Val Gly Gln Lys Val Gly Asn Glu Ile Asp	85	90	95	
cga tcc tcc tgc att tgg aga atg aac aat gcc ccc acc aaa ggt tat				510
Arg Ser Ser Cys Ile Trp Arg Met Asn Asn Ala Pro Thr Lys Gly Tyr	100	105	110	115
gaa gaa gat gtc ggc cgc atg acc atg att cga gtt gtg tcc cat acc				558
Glu Glu Asp Val Gly Arg Met Thr Met Ile Arg Val Val Ser His Thr	120	125	130	
agc gtt cct ctt ttg cta aaa aac cct gat tat ttt ttc aag gaa gcg				606
Ser Val Pro Leu Leu Leu Lys Asn Pro Asp Tyr Phe Phe Lys Glu Ala	135	140	145	
aat act act att tgt gtt att tgg gga cct ttc cgc aat atg agg aaa				654
Asn Thr Thr Ile Cys Val Ile Trp Gly Pro Phe Arg Asn Met Arg Lys	150	155	160	
gat ggc aat ggc atc gtt tac aac atg ttg aaa aag aca gtt ggt atc				702
Asp Gly Asn Gly Ile Val Tyr Asn Met Leu Lys Lys Thr Val Gly Ile	165	170	175	
tat ccg aat gcc caa ata tac gtg acc aca gag aag cgc atg agt tac				750
Tyr Pro Asn Ala Gln Ile Tyr Val Thr Thr Glu Lys Arg Met Ser Tyr	180	185	190	195
tgt gat gga gtt ttt aag aag gaa act ggg aag gac agg ggg cat gca				798
Cys Asp Gly Val Phe Lys Lys Glu Thr Gly Lys Asp Arg Gly His Ala	200	205	210	
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Arg Arg Leu Leu Ile Ser Thr Asp Thr Phe *	215	220		
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 atg ccc ttg aag ctc tac ttg cct ggt ggt aat tcc agg atg acc cag 226
 Met Pro Leu Lys Leu Tyr Leu Pro Gly Gly Asn Ser Arg Met Thr Gln
 1 5 10 15
 gag agg ctg gaa aga gcg ttc aaa cgg cag ggc agc cag ccc gca cct 274
 Glu Arg Leu Glu Arg Ala Phe Lys Arg Gln Gly Ser Gln Pro Ala Pro
 20 25 30
 gtc agg aaa aat cag ttg ctg ccg tct gac aag gtg gat ggt gag ctg 322
 Val Arg Lys Asn Gln Leu Leu Pro Ser Asp Lys Val Asp Gly Glu Leu
 35 40 45
 ggt gcc ctg cgg ctc gag gat gtg gag gat gag ttg ata agg gaa gag 370
 Gly Ala Leu Arg Leu Glu Asp Val Glu Asp Glu Leu Ile Arg Glu Glu
 50 55 60
 gtc atc ctg tcg cca gtc cca tca gtg ctc aag ttg cag aca gca tca 418
 Val Ile Leu Ser Pro Val Pro Ser Val Leu Lys Leu Gln Thr Ala Ser
 65 70 75 80
 aaa cca att gac ctc tca gta gca aag gaa ata aag acc ctt ctg ttt 466
 Lys Pro Ile Asp Leu Ser Val Ala Lys Glu Ile Lys Thr Leu Leu Phe
 85 90 95

ggt tcc agc ttt tgc tgt ttc aat gaa gaa tgg aaa ctt cag agt ttt Gly Ser Ser Phe Cys Cys Phe Asn Glu Glu Trp Lys Leu Gln Ser Phe 100 105 110	514
tcc ttt agt aac aca gcc tca tta aaa tac ggc ata gtg cag aac aag Ser Phe Ser Asn Thr Ala Ser Leu Lys Tyr Gly Ile Val Gln Asn Lys 115 120 125	562
ggt ggt cct tgc gga gtc ctg gca gct gtc caa ggc tgt gtc cta cag Gly Gly Pro Cys Gly Val Leu Ala Ala Val Gln Gly Cys Val Leu Gln 130 135 140	610
aaa ctc ctg ttt gaa gga gat agc aaa gcc gac tgt gct cag gga ctg Lys Leu Leu Phe Glu Gly Asp Ser Lys Ala Asp Cys Ala Gln Gly Leu 145 150 155 160	658
cag cct tca gat gcc cac cgg acc cgc tgc ctc gtc ctg gcc ctc gca Gln Pro Ser Asp Ala His Arg Thr Arg Cys Leu Val Leu Ala Leu Ala 165 170 175	706
gac att gtg tgg cgg gca ggg ggc cga gag aga gcc gtt gtt gca ctg Asp Ile Val Trp Arg Ala Gly Gly Arg Glu Arg Ala Val Val Ala Leu 180 185 190	754
gct tcg aga aca cag cag ttc agt cca aca ggg aaa tac aaa gca gat Ala Ser Arg Thr Gln Gln Phe Ser Pro Thr Gly Lys Tyr Lys Ala Asp 195 200 205	802
gga gtc tta gaa aca ctt acg ctt cac agt ttg acc tgc tat gag gac Gly Val Leu Glu Thr Leu Thr Leu His Ser Leu Thr Cys Tyr Glu Asp 210 215 220	850
ctg gtg act ttt ctt caa caa agc att cat cag ttt gaa gtg ggc ccc Leu Val Thr Phe Leu Gln Gln Ser Ile His Gln Phe Glu Val Gly Pro 225 230 235 240	898
tat ggc tgc atc ctg ctc acc ctt tct gcc atc ctg tcc agg tct aca Tyr Gly Cys Ile Leu Leu Thr Leu Ser Ala Ile Leu Ser Arg Ser Thr 245 250 255	946
gag ctc atc cgc cag gac ttt gat gtc ccc acc agc cac ctg att gga Glu Leu Ile Arg Gln Asp Phe Asp Val Pro Thr Ser His Leu Ile Gly 260 265 270	994
gca cat ggc tac tgt aca cag gaa ctt gtc aat ctg ctc ctg act ggg Ala His Gly Tyr Cys Thr Gln Glu Leu Val Asn Leu Leu Leu Thr Gly 275 280 285	1042
aaa gct gtg tcc aac gtt ttc aac gat gtg gtt gag ctg gat tct ggg Lys Ala Val Ser Asn Val Phe Asn Asp Val Val Glu Leu Asp Ser Gly 290 295 300	1090
gat ggg aac atc aca ctt ctc aga ggc att gct gca cgc agt gat att Asp Gly Asn Ile Thr Leu Leu Arg Gly Ile Ala Ala Arg Ser Asp Ile 305 310 315 320	1138
ggc ttc tta tct ctc ttt gag cat tac aac atg tgc cag gtt ggc tgc	1186

Gly	Phe	Leu	Ser	Leu	Phe	Glu	His	Tyr	Asn	Met	Cys	Gln	Val	Gly	Cys	
				325					330					335		
ttc	ctg	aag	acc	ccg	agg	ttc	ccc	atc	tgg	gtg	gtt	tgc	agt	gag	agc	1234
Phe	Leu	Lys	Thr	Pro	Arg	Phe	Pro	Ile	Trp	Val	Val	Cys	Ser	Glu	Ser	
				340				345					350			
cac	ttc	agc	atc	ctc	ttt	agc	ctg	cag	ccg	ggg	ctc	ctg	cgt	gac	tgg	1282
His	Phe	Ser	Ile	Leu	Phe	Ser	Leu	Gln	Pro	Gly	Leu	Leu	Arg	Asp	Trp	
		355					360					365				
agg	act	gag	agg	ctc	ttt	gac	ttg	tac	tac	tac	gat	ggc	ctg	gcc	aac	1330
Arg	Thr	Glu	Arg	Leu	Phe	Asp	Leu	Tyr	Tyr	Tyr	Asp	Gly	Leu	Ala	Asn	
	370					375					380					
cag	cag	gag	cag	atc	cgg	ctg	acc	att	gac	acc	acc	caa	acc	atc	tct	1378
Gln	Gln	Glu	Gln	Ile	Arg	Leu	Thr	Ile	Asp	Thr	Thr	Gln	Thr	Ile	Ser	
385					390				395					400		
gag	gac	aca	gac	aac	gac	ctt	gtc	cca	ccc	ctc	gag	ctc	tgc	atc	aga	1426
Glu	Asp	Thr	Asp	Asn	Asp	Leu	Val	Pro	Pro	Leu	Glu	Leu	Cys	Ile	Arg	
				405				410					415			
acc	aag	tgg	aag	ggg	gca	tca	gtg	aac	tgg	aac	ggc	tca	gac	ccc	atc	1474
Thr	Lys	Trp	Lys	Gly	Ala	Ser	Val	Asn	Trp	Asn	Gly	Ser	Asp	Pro	Ile	
			420					425					430			
ctg	tga	ccgttgatg	tgggtaaacc	ctgtggtcca	ccactcatca	cctcatcacc										1530
Leu	*															
gaggatgaca	gctgaacccc	aagcctctgg	ggcaggtctc	atgtacccca	acctgggtca											1590
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tgtgctgggg	accagtgtg	ttgctgggtc	ccctcccagc	tgagctgtga	ctgctgagta											1710
ctggaaggag	gttgccaggg	tctctgctac	ctttgtctgc	atccctccct	tgctccctgc											1770
tgggtggtcc	ctcaccagc	cctccaatgt	ggttggccct	ggggactcat	tacttctggt											1830
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (371)..(595)

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agaacagcta cccatctcaa accccaggag tcaccagccc ttggggccctc acatccctgg 180
agcctcagcc ccctccacac acgtgctgtg aatcataggg ggatcaggat actcctgctc 240
acagacaccc atctccccct accaaaaata acgctggggt cctccttcca ccttgactct 300
gcctctctgt ctgcaggagc ctggtcgggg tgctccacag aagctgtgcc tgggcttggg 360
agccaaggcc  atg tcc ctc tcc cgg cca ggg gag acg gag ccc atc cac 409
              Met Ser Leu Ser Arg Pro Gly Glu Thr Glu Pro Ile His
              1             5             10

agt gtc agc tat ggc cat gtg gcc gcc tgc cag cta atg ggc ccc cac 457
Ser Val Ser Tyr Gly His Val Ala Ala Cys Gln Leu Met Gly Pro His
    15             20             25

acc ctg gcc ttg agg gtg gga gag agc cag ctc ctc ctg cag agc ccc 505
Thr Leu Ala Leu Arg Val Gly Glu Ser Gln Leu Leu Leu Gln Ser Pro
    30             35             40             45

cag gtg agt gag aag agg agt tgt ggg agg agg aga gaa ggg aag cga 553
Gln Val Ser Glu Lys Arg Ser Cys Gly Arg Arg Arg Glu Gly Lys Arg
          50             55             60

tgt cag gaa gca ttt aca gaa cac caa acc tgg gcc agg tag agctcta 602
Cys Gln Glu Ala Phe Thr Glu His Gln Thr Trp Ala Arg  *
          65             70             75

agcactgggg atccagcagt gatcacagac aagctgaagg agcttacact agagtggagt 662
cagacaataa acaaggaatc ccaggctatg aagacagtga gaaatgctac aaaggaaaga 722
gtgatgtgac aggaagccag ggaagggttc tcaaaaaggg tgccatttaa gctagccagg 782
gaaga 787

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<210> 222
 <211> 1184
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (66)..(425)

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<400> 222
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aggag  atg ccc agc ctg gag gtg atc acg ctc agg tac ctc gct cct 107
        Met Pro Ser Leu Val Ile Thr Leu Arg Tyr Leu Ala Pro
        1             5             10

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gct gtc atg ctc agc ctg ggg cct gga agc cgg ggc aga gcc tca cgt	155
Ala Val Met Leu Ser Leu Gly Pro Gly Ser Arg Gly Arg Ala Ser Arg	
15 20 25 30	
ccc tcc agt ggg acc cag cac tgt gac ata acc tgg aaa cct cca aca	203
Pro Ser Ser Gly Thr Gln His Cys Asp Ile Thr Trp Lys Pro Pro Thr	
35 40 45	
cag act gag ggc ggc ttc cag aag ggg agg ggc cgg gac agc gag agc	251
Gln Thr Glu Gly Gly Phe Gln Lys Gly Arg Gly Arg Asp Ser Glu Ser	
50 55 60	
tgg gcc tac cct gtg gcc ccc atg ttc agc cct cct tcc tca gag cct	299
Trp Ala Tyr Pro Val Ala Pro Met Phe Ser Pro Pro Ser Ser Glu Pro	
65 70 75	
cac ctg ggc ctc ctg atg gct cct gtc ccc tgc ctg ccc tgc tgt acg	347
His Leu Gly Leu Leu Met Ala Pro Val Pro Cys Leu Pro Cys Cys Thr	
80 85 90	
cct gcc cac cct tgg cct gtg tgc tcc gat aag cca ttg ctg tgt tca	395
Pro Ala His Pro Trp Pro Val Cys Ser Asp Lys Pro Leu Leu Cys Ser	
95 100 105 110	
ctg ggc cag tgc gtg gtg gag ccc tcc taa g gattcacggt ggccccgcct	446
Leu Gly Gln Ser Val Val Glu Pro Ser *	
115 120	
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ccccagtgcc accactgcct accagtttct ctgcaccccc tgacctgtgc ccgtcttctg	566
gggtcactgc cctcccagca gactaaggga agcttgaatg aacaaatgtt actggacttt	626
caggcagttg ggggtgtattt gggggctctg gggaagagaa gagctccctt tatccctgaa	686
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catgttgatg cccgtgcccc gctgtctgcc cgccatgggc tgaggccagt ccatctggtg	1046
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ccttggggcga ggcattggc	1184

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 <211> 4716
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (74)..(1732)

<400> 223

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agagccttgg gag atg acg agt gag atg aca aga agc cca ttc tca gat	109
Met Thr Ser Glu Met Thr Arg Ser Pro Phe Ser Asp	
1 5 10	
tgg gaa tct ata tat gtg aca cag gaa tta cct ctg aag cag ttc atg	157
Trp Glu Ser Ile Tyr Val Thr Gln Glu Leu Pro Leu Lys Gln Phe Met	
15 20 25	
tat gat gat gca tgc atg gag gga att act agc tat gga ctt gag tgt	205
Tyr Asp Asp Ala Cys Met Glu Gly Ile Thr Ser Tyr Gly Leu Glu Cys	
30 35 40	
tcc act ttt gaa gaa aat tgg aaa tgg gaa gac ctt ttt gag aag cag	253
Ser Thr Phe Glu Glu Asn Trp Lys Trp Glu Asp Leu Phe Glu Lys Gln	
45 50 55 60	
atg gga agt cat gag atg ttt agc aag aaa gaa ata atc act cat aaa	301
Met Gly Ser His Glu Met Phe Ser Lys Lys Glu Ile Ile Thr His Lys	
65 70 75	
gaa acc atc act aag gaa aca gaa ttc aaa tat act aaa ttt ggg aaa	349
Glu Thr Ile Thr Lys Glu Thr Glu Phe Lys Tyr Thr Lys Phe Gly Lys	
80 85 90	
tgt atc cat ctg gaa aac ata gaa gag agt att tat aat cac aca tca	397
Cys Ile His Leu Glu Asn Ile Glu Glu Ser Ile Tyr Asn His Thr Ser	
95 100 105	
gat aaa aaa agc ttc tcc aaa aat tct att gta ata aaa cac aag aaa	445
Asp Lys Lys Ser Phe Ser Lys Asn Ser Ile Val Ile Lys His Lys Lys	
110 115 120	
gtc tat gta gga aag aag ctt ttt aaa tgt aat gaa tgt gac aaa acc	493
Val Tyr Val Gly Lys Lys Leu Phe Lys Cys Asn Glu Cys Asp Lys Thr	
125 130 135 140	
ttc acc cat agc tca tcc ctt act gtt cat ttt aga att cat act ggt	541
Phe Thr His Ser Ser Ser Leu Thr Val His Phe Arg Ile His Thr Gly	
145 150 155	
gaa aaa cca tat gca tgt gag gaa tgt gga aaa gcc ttc aag caa agg	589
Glu Lys Pro Tyr Ala Cys Glu Glu Cys Gly Lys Ala Phe Lys Gln Arg	
160 165 170	

aatgccagtg aaacagaacc gcttactccc ttgttaaggg ggctgaagcc ggggagccaa	2342
gtggttccca tgcccactga gccagcaag ctaagatcca ctggcttgga attctccctg	2402
ccagcacagc agtctgaagt caacctggga tgatcaagct tgggtggggg aggggcgcca	2462
accattacca aagcttgaat aggtgggtttt cccctcacag cgtaaacaaa gccatgggga	2522
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tgcagcctcc actggtgata cccaggcaga cagggtctgg agtggacctc cagcaaactc	3002
cagcagacct gcagccgagg ggcctcactg ttagaaggaa aactaacagg aatataatca	3062
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cacattcaat gggttgcata cccatgaatt ctaaaacttc atcctctttt gtccctttcg	3962
agttaacatt acagccacag tgacctttca aaaatgcaaa ttaagttact cttaaaactc	4022

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tcttgaaagc agtatggcag tcataaaaat tttggaacca aaacagtatc tttttttaag 4202
ctaaaaaaaa gttttaaatg gtgtctttct atgttgccca ggttggtctc aaactcctgt 4262
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ttaaacacgt atcttaaggt agatgggtgat tagcacatgt agtatgctta acatttaata 4382
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gaaattaatt atgacttgat aaatagaaca tgttttaaga agtggctata tagctctgga 4502
taaaacgaac aaaagaatta gaattcctgc ggggaatata tacaagactt tatttagtca 4562
agtaaaaaaa aatcactaat gtttaactga agaaagagaa attgaataat atagttctat 4622
ttcaacatgt gggttcacag atttattcta accttccaag taaagttggt ccactagtaa 4682
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<210> 224
<211> 1026
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (578)..(916)

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gcagaggagg cttaaggctg gcctgggaga gattcttggt ctagctccca gcacggagcc 180
ttgcttgtgt cccagggcgg cactaaccag aaccagaaaa ggaaatcttt ggccctcggg 240
gagaattatg ccaattatct gtctgggtcc tgtctttgaa aatgcccgaga tgttggttta 300
caaatcagga agctgtcttg gggcaatctc tgttccctct ttgatgcaga gagcctttct 360
ctgtaaacac tggagagcag ggcttcactg tctggctccc ctccgcctc ttgcaggaag 420
gactagatgc tgctgatcag ctgatcatgg ctgagccggg tagagcttgg ggctctccta 480
agaggtcacc cactgggagg gagcttcaca gctgttcttt tgaccagga aggagctctt 540
tcaggactgt ggcaccagga gccgtggccc tctgcc atg cca ttg ttc cca ctt 595

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Met Pro Leu Phe Pro Leu
1 5

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ccc tgc cct tgg gag tct tgg aga cag ctg act agc tgc cct gag ggg      643
Pro Cys Pro Trp Glu Ser Trp Arg Gln Leu Thr Ser Cys Pro Glu Gly
          10          15          20

tcc acc gct ctc acc ttc tca ctg gtg gct gct gcc att ctc ctg ggc      691
Ser Thr Ala Leu Thr Phe Ser Leu Val Ala Ala Ala Ile Leu Leu Gly
          25          30          35

tct gca cag aaa gct ttg gtc ctt ctg aaa gcc act ctg ccc ctt cct      739
Ser Ala Gln Lys Ala Leu Val Leu Leu Lys Ala Thr Leu Pro Leu Pro
          40          45          50

gca gca cca gat ccc cct gag ccg gta ctg ctg cct cca cct ggg cca      787
Ala Ala Pro Asp Pro Pro Glu Pro Val Leu Leu Pro Pro Pro Gly Pro
          55          60          65          70

aga cta gtc ttg gtg ttc acc ctt ctt cgt gct tca gaa agt agg gat      835
Arg Leu Val Leu Val Phe Thr Leu Leu Arg Ala Ser Glu Ser Arg Asp
          75          80          85

atc tgg gga cat gac tgt gtt tcc ctg ggg tcc ttt cag aag aga ctt      883
Ile Trp Gly His Asp Cys Val Ser Leu Gly Ser Phe Gln Lys Arg Leu
          90          95          100

agg aag ctc ctg ctc agg aat ctg gcc ctc tga aagagccc cttcaaagca      934
Arg Lys Leu Leu Leu Arg Asn Leu Ala Leu *
          105          110

gcctggggcag caggtaacgt gggtttccctt gcggccccct cctcccagct gcatagactc      994

gtgggtttgaa gtgaacagat cttgtccgga ac      1026

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<210> 225
<211> 1267
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (70)..(609)

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<400> 225
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accgccaag      atg gtg gtg ggc gcg ttc cct atg gcg aag ctg cta tac      108
                Met Val Val Gly Ala Phe Pro Met Ala Lys Leu Leu Tyr
                1          5          10

ttg ggc atc cgg cag gtc agc aag ccg ctt gcc aac cgt att aag gag      156
Leu Gly Ile Arg Gln Val Ser Lys Pro Leu Ala Asn Arg Ile Lys Glu
          15          20          25

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gcc gcc cgc cga agc gag ttc ttc aag acc tat atc tgc ctc ccg ccg 204
 Ala Ala Arg Arg Ser Glu Phe Phe Lys Thr Tyr Ile Cys Leu Pro Pro
 30 35 40 45
 gct caa ctg tat cac tgg gtg gag atg cgg acc aag atg cgc atc atg 252
 Ala Gln Leu Tyr His Trp Val Glu Met Arg Thr Lys Met Arg Ile Met
 50 55 60
 ggc ttc cgg ggc acg gtc atc aag ccg ctg aac gag gag gcg gca gct 300
 Gly Phe Arg Gly Thr Val Ile Lys Pro Leu Asn Glu Glu Ala Ala Ala
 65 70 75
 gag ctg ggc gca gag ctg ctg ggc gaa gcc acc atc ttc atc gtg ggc 348
 Glu Leu Gly Ala Glu Leu Leu Gly Glu Ala Thr Ile Phe Ile Val Gly
 80 85 90
 ggc ggc tgc cta gtg ctg gag tac tgg cgc cac cag gcg cag cag cgc 396
 Gly Gly Cys Leu Val Leu Glu Tyr Trp Arg His Gln Ala Gln Gln Arg
 95 100 105
 cac aag gag gag gag cag cgt gct gcc tgg aac gcg ctg cgg gac gag 444
 His Lys Glu Glu Glu Gln Arg Ala Ala Trp Asn Ala Leu Arg Asp Glu
 110 115 120 125
 gtg ggc cac ctg gcg ctg gcg ctg gaa gcg ctg cag gcg cag gtg cag 492
 Val Gly His Leu Ala Leu Ala Leu Glu Ala Leu Gln Ala Gln Val Gln
 130 135 140
 gcg gcg ccg cca cag ggc gcc ctg gag gaa ctg cgc aca gag ctg caa 540
 Ala Ala Pro Pro Gln Gly Ala Leu Glu Glu Leu Arg Thr Glu Leu Gln
 145 150 155
 gag gtg cgc gcc cag ctc tgc aat ccc ggc cgg tcc gct tcc cac gca 588
 Glu Val Arg Ala Gln Leu Cys Asn Pro Gly Arg Ser Ala Ser His Ala
 160 165 170
 gtg cct gcg tcc aag aaa tag ga gcttgctgga tggaacctga atttggacat 641
 Val Pro Ala Ser Lys Lys *
 175 180
 ggccatatgta cctaacgtgg ccttcttccc gcaccaccct tgccctgcgct ggcccagtg 701
 aaaccaccag gatcttgatg caacttggca tttggttacc cctgctgata agagcagcca 761
 ttacctgcca ctgggaccag caggtgaagc gttgcaacat agccccctcc atcatccttc 821
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Cys Phe Cys Trp Cys Cys Cys Cys Ser Cys Ser Cys Leu Thr Val Arg
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Asn Glu Glu Arg Gly Glu Asn Ala Gly Arg Pro Thr His Thr Thr Lys
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Glu Val Ile Asn Arg Asn Leu Leu Asp Pro Asn Pro His Met Tyr Glu			
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Asp Ala Gln Leu Gln Ile Tyr Thr Leu Met His Arg Asp Ser Phe Pro			
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Met Ala
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5 10 15
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Pro Thr Cys Ser Pro Thr Ser Asp Ser Glu Asn Leu Ser Pro Asp Glu
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Leu Glu Leu Leu Ala Lys Leu Glu Glu Gln Asn Arg Leu Leu Glu Ala
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Asp Ser Lys Ser Met Arg Ser Met Asn Gly Ser Arg Arg Asn Ser Gly
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Glu Glu Asp Thr Trp Ile Leu Trp Gly Arg Ile Ala Asn Glu Trp Glu
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Gly Ile Pro His His Phe Arg Ala Ile Val Trp Gln Leu Leu Cys Ser
115 120 125 130
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Pro	Glu	His	Glu	Phe	Phe	Lys	Gly	Gln	Asp	Ser	Leu	Gly	Gln	Glu	Val	
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ctc	ttc	aac	gtc	atg	aag	gca	tac	tcg	ctg	gta	gac	cgg	gag	gtg	ggc	751
Leu	Phe	Asn	Val	Met	Lys	Ala	Tyr	Ser	Leu	Val	Asp	Arg	Glu	Val	Gly	
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tac	tgc	cag	gga	agc	gcc	ttc	atc	gtg	ggc	ctg	ctc	ctc	atg	cag	atg	799
Tyr	Cys	Gln	Gly	Ser	Ala	Phe	Ile	Val	Gly	Leu	Leu	Leu	Met	Gln	Met	
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Pro	Glu	Glu	Glu	Ala	Phe	Cys	Val	Phe	Val	Arg	Leu	Met	Gln	Glu	Tyr	
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Ile	Tyr	Gln	Phe	Glu	Tyr	Met	Leu	Gln	Glu	Gln	Leu	Pro	Asp	Leu	Asn	
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Thr	His	Phe	Arg	Ser	Gln	Ser	Phe	His	Thr	Ser	Met	Tyr	Ala	Ser	Ser	
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Trp	Phe	Leu	Thr	Leu	Phe	Leu	Thr	Thr	Phe	Pro	Leu	Pro	Val	Ala	Thr	
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Val	Gly	Leu	Ala	Leu	Leu	Gln	Val	Asn	Gln	Ala	Glu	Leu	Met	Gln	Leu	
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Asp	Met	Glu	Gly	Met	Ser	Gln	Tyr	Phe	Gln	Arg	Val	Ile	Pro	His	Gln	
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Phe	Asp	Ser	Cys	Pro	Asp	Lys	Leu	Val	Leu	Lys	Ala	Tyr	Gln	Val	Lys	
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Tyr	Asn	Pro	Lys	Lys	Met	Lys	Arg	Leu	Glu	Lys	Glu	Tyr	Ala	Ala	Met	
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Thr His Leu Gln Ala Gly Leu Ser Pro Glu Thr Ile Glu Lys Ala Arg
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Asn Leu Asp Met Phe Lys Asn Phe Lys Ala Asp Asp Pro Gly Ile Lys
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Ile Phe Leu His Gly Asn Asn Leu Asn Ser Leu His Gln Leu Ile His	
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 Ser Leu Gly Val Lys Ala Glu Val Leu Pro Ala Ala Tyr Gln Val Leu
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 His Asp Pro Asp Ser Phe Leu Ala Leu Trp Leu Ser Cys Cys Ser Pro
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 Cys Ser Val Tyr Thr Ile Leu Gln Asn Ile His Met Val Cys Pro Pro
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 Ser Phe Thr Phe Leu Asn Ser Thr Val Ser Val Arg Leu Pro Trp His
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 Pro Ser *
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 ccttgatatgt tttgctgag 546

<210> 230
 <211> 3543
 <212> DNA
 <213> Homo sapiens

<220>

[illegible]

514

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Leu Phe Asp Ala His Lys Leu Glu Ile Ser Asp Glu Phe Ser Glu Ala	
190 195 200	
atc ggc gcg ttg cgg ggc cat gag gac aag atc cgc gtg gtg ctc aac	854
Ile Gly Ala Leu Arg Gly His Glu Asp Lys Ile Arg Val Val Leu Asn	
205 210 215	
aag gcc gac atg gtg gag acg cag cag ctg atg cgc gtc tac ggc gcg	902
Lys Ala Asp Met Val Glu Thr Gln Gln Leu Met Arg Val Tyr Gly Ala	
220 225 230 235	
ctc atg tgg gcg ctg ggc aag gtg gtg ggc acg ccc gag gtg ctg cgc	950
Leu Met Trp Ala Leu Gly Lys Val Val Gly Thr Pro Glu Val Leu Arg	
240 245 250	
gtc tac atc ggc tcc ttc tgg tcc cag ccc ctc ctc gtg ccc gac aac	998
Val Tyr Ile Gly Ser Phe Trp Ser Gln Pro Leu Leu Val Pro Asp Asn	
255 260 265	
cgg cgc ctc ttc gag ctg gag gag cag gac ctc ttc cgc gac atc cag	1046
Arg Arg Leu Phe Glu Leu Glu Glu Gln Asp Leu Phe Arg Asp Ile Gln	
270 275 280	
ggc ctg ccc cgg cac gca gcc ttg cgc aag ctc aac gac ctg gtg aag	1094
Gly Leu Pro Arg His Ala Ala Leu Arg Lys Leu Asn Asp Leu Val Lys	
285 290 295	
agg gcc cgg ctg gtg cga gtt cac gct tac atc atc agc tac ctg aag	1142
Arg Ala Arg Leu Val Arg Val His Ala Tyr Ile Ile Ser Tyr Leu Lys	
300 305 310 315	
aag gag atg ccc tct gtg ttt ggg aag gag aac aag aag aag cag ctg	1190
Lys Glu Met Pro Ser Val Phe Gly Lys Glu Asn Lys Lys Lys Gln Leu	
320 325 330	
atc ctc aaa ctg ccc gtc atc ttt gcg aag att cag ctg gaa cat cac	1238
Ile Leu Lys Leu Pro Val Ile Phe Ala Lys Ile Gln Leu Glu His His	
335 340 345	
atc tcc cct ggg gac ttt cct gat tgc cag aaa atg cag gag ctg ctg	1286
Ile Ser Pro Gly Asp Phe Pro Asp Cys Gln Lys Met Gln Glu Leu Leu	
350 355 360	
atg gcg cac gac ttc acc aag ttt cac tcg ctg aag ccg aag ctg cta	1334
Met Ala His Asp Phe Thr Lys Phe His Ser Leu Lys Pro Lys Leu Leu	
365 370 375	
gag gca ctg gac gag atg ctg acg cac gac atc gcc aag ctc atg ccc	1382
Glu Ala Leu Asp Glu Met Leu Thr His Asp Ile Ala Lys Leu Met Pro	
380 385 390 395	
ctg ctg cgg cag gag gag ctg gag agc acc gag gtg ggc gtg cag ggg	1430
Leu Leu Arg Gln Glu Glu Leu Glu Ser Thr Glu Val Gly Val Gln Gly	
400 405 410	

ggc gct ttt gag ggc acc cac atg ggc ccg ttt gtg gag cgg gga cct Gly Ala Phe Glu Gly Thr His Met Gly Pro Phe Val Glu Arg Gly Pro 415 420 425	1478
gac gag gcc atg gag gac ggc gag gag ggc tcg gac gac gag gcc gag Asp Glu Ala Met Glu Asp Gly Glu Glu Gly Ser Asp Asp Glu Ala Glu 430 435 440	1526
tgg gtg gtg acc aaa gac aag tcc aaa tac gac gag atc ttc tac aac Trp Val Val Thr Lys Asp Lys Ser Lys Tyr Asp Glu Ile Phe Tyr Asn 445 450 455	1574
ctg gcg cct gcc gac ggc aag ctg agc ggc tcc aag gcc aag acc tgg Leu Ala Pro Ala Asp Gly Lys Leu Ser Gly Ser Lys Ala Lys Thr Trp 460 465 470 475	1622
atg gtg ggg acc aag ctc ccc aac tca gtg ctg ggg cgc atc tgg aag Met Val Gly Thr Lys Leu Pro Asn Ser Val Leu Gly Arg Ile Trp Lys 480 485 490	1670
ctc agc gat gtg gac cgc gac ggc atg ctg gat gat gaa gag ttc gcg Leu Ser Asp Val Asp Arg Asp Gly Met Leu Asp Asp Glu Glu Phe Ala 495 500 505	1718
ctg gcc agc cac ctc atc gag gcc aag ctg gaa ggc cac ggg ctg ccc Leu Ala Ser His Leu Ile Glu Ala Lys Leu Glu Gly His Gly Leu Pro 510 515 520	1766
gcc aac ctg ccc cgt cgc ctg gtg cca ccc tcc aag cga cgc cac aag Ala Asn Leu Pro Arg Arg Leu Val Pro Pro Ser Lys Arg Arg His Lys 525 530 535	1814
ggc tcc gcc gag tga gccgggcccc cctcccatgg ccttgcctgtg gctccccagc Gly Ser Ala Glu *	1869
540	
tccagtcggc tgcacgcaca ccctgtctcc ggctcacaca cgccctgcct gccctccctg	1929
cccagctgta aggaccgggg gtctccctcc tctactaccgc cagacacccc ggtggaagca	1989
tttagagggg accacgggag ggacaaggct tctctgtccg cccttcacac ctccagcctc	2049
acgttcactt aggcacatca cacacacact ggacacgcga ggcattccatc catccgtcat	2109
tcattcaaatt atttattgag cacctactat gtgcccagcc ctgtttctagg cactgggcat	2169
taccatagag aacaaaatag acaaatacat ctgccctcat ggaaggtgac gttcccagga	2229
gagggcacct acacagtcac gcaaacacac actaattcct ggcagggccc ccagcccctc	2289
ccctggctga gcagccctgt ggctgaaatg actagcagat aaacagaccc ccttctgtctc	2349
cgcttcctcc tgcccagcca ggcaacaccc tcaaccggct ccatcacatc ctcaggtctc	2409
gggaccatgg ggggctcaga ggggagacac acctactgct tcctcagatg ggcccctccg	2469
cagccccttc ccttgctcgg ggaaagcccc caattctgcc cacacccatt tatttccttc	2529

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cttccttcc tcttttcttt ccttccttcc ttcttttttg tttttgcccc caattctgcc 2589
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acaccccttc cctttcctgt cctgtccttt ctttcttttt tgatagaatc ttgctctgtc 2709
gcccaggctg gagtgcagtg gtgagatctc agctcactgc aacctccacc tcctgggttg 2769
aagtgattct cgtgcctcag cctcctgagt agctgggact gcaggcacgc gccaccacgc 2829
ccagctaatt tttgtatttg agtagagacg gggtttcacc atgttggcca ggctgggtctc 2889
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cagctggtaa tctggactta aggattgctg gccaccgcc tctctgcta ccaccattcc 3189
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ggacgccgac gctgtttgct gccttcacca catattagt cttgacctg gcaggggacc 3369
ccatggaaaa gatggggaag agcaaaatac atggagacga cgcaccctcc aggatgctcg 3429
ctgggattcc cagcccacc actgtcccc acccatggc tgggaggggc ctctgaacgg 3489
aacagtgtcc ccacagagcg aataaagcca aggtcttctc ccaaaaaaaaa aaaa 3543

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<210> 231
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 <212> DNA
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<220>
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 <222> (190)..(1014)

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tgacagctga ctctgccggg gggagtgcg tgcctccca ccgtgctggc gctgaactga 120
ctgtccgctg ccaaggggaag tgacagccgc agccgggctc tcagccagcg gccgggcgcc 180
ccgcggaacc      atg ctc tcc agt acg cag aac gcg ggc ggc tcc tat cag 228
                  Met Leu Ser Ser Thr Gln Asn Ala Gly Gly Ser Tyr Gln
                   1                      5                      10

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cgg gtc cgc ggg gcg ctt gat aca cag aaa tgc agt cca gag aaa agt	276
Arg Val Arg Gly Ala Leu Asp Thr Gln Lys Cys Ser Pro Glu Lys Ser	
15 20 25	
gcc tca ttt ttc agt aaa gtg aca tat tcc tgg ttt agc aga gta att	324
Ala Ser Phe Phe Ser Lys Val Thr Tyr Ser Trp Phe Ser Arg Val Ile	
30 35 40 45	
act tta ggc tat aag aga cct ttg gaa aga gag gat ctt ttt gaa cta	372
Thr Leu Gly Tyr Lys Arg Pro Leu Glu Arg Glu Asp Leu Phe Glu Leu	
50 55 60	
aag gaa agt gat tcc ttc tgc act gcg tgt ccc atc ttt gaa aaa caa	420
Lys Glu Ser Asp Ser Phe Cys Thr Ala Cys Pro Ile Phe Glu Lys Gln	
65 70 75	
tgg aga aag gaa gtt tta agg aat caa gag agg caa aaa gta aag gta	468
Trp Arg Lys Glu Val Leu Arg Asn Gln Glu Arg Gln Lys Val Lys Val	
80 85 90	
tct tgt tat aaa gag gca cat atc aag aaa cca tct cta ctc tat gca	516
Ser Cys Tyr Lys Glu Ala His Ile Lys Lys Pro Ser Leu Leu Tyr Ala	
95 100 105	
ttg tgg aac acc ttt aaa tcc atc ctg att caa gtt gcc tta ttc aaa	564
Leu Trp Asn Thr Phe Lys Ser Ile Leu Ile Gln Val Ala Leu Phe Lys	
110 115 120 125	
gtg ttt gct gat att ttg tcc ttc act agc cca ctc ata atg aag caa	612
Val Phe Ala Asp Ile Leu Ser Phe Thr Ser Pro Leu Ile Met Lys Gln	
130 135 140	
att atc att ttc tgt gaa cac agc tca gat ttt ggc tgg aat ggc tat	660
Ile Ile Ile Phe Cys Glu His Ser Ser Asp Phe Gly Trp Asn Gly Tyr	
145 150 155	
ggc tat gca gtg gca ctt ctt gtt gta gtc ttt ttg caa act ctg att	708
Gly Tyr Ala Val Ala Leu Leu Val Val Phe Leu Gln Thr Leu Ile	
160 165 170	
ctt cag caa tat caa cgt ttt aac atg ctc acc tca gca aaa gtt aag	756
Leu Gln Gln Tyr Gln Arg Phe Asn Met Leu Thr Ser Ala Lys Val Lys	
175 180 185	
aca gct gta aat gga ctg atc tac aaa aag gcc tta ctt tta tca aat	804
Thr Ala Val Asn Gly Leu Ile Tyr Lys Lys Ala Leu Leu Leu Ser Asn	
190 195 200 205	
gtt tct cga caa aag ttt tcc act ggg gaa att att aac ttg atg tca	852
Val Ser Arg Gln Lys Phe Ser Thr Gly Glu Ile Ile Asn Leu Met Ser	
210 215 220	
gca act cat gga ctt gac agc aaa cct caa tct cct ctg gtc tgc ccc	900
Ala Thr His Gly Leu Asp Ser Lys Pro Gln Ser Pro Leu Val Cys Pro	
225 230 235	

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ttt tca aat cct aat ggc cgt ata tct cct ttg gca aga gct ggg tcc      948
Phe Ser Asn Pro Asn Gly Arg Ile Ser Pro Leu Ala Arg Ala Gly Ser
      240                      245                      250

agc agt gtt agc agg ggt ggc agt cct tgt gtt tgt tat acc aat aaa      996
Ser Ser Val Ser Arg Gly Gly Ser Pro Cys Val Cys Tyr Thr Asn Lys
      255                      260                      265

tgc ttt agc tgc aac taa aataaa aaagttaaag gtaaaaaaat gactgcctca    1050
Cys Phe Ser Cys Asn *
      270                      275

tgttacatgt gtcaaacagg agctgagttt tctgacttga gttaacaatc accatctcgc    1110

taattatata gagagagtta caaatggaag tcatcgaatt ttatcattta cttattcact    1170

caaccagtat tgaacaagca tgtatcttat gtcagccagt gtttcaggca caggaagtac    1230

agcagtgagg ggaaatgaca agtccagctc tcatgagggg tagtggagga gacaggcatt    1290

aagcaagtac ataaatagag agaaaacatt tgtatatgaa aaagatttag taaaatacag    1350

tgatgaagag acaaaggatg ccattttaca ttttaagatc                        1389

<210> 232
<211> 707
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (56)..(439)

<400> 232
ctactactac tactactaaa ttcgcggccg cgtcgaccat agcgctcacg caagc atg      58
                                   Met
                                   1

gtt aac gtc cct aaa acc cgc cgg act ttc tgt aag aag tgt ggc aag      106
Val Asn Val Pro Lys Thr Arg Arg Thr Phe Cys Lys Lys Cys Gly Lys
      5                      10                      15

cac caa ccc cat aaa gtg aca cag tac aag aag ggc aag gat tct ctg      154
His Gln Pro His Lys Val Thr Gln Tyr Lys Lys Gly Lys Asp Ser Leu
      20                      25                      30

tac gcc cag gga aag cgg cgt tat gac agg aag cag agt ggc tat ggt      202
Tyr Ala Gln Gly Lys Arg Arg Tyr Asp Arg Lys Gln Ser Gly Tyr Gly
      35                      40                      45

ggg caa act aag ccg att ttc cgg aaa aag gct aaa act aca aag aag      250
Gly Gln Thr Lys Pro Ile Phe Arg Lys Lys Ala Lys Thr Thr Lys Lys
      50                      55                      60                      65

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att gtg cta agg ctt gag tgc gtt gag ccc aac tgc aga tct aag aga      298
Ile Val Leu Arg Leu Glu Cys Val Glu Pro Asn Cys Arg Ser Lys Arg
              70                      75                      80

atg ctg gct att aaa aga tgc aag cat ttt gaa ctg gga gga gat aag      346
Met Leu Ala Ile Lys Arg Cys Lys His Phe Glu Leu Gly Gly Asp Lys
              85                      90                      95

aag aga aag gta tat aat tat ggg tgc gaa ggt gca atc ttt ctc ata      394
Lys Arg Lys Val Tyr Asn Tyr Gly Ser Glu Gly Ala Ile Phe Leu Ile
              100                     105                     110

gct tta tta ttt cga aaa ggt gaa cat cta ttc ctt gtg gca tag agc      442
Ala Leu Leu Phe Arg Lys Gly Glu His Leu Phe Leu Val Ala  *
              115                     120                     125

tcaggggtaa tcctctaaaa atattagatc tatagctaaa gatatgtgag gtcttttgct      502

acaaggagga aaggaagaat gaggaagctt aacagcatgg tgactatttt aggaacagat      562

aatgtttctta atggggcagt agttcatggc aaaatacaaaa acaacttttt tctgttctgc      622

ttacagggcc aagtgatcca gttttaagtg tcattcttta ttatgaagac aataaaatct      682

tgagtttatg ttcaaaaaaa aaaaaa                                          707

<210> 233
<211> 824
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (101)..(688)

<400> 233
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cgagctcgga tccactagtc cagtgtggtg gaattccata  atg tat agt att tct      115
                                         Met Tyr Ser Ile Ser
                                         1                      5

cct gcc aac tct gag gaa ggc cag gaa ctt tat gtc tgc aca gtc aag      163
Pro Ala Asn Ser Glu Glu Gly Gln Glu Leu Tyr Val Cys Thr Val Lys
              10                      15                      20

gat gat gtg aac ttg gat aca gta ctt ctc cta ccc ttt ttg aaa gaa      211
Asp Asp Val Asn Leu Asp Thr Val Leu Leu Leu Pro Phe Leu Lys Glu
              25                      30                      35

ata gca gta agc caa ctg gat caa ctg agc cca gag gaa cag ttg ctg      259
Ile Ala Val Ser Gln Leu Asp Gln Leu Ser Pro Glu Glu Gln Leu Leu
              40                      45                      50

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gtc aag tgt gct gca atc att ggt cac tcc ttc cat ata gat ttg ctg 307
Val Lys Cys Ala Ala Ile Ile Gly His Ser Phe His Ile Asp Leu Leu
55 60 65

cag cac ctc ctg cct ggc tgg gat aaa aat aag cta ctt cag gtc ttg 355
Gln His Leu Leu Pro Gly Trp Asp Lys Asn Lys Leu Leu Gln Val Leu
70 75 80 85

aga gct ctt gtg gat ata cat gtg ctc tgc tgg tct gac aag agc caa 403
Arg Ala Leu Val Asp Ile His Val Leu Cys Trp Ser Asp Lys Ser Gln
90 95 100

gag ctt cct gct gag ccc ata tta atg cct tcc tct atc gac atc att 451
Glu Leu Pro Ala Glu Pro Ile Leu Met Pro Ser Ser Ile Asp Ile Ile
105 110 115

gat gga acc aaa gag aag aag aca aag tta gat ggt ggg tca gcc tct 499
Asp Gly Thr Lys Glu Lys Lys Thr Lys Leu Asp Gly Gly Ser Ala Ser
120 125 130

ctt ctc agg cta caa gaa gaa tta tcc cta cca cag gca gca ctg aaa 547
Leu Leu Arg Leu Gln Glu Leu Ser Leu Pro Gln Ala Ala Leu Lys
135 140 145

cag aca ata gac agc ttc cac ccc act aca cgc ctg cag caa cac agc 595
Gln Thr Ile Asp Ser Phe His Pro Thr Thr Arg Leu Gln Gln His Ser
150 155 160 165

ccg gct gca cag gct ctc gta tgc gac cat cat gct tgc agt agc ccg 643
Pro Ala Ala Gln Ala Leu Val Cys Asp His His Ala Cys Ser Ser Pro
170 175 180

gtc ttt gca cgg cta cct cta gag cac ctt cag aaa tgc cct taa gca 691
Val Phe Ala Arg Leu Pro Leu Glu His Leu Gln Lys Cys Pro *
185 190 195

tgctgggggtc acgtgtcatg caaaccttgg acagatgact gaacctctct atgccttggt 751

ttcttcatct gtgtagacgc cagtgcgat gtctccttcc tcaggtcggg gactatctgg 811

gaccaaggt tct 824

<210> 234
<211> 1077
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (239)..(946)

<400> 234
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gctgcccttc	cccagatccc	gaatatactc	ctggccaggt	ggagcagaga	acagttcctc	120
agctgggtcat	gctgagctca	taccctgatg	gctgctccat	gaggtcaaga	ctgggtctcc	180
tccctcctcc	cccttcacca	atgcctgggc	tcacggggct	agttttgacc	cccacgct	238
atg gca tca tgc acc tcc ctc cca gct cct ggc tct cgg cct aag aag	286					
Met Ala Ser Ser Thr Ser Leu Pro Ala Pro Gly Ser Arg Pro Lys Lys						
1 5 10 15						
cct cta ggc aag atg gct gac tgg ttc agg cag acc ctg ctg aag aag	334					
Pro Leu Gly Lys Met Ala Asp Trp Phe Arg Gln Thr Leu Leu Lys Lys						
20 25 30						
ccc aag aag agg ccc aac tcc cca gaa agc acc tcc agc gat gct tca	382					
Pro Lys Lys Arg Pro Asn Ser Pro Glu Ser Thr Ser Ser Asp Ala Ser						
35 40 45						
cag cct acc tca cag gac agc cca cta ccc cca agc ctc agc tca gtc	430					
Gln Pro Thr Ser Gln Asp Ser Pro Leu Pro Pro Ser Leu Ser Ser Val						
50 55 60						
acg tct ccc agc ctg cca ccc aca cat gcg agt gac agt ggc agt agt	478					
Thr Ser Pro Ser Leu Pro Thr His Ala Ser Asp Ser Gly Ser Ser						
65 70 75 80						
cgc tgg agc aaa gac tat gac gtc tgc gtg tgc cac agt gag gaa gac	526					
Arg Trp Ser Lys Asp Tyr Asp Val Cys Val Cys His Ser Glu Glu Asp						
85 90 95						
ctg gtg gcc gcc cag gac ctg gtc tcc tac ttg gaa ggc agc act gcc	574					
Leu Val Ala Ala Gln Asp Leu Val Ser Tyr Leu Glu Gly Ser Thr Ala						
100 105 110						
agc ctg cgc tgc ttc ctg caa ctc cgg gat gca acc cca ggc ggc gct	622					
Ser Leu Arg Cys Phe Leu Gln Leu Arg Asp Ala Thr Pro Gly Gly Ala						
115 120 125						
ata gtg tcc gag ctg tgc cag gca ctg agc agt agt cac tgc cgg gtg	670					
Ile Val Ser Glu Leu Cys Gln Ala Leu Ser Ser Ser His Cys Arg Val						
130 135 140						
ctg ctc atc acg ccg ggc ttc ctt cag gac ccc tgg tgc aag tac cag	718					
Leu Leu Ile Thr Pro Gly Phe Leu Gln Asp Pro Trp Cys Lys Tyr Gln						
145 150 155 160						
atg ctg cag gcc ctg acc gag gct cca ggg gcc gag ggc tgc acc atc	766					
Met Leu Gln Ala Leu Thr Glu Ala Pro Gly Ala Glu Gly Cys Thr Ile						
165 170 175						
ccc ctg ctg tgc ggc ctc agc aga gct gct tac cca cct gag ctc cga	814					
Pro Leu Leu Ser Gly Leu Ser Arg Ala Ala Tyr Pro Pro Glu Leu Arg						
180 185 190						
ttc atg tac tac gtc gat ggc agg ggc cct gat ggt ggc ttt cgt caa	862					
Phe Met Tyr Tyr Val Asp Gly Arg Gly Pro Asp Gly Gly Phe Arg Gln						
195 200 205						

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gtc aaa gaa gct gtc atg cgt tgt aag cta cta cag gag gga gaa ggg      910
Val Lys Glu Ala Val Met Arg Cys Lys Leu Leu Gln Glu Gly Glu Gly
    210                      215                      220

gaa cgg gat tca gct aca gta ttt gat cta ctt tga cttt taggagacag      960
Glu Arg Asp Ser Ala Thr Val Phe Asp Leu Leu *
    225                      230                      235

ccctgtagcc tagtagttca aagcgcagct tctggaagag gctgtcgggg tttgtatcct    1020

ggctcctgcc cttattaacc cataaaaagt aacttggtca agttaaaaaa aaaaaaa      1077

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<210> 235
<211> 916
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (169)..(738)

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<400> 235
agctggctag cgtttaaact taagcttggg accgagctcg gatccactag tccagtgtgg      60

tggaattcca cagccagta actttgctag tacctcttga gtgcaagggtg gagaattaag    120

atctggattt gagacggagc acggaacatt tcactcaggg gaagagct atg aac atg      177
                               Met Asn Met
                               1

ctg act gcc agc ctg ttg agg gca gtc ata gcc tcc atc tgt gtt gta      225
Leu Thr Ala Ser Leu Leu Arg Ala Val Ile Ala Ser Ile Cys Val Val
    5                      10                      15

tcc agc atg gct cag aag gta act caa gcg cag act gaa att tct gtg      273
Ser Ser Met Ala Gln Lys Val Thr Gln Ala Gln Thr Glu Ile Ser Val
    20                      25                      30                      35

gtg gag aag gag gat gtg acc ttg gac tgt gtg tat gaa acc cgt gat      321
Val Glu Lys Glu Asp Val Thr Leu Asp Cys Val Tyr Glu Thr Arg Asp
                40                      45                      50

act act tat tac tta ttc tgg tac aag caa cca cca agt gga gaa ttg      369
Thr Thr Tyr Tyr Leu Phe Trp Tyr Lys Gln Pro Pro Ser Gly Glu Leu
                55                      60                      65

gtt ttc ctt att cgt cgg aac tct ttt gat gag caa aat gaa ata agt      417
Val Phe Leu Ile Arg Arg Asn Ser Phe Asp Glu Gln Asn Glu Ile Ser
                70                      75                      80

ggg cgg tat tct tgg aac ttc cag aaa tcc acc agt tcc ttc aac ttc      465
Gly Arg Tyr Ser Trp Asn Phe Gln Lys Ser Thr Ser Ser Phe Asn Phe
    85                      90                      95

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acc atc aca gcc tca caa gtc gtg gac tca gca gta tac ttc tgt gct      513
Thr Ile Thr Ala Ser Gln Val Val Asp Ser Ala Val Tyr Phe Cys Ala
100                      105                      110                      115

ctg agt gag gcg gcc caa gaa acc agt ggc tct agg ttg acc ttt ggg      561
Leu Ser Glu Ala Ala Gln Glu Thr Ser Gly Ser Arg Leu Thr Phe Gly
                      120                      125                      130

gaa gga aca cag ctc aca gtg aat cct gat atc cag aac cct gac cct      609
Glu Gly Thr Gln Leu Thr Val Asn Pro Asp Ile Gln Asn Pro Asp Pro
                      135                      140                      145

gcc gtg tac cag ctg aga gac tct aaa tcc agt gac aag tct gtc tgc      657
Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys
                      150                      155                      160

cta ttc acc gat ttt gat tct caa aca aat gtg tca caa agt aag gat      705
Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp
                      165                      170                      175

tct gat gtg tat atc aca gac aaa ctg tgc tag actgtgag gctagggatt      756
Ser Asp Val Tyr Ile Thr Asp Lys Leu Cys *
180                      185                      190

tcagaaccac cggggtgggc ctggagcaac aaatctgact ttgcatgggc aacgccttca      816

acaacaggct tatttcagaa gaacccttct tccccagccc caaaagggtcc cttgatggca      876

agctgcccga gaaagctttg aaacagatac caacctaaac                        916

<210> 236
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<212> DNA
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<220>
<221> CDS
<222> (38)..(547)

<400> 236
agtgtggtgg aattcgggag cctgccccca ggggccc atg cag aat gcc acc aag      55
Met Gln Asn Ala Thr Lys
                      1                      5

tat ggc aac atg aca gag gac cat gtg atg cac ctg ctc cag aat gct      103
Tyr Gly Asn Met Thr Glu Asp His Val Met His Leu Leu Gln Asn Ala
                      10                      15                      20

gac ccc ctg aag gtg tac ccg cca ctg aag ggg agc ttc ccg gag aac      151
Asp Pro Leu Lys Val Tyr Pro Pro Leu Lys Gly Ser Phe Pro Glu Asn
                      25                      30                      35

ctg aga cac ctt aag aac acc atg gag acc ata gac tgg aag gtc ttt      199
Leu Arg His Leu Lys Asn Thr Met Glu Thr Ile Asp Trp Lys Val Phe

```

40	45	50	
gag agc tgg atg cac cat tgg ctc ctg ttt gaa atg agc agg cac tcc			247
Glu Ser Trp Met His His Trp Leu Leu Phe Glu Met Ser Arg His Ser			
55	60	65	70
ttg gag caa aag ccc act gac gct cca ccg aaa gta ctg acc aag tgc			295
Leu Glu Gln Lys Pro Thr Asp Ala Pro Pro Lys Val Leu Thr Lys Cys			
	75	80	85
cag gaa gag gtc agc cac atc cct gct gtc cac ccg ggt tca ttc agg			343
Gln Glu Glu Val Ser His Ile Pro Ala Val His Pro Gly Ser Phe Arg			
	90	95	100
ccc aag tgc gac gag aac ggc aac tat ctg cca ctc cag tgc tat ggg			391
Pro Lys Cys Asp Glu Asn Gly Asn Tyr Leu Pro Leu Gln Cys Tyr Gly			
	105	110	115
agc atc ggc tac tgc tgg tgt gtc ttc ccc aac ggc acg gag gtc ccc			439
Ser Ile Gly Tyr Cys Trp Cys Val Phe Pro Asn Gly Thr Glu Val Pro			
	120	125	130
aac acc aga agc cgc ggg cac cat aac tgc agt gag tca ctg gaa ctg			487
Asn Thr Arg Ser Arg Gly His His Asn Cys Ser Glu Ser Leu Glu Leu			
	135	140	145
gag gac ccg tct tct ggg ctg ggt gtg acc aag cag gat ctg ggc cca			535
Glu Asp Pro Ser Ser Gly Leu Gly Val Thr Lys Gln Asp Leu Gly Pro			
	155	160	165
gtc ccc atg tga gag cagcagaggc ggtcttcaac atcctgccag cccacacag			590
Val Pro Met *			
	170		
ctacagcttt cttgctccct tcagcccca gccctcccc catctccac cctgtacctc			650
atcccatgag accctggtgc ctggctcttt cgtcaccctt ggacaagaca aaccaagtcg			710
gaacagcaga taacaatgca gcaaggccct gctgcccaat ctccatctgt caacaggggc			770
ggtcgacgcg gccgcgaatt cggatcctcg agagatctct ttttttgggt ttggtggggt			830
gtcttcatca tcggatatata taggtatata catcggccta tcaagg			876

<210> 237
 <211> 753
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (168)..(419)

 <400> 237

CCDS: C12345.1

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gtccgtgcgc accgcccggc gtccaggtga gtctcccatc tgcagagacg cggacgcgcc      60
ggccccgcagt tggcctgcgg agcgcggtgg acggtttggc gcccaccagg cgatcaatac      120
tttggaatttt taattttctag atttggcaat tcttcgctga agtcacac  atg agc ttt      176
                                     Met Ser Phe
                                     1

ttc caa ctc ctg atg aaa agg aag gaa ctc att ccc ttg gtg gtg ttc      224
Phe Gln Leu Leu Met Lys Arg Lys Glu Leu Ile Pro Leu Val Val Phe
      5                      10                      15

atg act gtg gcg gcg ggt gga gcc tca tct ttc gct gtg tat tct ctt      272
Met Thr Val Ala Ala Gly Gly Ala Ser Ser Phe Ala Val Tyr Ser Leu
      20                      25                      30                      35

tgg aaa acc gat gtg atc ctt gat cga aaa aaa aat cca gaa cct tgg      320
Trp Lys Thr Asp Val Ile Leu Asp Arg Lys Lys Asn Pro Glu Pro Trp
                      40                      45                      50

gaa act gtg gac cct act gta cct caa aag ctt ata aca atc aac caa      368
Glu Thr Val Asp Pro Thr Val Pro Gln Lys Leu Ile Thr Ile Asn Gln
                      55                      60                      65

caa tgg aaa ccc att gaa gag ttg caa aat gtc caa agg gtg acc aaa      416
Gln Trp Lys Pro Ile Glu Glu Leu Gln Asn Val Gln Arg Val Thr Lys
                      70                      75                      80

tga cgag cctcgcctc tttcttctga agagtactct ataaatctag tggaaacatt      473
*

tctgcacaaa ctagattctg gacaccagtg tgcggaaatg cttctgctac attttttaggg      533

tttgtctaca ttttttgggc tctggataag gaattaaagg agtgcagcaa taactgcact      593

gtctaaaagt ttgtgcttat tttcttgtaa atttgaatat tgcattattga aatttttggt      653

tatgatctat gaatgttttt cttaaaattt acaaagcttt gtaaattaga ttttctttaa      713

taaaatgccca tttgtgcaag atttctcaaa aaaaaaaaaa      753

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<210> 238
 <211> 1395
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (50)..(1060)

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<400> 238
gagtgggtgga attccgctgg cctcgcctcg tgcgcgcctc cctccccgc  atg cag      55
                                     Met Gln

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ccc gcc gag cgc tcg cgg gtc ccc agg atc gac ccg tac gga ttc gag	103
Pro Ala Glu Arg Ser Arg Val Pro Arg Ile Asp Pro Tyr Gly Phe Glu	
5 10 15	
cgg cct gag gac ttc gac gac gcc gcc tac gag aag ttt ttc tcc agc	151
Arg Pro Glu Asp Phe Asp Asp Ala Ala Tyr Glu Lys Phe Phe Ser Ser	
20 25 30	
tac ctg gtc acg ctc acc cgc agg gcg atc aaa tgg tcc cgg ctg ctg	199
Tyr Leu Val Thr Leu Thr Arg Arg Ala Ile Lys Trp Ser Arg Leu Leu	
35 40 45 50	
cag ggc ggg ggc gtc ccc agg agc cgg aca gtg aag cgc tat gtc cgg	247
Gln Gly Gly Gly Val Pro Arg Ser Arg Thr Val Lys Arg Tyr Val Arg	
55 60 65	
aaa ggg gtc ccg ctg gag cac cgt gcc cgc gtc tgg atg gtg ctg agt	295
Lys Gly Val Pro Leu Glu His Arg Ala Arg Val Trp Met Val Leu Ser	
70 75 80	
ggg gcc cag gcg cag atg gac cag aat ccc ggc tac tac cac cag ctt	343
Gly Ala Gln Ala Gln Met Asp Gln Asn Pro Gly Tyr Tyr His Gln Leu	
85 90 95	
ctc cag gga gag aga aac ccc agg ctg gag gac gcc atc agg aca gac	391
Leu Gln Gly Glu Arg Asn Pro Arg Leu Glu Asp Ala Ile Arg Thr Asp	
100 105 110	
ctg aac cgg acc ttc ccc gac aac gtg aag ttc cgg aag acc acg gac	439
Leu Asn Arg Thr Phe Pro Asp Asn Val Lys Phe Arg Lys Thr Thr Asp	
115 120 125 130	
ccc tgc tta cag agg acc ctg tac aat gtg ctg ctg gca tat ggg cac	487
Pro Cys Leu Gln Arg Thr Leu Tyr Asn Val Leu Leu Ala Tyr Gly His	
135 140 145	
cat aac cag gga gtg ggc tac tgc cag gga atg aat ttt ata gca gga	535
His Asn Gln Gly Val Gly Tyr Cys Gln Gly Met Asn Phe Ile Ala Gly	
150 155 160	
tat ctg att ctt ata aca aat aat gaa gaa gaa tct ttt tgg ctg tta	583
Tyr Leu Ile Leu Ile Thr Asn Asn Glu Glu Glu Ser Phe Trp Leu Leu	
165 170 175	
gat gct ctt gtt gga aga ata cta cca gat tac tac agc ccg gcc atg	631
Asp Ala Leu Val Gly Arg Ile Leu Pro Asp Tyr Tyr Ser Pro Ala Met	
180 185 190	
ctg ggc ctg aag acc gac cag gag gtc ctc ggg gag ctg gtg cgg gcg	679
Leu Gly Leu Lys Thr Asp Gln Glu Val Leu Gly Glu Leu Val Arg Ala	
195 200 205 210	
aag ctg ccg gct gtg ggg gcc ctg atg gag cgt ctc ggt gtg ctg tgg	727
Lys Leu Pro Ala Val Gly Ala Leu Met Glu Arg Leu Gly Val Leu Trp	
215 220 225	

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acg ctg ctg gtg tcc cgc tgg ttc atc tgc ctg ttt gtg gac atc ttg      775
Thr Leu Leu Val Ser Arg Trp Phe Ile Cys Leu Phe Val Asp Ile Leu
      230                      235                      240

ccc gtg gag aca gtg ctt cgg atc tgg gac tgt ttg ttt aac gaa ggc      823
Pro Val Glu Thr Val Leu Arg Ile Trp Asp Cys Leu Phe Asn Glu Gly
      245                      250                      255

tcg aag att atc ttc cgg gtg gcc ctg acc tta att aag cag cac cag      871
Ser Lys Ile Ile Phe Arg Val Ala Leu Thr Leu Ile Lys Gln His Gln
      260                      265                      270

gag ttg att ttg gaa gcc acc agc gtt cca gac att tgc gat aag ttt      919
Glu Leu Ile Leu Glu Ala Thr Ser Val Pro Asp Ile Cys Asp Lys Phe
      275                      280                      285                      290

aag cag ata acc aaa ggg agt ttc gtg atg gag tgt cac acg ttt atg      967
Lys Gln Ile Thr Lys Gly Ser Phe Val Met Glu Cys His Thr Phe Met
      295                      300                      305

cag aaa ata ttt tca gaa cct gga agc tta tcc atg gcc acc gtc gcc      1015
Gln Lys Ile Phe Ser Glu Pro Gly Ser Leu Ser Met Ala Thr Val Ala
      310                      315                      320

aag ctc cgc gag agc tgc agg gcc cgg ctg ctg gca cag ggg tga gcg      1063
Lys Leu Arg Glu Ser Cys Arg Ala Arg Leu Leu Ala Gln Gly *
      325                      330                      335

tgccgtgcc ctgcgttgct cgtctctaca ctgacgatgc ccctttccag agttgacact      1123

ggaccaactt tcaactgcttt ccttttttagt gttgtaaata cttgacatca ctacacttta      1183

gttgtgaatt ttttaaaaga gcagtttaaa atcaggtcat tctaccagct tttgatgatt      1243

agctatgaag tcatactttt taaagaaaac ttattttttac ctgagagatc aataatatat      1303

aaaatgtgag tgtggggttg tatctaataa agtatgccaa cacctgtggt tgtgatcagt      1363

ttctcagctg actggaaatt aaaaaaaaaa aa                                  1395

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<210> 239
 <211> 767
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (78)..(326)

<220>
 <221> misc_feature
 <222> (1)...(767)
 <223> n = a,t,c or g

<400> 239
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 ttttcttgct cggcatc atg gct gcc ctc aga tcc ctt gtg aag ccc aag 110
 Met Ala Ala Leu Arg Ser Leu Val Lys Pro Lys
 1 5 10
 atc gtc aaa aag aga acc aag aaa ttc atc cgg cac cag tca gac cga 158
 Ile Val Lys Lys Arg Thr Lys Lys Phe Ile Arg His Gln Ser Asp Arg
 15 20 25
 tat gtc aaa atc aag atg aga aga ata atg tct ggg gtg aag gtg aag 206
 Tyr Val Lys Ile Lys Met Arg Arg Ile Met Ser Gly Val Lys Val Lys
 30 35 40
 cac cca gcc caa gac tca gca gcc agg aag tgg ccc agc gct ctt tat 254
 His Pro Ala Gln Asp Ser Ala Ala Arg Lys Trp Pro Ser Ala Leu Tyr
 45 50 55
 acc acg ggt gca gga att cac aca gaa aag tgg agg cca agg cgt gag 302
 Thr Thr Gly Ala Gly Ile His Thr Glu Lys Trp Arg Pro Arg Arg Glu
 60 65 70 75
 aat tcc tca atg act gcc ctc taa aggaagagat ccaaagaaat cctgaggaag 356
 Asn Ser Ser Met Thr Ala Leu *
 80
 cacaacaaac aaaaacactc tggatcagaa cttcctgtgc cagcgttaca tcagggtttt 416
 ctagcagcaa gggcgggctc cacatggctg aagcaggcaa ccaggaggac caggcttctt 476
 gtcagagact gaggaccag gaagaaacat gtctcggccc ctgtccccct ccacaattca 536
 gaggccacat tctaacaggg gaggctgacc aattaaacag ataatgacac ctcttagagc 596
 taagagctct ccgactatga accagatgcc tggagaacac ggatgaatgg tctgagcatg 656
 agcaggggtg ggaggcagcg ttaaggagg catcagagtc agaacctagc aaacaagtgt 716
 ttgtgaagaa gaattcatag aanagggcaa tgcgggcatc acatgggcta a 767

<210> 240
 <211> 526
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (187)..(324)

<400> 240
 gagttttaaa attcttttatt taaaaatctc taactgtaat gtttcataaa aaatatacac 60

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gtttctatattt acatattcca ttaattctat tagtttgaat tagatttttaa gtccaatttt 120
gaaaagcttg cagaattttct tctgaaatta cttaaaatta ctgtatgcat aaacttaciaa 180
aaacat atg cta tac caa ggc aga gaa aag aaa aaa agt gaa gtg gct 228
      Met Leu Tyr Gln Gly Arg Glu Lys Lys Lys Ser Glu Val Ala
        1             5             10

aca aag gtc cct ggg gca tca cct gct cac cta gga acc agg agt act 276
Thr Lys Val Pro Gly Ala Ser Pro Ala His Leu Gly Thr Arg Ser Thr
  15             20             25             30

gga tac tgt tcc gtt act ggt aac cta tct gga tgt aaa ggt tca taa 324
Gly Tyr Cys Ser Val Thr Gly Asn Leu Ser Gly Cys Lys Gly Ser *
          35             40             45

gttacaatgc tttttttgtt taaaaaaaaa aaaaagtctg tacttttaciaa gccaaaagtg 384
aaaatgccac acatcctctt tacgctttca tgtacactaa gtcactccat ttggttgata 444
ccaataatga tagctcctgt gtataatatt ttcataaaatc atactcagta agcaaattctc 504
tcaagcagcc agcatatgca gc 526

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<210> 241
 <211> 3744
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (27)..(3161)

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<400> 241
aagagctgcc tcccaggagggt gtctac atg gtg cag ccc cag ggg tgc agc gat 53
      Met Val Gln Pro Gln Gly Cys Ser Asp
        1             5

gag gaa gac cac gcg gag gag ccc tcc aag gac ggc ggt gcc ctg gag 101
Glu Glu Asp His Ala Glu Glu Pro Ser Lys Asp Gly Gly Ala Leu Glu
  10             15             20             25

gag aag gat tcg gac ggg gca gcc tcc aag gag gac agc ggc ccc agc 149
Glu Lys Asp Ser Asp Gly Ala Ala Ser Lys Glu Asp Ser Gly Pro Ser
          30             35             40

acc agg cag gct tca gga gag gcc tcc tcg ctg cgg gac tac gcg gcc 197
Thr Arg Gln Ala Ser Gly Glu Ala Ser Ser Leu Arg Asp Tyr Ala Ala
          45             50             55

tcc acc atg acc gag ttc ctc ggc atg ttt ggc tat gat gac cag aac 245
Ser Thr Met Thr Glu Phe Leu Gly Met Phe Gly Tyr Asp Asp Gln Asn
        60             65             70

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acg cgg gac gag ctg gcc agg aag atc agc ttt gag aag ctg cac gcg	293
Thr Arg Asp Glu Leu Ala Arg Lys Ile Ser Phe Glu Lys Leu His Ala	
75 80 85	
ggc tcc acc ccg gag gca gcc acc tcc tcc atg ctg ccc acc tcc gag	341
Gly Ser Thr Pro Glu Ala Ala Thr Ser Ser Met Leu Pro Thr Ser Glu	
90 95 100 105	
gat acc ctc agc aag cgg gcc cgg ttc tct aag tat gag gag tac atc	389
Asp Thr Leu Ser Lys Arg Ala Arg Phe Ser Lys Tyr Glu Glu Tyr Ile	
110 115 120	
cgc aag ctc aag gct gcc gag cag ctc tcc tgg ccg gcc ccc agc acc	437
Arg Lys Leu Lys Ala Gly Glu Gln Leu Ser Trp Pro Ala Pro Ser Thr	
125 130 135	
aag acc gag gag cgg gtg gcc aag gag gtg gtg gcc acc ctg ccc gcc	485
Lys Thr Glu Glu Arg Val Gly Lys Glu Val Val Gly Thr Leu Pro Gly	
140 145 150	
ctg cgg ctg ccc agc agc acg gcc cac ctg gag acc aag gcc acc atc	533
Leu Arg Leu Pro Ser Ser Thr Ala His Leu Glu Thr Lys Ala Thr Ile	
155 160 165	
ctg ccc ctg ccg tcg cac agc agt gtc cag atg cag aac ctg gta gcc	581
Leu Pro Leu Pro Ser His Ser Ser Val Gln Met Gln Asn Leu Val Ala	
170 175 180 185	
cgg gcc tcc aag tac gac ttc ttc atc caa aaa ctg aag acc gcc gag	629
Arg Ala Ser Lys Tyr Asp Phe Phe Ile Gln Lys Leu Lys Thr Gly Glu	
190 195 200	
aat ctg cgg ccc cag aac ggg agc acc tac aag aag cca tcc aag tac	677
Asn Leu Arg Pro Gln Asn Gly Ser Thr Tyr Lys Lys Pro Ser Lys Tyr	
205 210 215	
gac ctg gag aat gtc aag tac ctg cac ctc ttc aaa ccc ggg gag gcc	725
Asp Leu Glu Asn Val Lys Tyr Leu His Leu Phe Lys Pro Gly Glu Gly	
220 225 230	
agc ccc gac atg gcc ggg gcc atc gcc ttc aag aca gcc aag gtg ggg	773
Ser Pro Asp Met Gly Gly Ala Ile Ala Phe Lys Thr Gly Lys Val Gly	
235 240 245	
cgc cct tcc aag tac gac gtc cgg gcc atc cag aag cca gcc ccc gcc	821
Arg Pro Ser Lys Tyr Asp Val Arg Gly Ile Gln Lys Pro Gly Pro Ala	
250 255 260 265	
aag gtt ccg ccc acc ccc agc ctg gct ccc gca ccc ctc gcc agc gtg	869
Lys Val Pro Pro Thr Pro Ser Leu Ala Pro Ala Pro Leu Ala Ser Val	
270 275 280	
ccc agt gcc ccc aac gcc ccc ggg cca ggg cca gag cct cct gcc tcc	917
Pro Ser Ala Pro Asn Ala Pro Gly Pro Gly Pro Glu Pro Pro Ala Ser	
285 290 295	
ctg tcc ttc aac act ccc gag tac ctg aag tca acc ttc tcc aaa aca	965

Leu Ser Phe Asn Thr Pro Glu Tyr Leu Lys Ser Thr Phe Ser Lys Thr	
300 305 310	
gac tcc atc acc acg ggg acc gtc tcc act gtc aag aac gga ctg ccc	1013
Asp Ser Ile Thr Thr Gly Thr Val Ser Thr Val Lys Asn Gly Leu Pro	
315 320 325	
aca gat aaa cca gcc gtc act gaa gat gta aac att tac cag aaa tat	1061
Thr Asp Lys Pro Ala Val Thr Glu Asp Val Asn Ile Tyr Gln Lys Tyr	
330 335 340	
att gcc agg ttc tcg ggc agc cag cac tgt ggc cac atc cac tgt gcc	1109
Ile Ala Arg Phe Ser Gly Ser Gln His Cys Gly His Ile His Cys Ala	
350 355 360	
tac cag tac cgc gag cac tac cac tgc ctt gac cct gag tgt aac tac	1157
Tyr Gln Tyr Arg Glu His Tyr His Cys Leu Asp Pro Glu Cys Asn Tyr	
365 370 375	
cag agg ttc acg agt aag cag gac gtg atc cgc cac tac aac atg cac	1205
Gln Arg Phe Thr Ser Lys Gln Asp Val Ile Arg His Tyr Asn Met His	
380 385 390	
aag aag cgc gac aac tcc ctg cag cac ggc ttc atg cgt ttc agc ccg	1253
Lys Lys Arg Asp Asn Ser Leu Gln His Gly Phe Met Arg Phe Ser Pro	
395 400 405	
ctg gac gac tgc agc gtc tac tac cac ggc tgc cac ctc aat ggg aag	1301
Leu Asp Asp Cys Ser Val Tyr Tyr His Gly Cys His Leu Asn Gly Lys	
410 415 420 425	
agc acc cac tat cac tgc atg cag gtg ggc tgt aac aag gtg tac acg	1349
Ser Thr His Tyr His Cys Met Gln Val Gly Cys Asn Lys Val Tyr Thr	
430 435 440	
agc acg tct gac gtg atg acc cac gag aac ttc cac aag aag aat acc	1397
Ser Thr Ser Asp Val Met Thr His Glu Asn Phe His Lys Lys Asn Thr	
445 450 455	
cag ctc att aac gac ggc ttc cag cgc ttc cga gcc acc gaa gac tgt	1445
Gln Leu Ile Asn Asp Gly Phe Gln Arg Phe Arg Ala Thr Glu Asp Cys	
460 465 470	
ggc aca gcc gac tgc cag ttc tac gga cag aag acc acg cac ttc cac	1493
Gly Thr Ala Asp Cys Gln Phe Tyr Gly Gln Lys Thr Thr His Phe His	
475 480 485	
tgc agg cgc ccc ggc tgc aca ttc act ttc aag aac aag tgt gac atc	1541
Cys Arg Arg Pro Gly Cys Thr Phe Thr Phe Lys Asn Lys Cys Asp Ile	
490 495 500 505	
gag aag cac aag agc tac cac atc aag gac gat gcc tac gcc aag gac	1589
Glu Lys His Lys Ser Tyr His Ile Lys Asp Asp Ala Tyr Ala Lys Asp	
510 515 520	
ggc ttc aag aag ttc tac aag tac gag gag tgc aag tac gag ggc tgc	1637
Gly Phe Lys Lys Phe Tyr Lys Tyr Glu Glu Cys Lys Tyr Glu Gly Cys	

			525				530				535							
gtg	tac	agc	aag	gct	acc	aac	cac	ttc	cac	tgc	atc	cgc	gcc	ggc	tgc		1685	
Val	Tyr	Ser	Lys	Ala	Thr	Asn	His	Phe	His	Cys	Ile	Arg	Ala	Gly	Cys			
			540				545				550							
ggc	ttc	acc	ttc	acc	tcc	acc	agc	cag	atg	acc	tct	cac	aag	cgc	aag		1733	
Gly	Phe	Thr	Phe	Thr	Ser	Thr	Ser	Gln	Met	Thr	Ser	His	Lys	Arg	Lys			
			555				560				565							
cat	gag	cgc	cgg	cac	atc	cgc	tcc	tcg	ggc	gcg	ctg	ggg	ctg	ccg	ccc		1781	
His	Glu	Arg	Arg	His	Ile	Arg	Ser	Ser	Gly	Ala	Leu	Gly	Leu	Pro	Pro			
			570				575				580				585			
tcg	ctg	ctg	ggc	gcc	aag	gac	acg	gag	cac	gag	gag	tcc	agc	aac	gac		1829	
Ser	Leu	Leu	Gly	Ala	Lys	Asp	Thr	Glu	His	Glu	Glu	Ser	Ser	Asn	Asp			
			590				595				600							
gac	ctt	gtt	gac	ttc	tcc	gcc	ctg	agc	agc	aag	aac	tcc	agc	ctg	agc		1877	
Asp	Leu	Val	Asp	Phe	Ser	Ala	Leu	Ser	Ser	Lys	Asn	Ser	Ser	Leu	Ser			
			605				610				615							
gcc	tcc	cct	acc	agc	cag	cag	tcc	tct	gcg	tcc	ctg	gct	gcc	gcc	act		1925	
Ala	Ser	Pro	Thr	Ser	Gln	Gln	Ser	Ser	Ala	Ser	Leu	Ala	Ala	Ala	Thr			
			620				625				630							
gcc	gcc	acc	gag	gct	ggg	ccc	agt	gcc	acc	aaa	cct	ccc	aac	agc	aag		1973	
Ala	Ala	Thr	Glu	Ala	Gly	Pro	Ser	Ala	Thr	Lys	Pro	Pro	Asn	Ser	Lys			
			635				640				645							
atc	tcg	ggg	ctg	ctg	ccc	cag	ggc	ctg	cct	ggc	tcg	atc	ccc	ctg	gcc		2021	
Ile	Ser	Gly	Leu	Leu	Pro	Gln	Gly	Leu	Pro	Gly	Ser	Ile	Pro	Leu	Ala			
			650				655				660				665			
ctg	gcc	ctc	tcc	aac	tcg	ggc	ctg	ccc	acc	ccc	acg	ccc	tac	ttc	ccc		2069	
Leu	Ala	Leu	Ser	Asn	Ser	Gly	Leu	Pro	Thr	Pro	Thr	Pro	Tyr	Phe	Pro			
			670				675				680							
ata	ctg	gct	ggc	cgt	ggg	agc	acc	tcc	ctg	cct	gtg	ggc	acc	ccc	agc		2117	
Ile	Leu	Ala	Gly	Arg	Gly	Ser	Thr	Ser	Leu	Pro	Val	Gly	Thr	Pro	Ser			
			685				690				695							
ctc	ctg	ggt	gcc	gtg	tcg	tct	ggg	tca	gca	gcc	tca	gcc	acc	cct	gac		2165	
Leu	Leu	Gly	Ala	Val	Ser	Ser	Gly	Ser	Ala	Ala	Ser	Ala	Thr	Pro	Asp			
			700				705				710							
aca	ccc	acg	ctg	gtc	gcc	tcg	gga	gct	gga	gac	tca	gcc	ccc	gtg	gct		2213	
Thr	Pro	Thr	Leu	Val	Ala	Ser	Gly	Ala	Gly	Asp	Ser	Ala	Pro	Val	Ala			
			715				720				725							
gcc	gcc	tct	gtc	ccg	gca	cca	ccc	gcc	tcc	atc	atg	gag	agg	atc	tct		2261	
Ala	Ala	Ser	Val	Pro	Ala	Pro	Pro	Ala	Ser	Ile	Met	Glu	Arg	Ile	Ser			
			730				735				740				745			
gca	agc	aag	ggc	ctc	atc	tcg	ccc	atg	atg	gcc	agg	ctg	gct	gca	gct			

gcc ctc aag ccc tct gcc acc ttt gac cca gga agc ggg cag cag gtc Ala Leu Lys Pro Ser Ala Thr Phe Asp Pro Gly Ser Gly Gln Gln Val 765 770 775	2357
acc cca gcc agg ttc ccc ccg gcc caa gtg aag ccg gaa ccc ggt gag Thr Pro Ala Arg Phe Pro Pro Ala Gln Val Lys Pro Glu Pro Gly Glu 780 785 790	2405
agc acc ggc gcc cca ggc ccc cac gaa gcc tcc cag gac cgc agt cta Ser Thr Gly Ala Pro Gly Pro His Glu Ala Ser Gln Asp Arg Ser Leu 795 800 805	2453
gac ctg act gtg aag gag ccc agc aac gaa tca aat ggc cac gca gtc Asp Leu Thr Val Lys Glu Pro Ser Asn Glu Ser Asn Gly His Ala Val 810 815 820 825	2501
ccg gca aat tca tct ctt tta tcc tcg ctt atg aat aag atg tct cag Pro Ala Asn Ser Ser Leu Leu Ser Ser Leu Met Asn Lys Met Ser Gln 830 835 840	2549
ggc aac cct ggc ctg ggc agc ctg ctg aac atc aag gcg gaa gcg gag Gly Asn Pro Gly Leu Gly Ser Leu Leu Asn Ile Lys Ala Glu Ala Glu 845 850 855	2597
ggg agc ccc gct gcg gag ccc tcg ccc ttc cta ggc aag gcc gtg aag Gly Ser Pro Ala Ala Glu Pro Ser Pro Phe Leu Gly Lys Ala Val Lys 860 865 870	2645
gcg ctg gtt cag gag aag ttg gca gag ccc tgg aag gtg tac ctg cgc Ala Leu Val Gln Glu Lys Leu Ala Glu Pro Trp Lys Val Tyr Leu Arg 875 880 885	2693
agg ttt ggt aca aag gac ttc tgt gac ggc cag tgt gac ttc ctc cac Arg Phe Gly Thr Lys Asp Phe Cys Asp Gly Gln Cys Asp Phe Leu His 890 895 900 905	2741
aag gcc cac ttc cac tgc gtg gtg gag gaa tgc ggc gcg ctc ttc agc Lys Ala His Phe His Cys Val Val Glu Glu Cys Gly Ala Leu Phe Ser 910 915 920	2789
acc ttg gac ggg gcc atc aag cac gca aac ttc cac ttc cgg aca gag Thr Leu Asp Gly Ala Ile Lys His Ala Asn Phe His Phe Arg Thr Glu 925 930 935	2837
gga gga gca gca aaa gga aac aca gag gct gcc ttt ccg gcc tcg gcc Gly Gly Ala Ala Lys Gly Asn Thr Glu Ala Ala Phe Pro Ala Ser Ala 940 945 950	2885
gcc gag acc aaa cct ccc atg gcc ccc tcg tcc cct ccg gtc cct cct Ala Glu Thr Lys Pro Pro Met Ala Pro Ser Ser Pro Pro Val Pro Pro 955 960 965	2933
gtc acc acg gcc acg gtg tcc tct ctg gag ggg ccc gct ccc agc ccg Val Thr Thr Ala Thr Val Ser Ser Leu Glu Gly Pro Ala Pro Ser Pro 970 975 980 985	2981

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gcc tcc gtg ccc tcc acc ccc acc ctg ctc gcc tgg aag cag ctg gct      3029
Ala Ser Val Pro Ser Thr Pro Thr Leu Leu Ala Trp Lys Gln Leu Ala
          990                      995                      1000

tcc acc ata ccc cag atg cct cag atc cca gcg tca gtg cct cac ctg      3077
Ser Thr Ile Pro Gln Met Pro Gln Ile Pro Ala Ser Val Pro His Leu
          1005                      1010                      1015

ccc gcc tcg ccc ttg gca acg act tct cta gag aac gcc aag ccc cag      3125
Pro Ala Ser Pro Leu Ala Thr Thr Ser Leu Glu Asn Ala Lys Pro Gln
          1020                      1025                      1030

gtc aaa ccc gga ttc ctc cag ttc cag gag aag tga gtcc ctgatgagc      3175
Val Lys Pro Gly Phe Leu Gln Phe Gln Glu Lys *
          1035                      1040                      1045

cgggagtcctc gcgttcccct cgcgtctcgg gagtaggtgc tagcaagggc gctaggaggc      3235

cctgttcctc actgcggatg gtgctgctgt cccagcctc tctggggcat ggccatcggg      3295

tgatgtcctt ctagccaaag atgctgctgc tcctacctca ctgcctgtcc cagagcaggc      3355

cagcccgcgt gggccgatgg tggcggcagt ggctactgct cctgcagggc atgtggtgat      3415

cctgccaggg ccaggtgggg tggactgggc gtggtggtcc tcagaggaca actcccagcc      3475

tgacaaggag ggctgcgtct cctccgagc ctccgtattg gcctcctctg tggctcacac      3535

ccatggctga atctctgcag ggcacgtgaa gtcacgggta ggggccaggc cctccaggc      3595

cgtcactggc ctgcacagtg gtctgagctc ttgggtggaa gggaccctcc tcaactggatg      3655

gtggtggctc cttgcagggg gaacggtgac tttgtattgt catgtgtgcg gcttcctgtt      3715

ctcaataaaa gtaataaatt ggattatatt      3744

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<210> 242
<211> 2450
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (192)..(2438)

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<400> 242
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atctttttaa gtatgcatat cattagtggg aaataatagg taacaaaaga aattggggga      120

aaagctttta gagttctgat gcctatttaa gtaaattaac tcttttcccc ccaaattct      180

taggcttgaa g atg cag tgg acg cca gag cat gcc cag tgg cca gaa cag      230
          Met Gln Trp Thr Pro Glu His Ala Gln Trp Pro Glu Gln

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1	5	10	
cac ttt gac atc acc tca acc act cgg tct cct gcc cac aaa gtt gaa			278
His Phe Asp Ile Thr Ser Thr Thr Arg Ser Pro Ala His Lys Val Glu			
15	20	25	
gcc tac aga ggt cat ctg cag cgc acc tat cag tac gcc tgg gcg aat			326
Ala Tyr Arg Gly His Leu Gln Arg Thr Tyr Gln Tyr Ala Trp Ala Asn			
30	35	40	45
gat gac ata tct gct ctg act gca tcc aac cta cta aaa aaa tat gca			374
Asp Asp Ile Ser Ala Leu Thr Ala Ser Asn Leu Leu Lys Lys Tyr Ala			
50	55	60	
gag aag tat tcc ggc att ttg gaa ggt cct gtg gac cga ccc gta ctc			422
Glu Lys Tyr Ser Gly Ile Leu Glu Gly Pro Val Asp Arg Pro Val Leu			
65	70	75	
agc aac tat tcg gac aca cca tca gga cta gtg aac ggt cgg aaa aat			470
Ser Asn Tyr Ser Asp Thr Pro Ser Gly Leu Val Asn Gly Arg Lys Asn			
80	85	90	
gaa agt gaa ccc tgg cag cct tcc ttg aat tca gaa gct gtt tat ccc			518
Glu Ser Glu Pro Trp Gln Pro Ser Leu Asn Ser Glu Ala Val Tyr Pro			
95	100	105	
atg aac tgt gtt ccg gat gtt atc act gcc agc aaa gct gga gtc agt			566
Met Asn Cys Val Pro Asp Val Ile Thr Ala Ser Lys Ala Gly Val Ser			
110	115	120	125
tca gcc ctc cct cca gca gat gtc tct gcg agt ata gga agc tct cct			614
Ser Ala Leu Pro Pro Ala Asp Val Ser Ala Ser Ile Gly Ser Ser Pro			
130	135	140	
ggg gta gcc agc aac ctg aca gaa cct agt tat tca agt agt acc tgt			662
Gly Val Ala Ser Asn Leu Thr Glu Pro Ser Tyr Ser Ser Ser Thr Cys			
145	150	155	
gga agc cac act gta ccc agt ctt cat gca ggg ctc cca tct cag gaa			710
Gly Ser His Thr Val Pro Ser Leu His Ala Gly Leu Pro Ser Gln Glu			
160	165	170	
tat gcc cca gga tac aac gga tca tat ttg cat tct act tat agt agc			758
Tyr Ala Pro Gly Tyr Asn Gly Ser Tyr Leu His Ser Thr Tyr Ser Ser			
175	180	185	
cag cca gca cct gca ctt cct tca cct cat ccg tct cct ttg cat agc			806
Gln Pro Ala Pro Ala Leu Pro Ser Pro His Pro Ser Pro Leu His Ser			
190	195	200	205
tct ggg cta cta cag ccc cca cca cca cct cct ccg cca cca gcc ttg			854
Ser Gly Leu Leu Gln Pro Pro Pro Pro Pro Pro Pro Pro Pro Ala Leu			
210	215	220	
gtc cca ggc tac aat ggg act tct aac ctc tcc agt tac agc tat ccg			902
Val Pro Gly Tyr Asn Gly Thr Ser Asn Leu Ser Ser Tyr Ser Tyr Pro			
225	230	235	

tct gct agc tat cct cct cag act gct gtg ggg tct ggg tac agc cct Ser Ala Ser Tyr Pro Pro Gln Thr Ala Val Gly Ser Gly Tyr Ser Pro 240 245 250	950
ggg ggg gca ccg cct ccg cct tca gcg tac ctg cct tca gga att cct Gly Gly Ala Pro Pro Pro Pro Ser Ala Tyr Leu Pro Ser Gly Ile Pro 255 260 265	998
gct ccc acc ccc cta ccc ccc acc act gtt cct ggc tac acc tac cag Ala Pro Thr Pro Leu Pro Pro Thr Thr Val Pro Gly Tyr Thr Tyr Gln 270 275 280 285	1046
ggc cat ggt ttg aca cct att gca ccg tcg gct ctg aca aac agt tca Gly His Gly Leu Thr Pro Ile Ala Pro Ser Ala Leu Thr Asn Ser Ser 290 295 300	1094
gca agt tct ctc aaa agg aaa gct ttc tac atg gca ggg caa gga gat Ala Ser Ser Leu Lys Arg Lys Ala Phe Tyr Met Ala Gly Gln Gly Asp 305 310 315	1142
atg gac tcc agt tat gga aat tac agc tat ggc caa cag aga tct aca Met Asp Ser Ser Tyr Gly Asn Tyr Ser Tyr Gly Gln Gln Arg Ser Thr 320 325 330	1190
cag agt cct atg tac aga atg ccc gac aac agc att tca aac aca aat Gln Ser Pro Met Tyr Arg Met Pro Asp Asn Ser Ile Ser Asn Thr Asn 335 340 345	1238
cgg ggg aat ggc ttt gac aga agt gct gaa aca tca tcc tta gca ttt Arg Gly Asn Gly Phe Asp Arg Ser Ala Glu Thr Ser Ser Leu Ala Phe 350 355 360 365	1286
aag cca acg aag cag cta atg tcc tct gaa cag caa agg aaa ttc agc Lys Pro Thr Lys Gln Leu Met Ser Ser Glu Gln Gln Arg Lys Phe Ser 370 375 380	1334
agc cag tcc agt agg gct ctg acc cct cct tcc tac agt act gct aaa Ser Gln Ser Ser Arg Ala Leu Thr Pro Pro Ser Tyr Ser Thr Ala Lys 385 390 395	1382
aat tca ttg gga tca aga tcc agt gaa tcc ttt ggg aag tac aca tcg Asn Ser Leu Gly Ser Arg Ser Ser Glu Ser Phe Gly Lys Tyr Thr Ser 400 405 410	1430
cca gta atg agt gag cat ggg gac gag cac agg cag ctc ctc tct cac Pro Val Met Ser Glu His Gly Asp Glu His Arg Gln Leu Leu Ser His 415 420 425	1478
cca atg caa ggc cct gga ctc cgt gca gct acc tca tcc aac cac tct Pro Met Gln Gly Pro Gly Leu Arg Ala Ala Thr Ser Ser Asn His Ser 430 435 440 445	1526
gtg gac gag caa ctg aag aat act gac acg cac ctc atc gac ctg gta Val Asp Glu Gln Leu Lys Asn Thr Asp Thr His Leu Ile Asp Leu Val 450 455 460	1574

acc aat gag att atc acc caa gga cct cca gtg gac tgg aat gac att	1622
Thr Asn Glu Ile Ile Thr Gln Gly Pro Pro Val Asp Trp Asn Asp Ile	
465 470 475	
gct ggt ctc gac ctg gtg aag gct gtc att aaa gag gag gtt tta tgg	1670
Ala Gly Leu Asp Leu Val Lys Ala Val Ile Lys Glu Glu Val Leu Trp	
480 485 490	
cca gtg ttg agg tca gac gcg ttc agt gga ctg acg gcc tta cct cgg	1718
Pro Val Leu Arg Ser Asp Ala Phe Ser Gly Leu Thr Ala Leu Pro Arg	
495 500 505	
agc atc ctt tta ttt gga cct cgg ggg aca ggc aaa aca tta ttg ggc	1766
Ser Ile Leu Leu Phe Gly Pro Arg Gly Thr Gly Lys Thr Leu Leu Gly	
510 515 520 525	
aga tgc atc gct agt cag ctg ggg gcc aca ttt ttc aaa att gcc ggt	1814
Arg Cys Ile Ala Ser Gln Leu Gly Ala Thr Phe Phe Lys Ile Ala Gly	
530 535 540	
tct gga cta gtc gcc aag tgg tta gga gaa gca gag aaa att atc cat	1862
Ser Gly Leu Val Ala Lys Trp Leu Gly Glu Ala Glu Lys Ile Ile His	
545 550 555	
gcc tct ttt ctt gtg gcc agg tgt cgc cag ccc tcg gtg att ttt gtt	1910
Ala Ser Phe Leu Val Ala Arg Cys Arg Gln Pro Ser Val Ile Phe Val	
560 565 570	
agt gac att gac atg ctt ctc tcc tct caa gtg aat gag gaa cat agt	1958
Ser Asp Ile Asp Met Leu Leu Ser Ser Gln Val Asn Glu Glu His Ser	
575 580 585	
cca gtc agt cgg atg aga acc gaa ttt ctg atg caa ctg gac act gta	2006
Pro Val Ser Arg Met Arg Thr Glu Phe Leu Met Gln Leu Asp Thr Val	
590 595 600 605	
cta act tcg gct gag gac caa atc gta gta att tgt gcc acc agt aaa	2054
Leu Thr Ser Ala Glu Asp Gln Ile Val Val Ile Cys Ala Thr Ser Lys	
610 615 620	
cca gaa gaa ata gat gaa tcc ctt cgg agg tac ttc atg aaa cga ctt	2102
Pro Glu Glu Ile Asp Glu Ser Leu Arg Arg Tyr Phe Met Lys Arg Leu	
625 630 635	
tta atc cca ctt cct gac agc aca gcg agg cac cag ata ata gta caa	2150
Leu Ile Pro Leu Pro Asp Ser Thr Ala Arg His Gln Ile Ile Val Gln	
640 645 650	
ctg ctc tca cag cac aat tac tgt ctc aat gac aag gag ttt gca ctg	2198
Leu Leu Ser Gln His Asn Tyr Cys Leu Asn Asp Lys Glu Phe Ala Leu	
655 660 665	
ctc gtc cag cgc aca gaa ggc ttt tct gga cta gat gtg gct cat ttg	2246
Leu Val Gln Arg Thr Glu Gly Phe Ser Gly Leu Asp Val Ala His Leu	
670 675 680 685	
tgt cag gaa gca gtg gtg ggc ccc ctc cat gcc atg cca gcc aca gac	2294

Cys Gln Glu Ala Val Val Gly Pro Leu His Ala Met Pro Ala Thr Asp	
690 695 700	
ctt tca gcc att atg ccc agc cag ttg agg ccc gtt aca tat caa gac	2342
Leu Ser Ala Ile Met Pro Ser Gln Leu Arg Pro Val Thr Tyr Gln Asp	
705 710 715	
ttt gaa aat gct ttc tgc aag att cag cct agc ata tct caa aag gag	2390
Phe Glu Asn Ala Phe Cys Lys Ile Gln Pro Ser Ile Ser Gln Lys Glu	
720 725 730	
ctt gat atg tat gtt gaa tgg aac aaa atg ttt ggt tgc agt cag tga	2438
Leu Asp Met Tyr Val Glu Trp Asn Lys Met Phe Gly Cys Ser Gln *	
735 740 745	
taactttcttt ag	2450

<210> 243
 <211> 465
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (168)..(437)

<400> 243

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aagatgcctg taaatcaaata ttactataa ttgtaaagaa acctgaggca attagttaaa	120
aagttttaag tattcaggca attcatgata ccttgttgaa ataaagc atg cag act	176
Met Gln Thr	
1	
cat aaa aac ttg tat ata atc aaa ata aag ttc tac aaa tgg gaa aga	224
His Lys Asn Leu Tyr Ile Ile Lys Ile Lys Phe Tyr Lys Trp Glu Arg	
5 10 15	
gga tta tta tca ggg tat att aag gtg tta gac tta caa aag aag tgc	272
Gly Leu Leu Ser Gly Tyr Ile Lys Val Leu Asp Leu Gln Lys Lys Cys	
20 25 30 35	
ata att aat tac tca ttt aaa att aat tct ata ccc att agc ttg gca	320
Ile Ile Asn Tyr Ser Phe Lys Ile Asn Ser Ile Pro Ile Ser Leu Ala	
40 45 50	
aca gat aaa ata aaa gca tgc aac agt gct ttc tta gtc gac gcg gcc	368
Thr Asp Lys Ile Lys Ala Cys Asn Ser Ala Phe Leu Val Asp Ala Ala	
55 60 65	
gcg aat tcg gat cct cga gag atc tct ttt ttt ggg ttt ggt ggg gta	416
Ala Asn Ser Asp Pro Arg Glu Ile Ser Phe Phe Gly Phe Gly Gly Val	
70 75 80	

tct tca tca tcg aat aga tag ttatatatcat catgctcttc aattaaaa	465
Ser Ser Ser Ser Asn Arg *	
85 90	

<210> 244
 <211> 1080
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (83)..(829)

<400> 244

ctaggggagc tgaattctgc gtcttccttt aggctgcggc gagacaatcc ccagagcccc	60
gcggcccggc ctcggggcag cc atg gac tcg cag gaa ttg aag act ttg att	112
Met Asp Ser Gln Glu Leu Lys Thr Leu Ile	
1 5 10	
aat tac tat tgt caa gag aga tat ttc cat cat gta tta ctg gtt gcc	160
Asn Tyr Tyr Cys Gln Glu Arg Tyr Phe His His Val Leu Leu Val Ala	
15 20 25	
agt gaa gga att aag agg tat gga agt gat cca gtc ttc agg ttt tat	208
Ser Glu Gly Ile Lys Arg Tyr Gly Ser Asp Pro Val Phe Arg Phe Tyr	
30 35 40	
cat gcc tat ggc aca tta atg gaa ggt aaa act caa gaa gct ctt cga	256
His Ala Tyr Gly Thr Leu Met Glu Gly Lys Thr Gln Glu Ala Leu Arg	
45 50 55	
gaa ttt gag gct att aaa aat aaa caa gat gta tca ctt tgt tct cta	304
Glu Phe Glu Ala Ile Lys Asn Lys Gln Asp Val Ser Leu Cys Ser Leu	
60 65 70	
ctt gca ctg ata tat gcc cat aaa atg agt cct aat cca gat aga gaa	352
Leu Ala Leu Ile Tyr Ala His Lys Met Ser Pro Asn Pro Asp Arg Glu	
75 80 85 90	
gct att ctg gaa tca gat gcc aga gtg aag gaa caa cgt aaa gga gct	400
Ala Ile Leu Glu Ser Asp Ala Arg Val Lys Glu Gln Arg Lys Gly Ala	
95 100 105	
gga gag aaa gcc tta tac cat gca ggc tta ttt tta tgg cac att ggt	448
Gly Glu Lys Ala Leu Tyr His Ala Gly Leu Phe Leu Trp His Ile Gly	
110 115 120	
cgc cat gat aaa gca agg gaa tat att gac aga atg atc aaa ata tca	496
Arg His Asp Lys Ala Arg Glu Tyr Ile Asp Arg Met Ile Lys Ile Ser	
125 130 135	

gat ggt agt aaa cag gga cac gtt ttg aaa gca tgg ctt gat att aca	544
Asp Gly Ser Lys Gln Gly His Val Leu Lys Ala Trp Leu Asp Ile Thr	
140 145 150	
aga gga aaa gag cct tac act aaa aaa gca ctg aag tat ttt gaa gag	592
Arg Gly Lys Glu Pro Tyr Thr Lys Lys Ala Leu Lys Tyr Phe Glu Glu	
155 160 165 170	
gga ctc caa gat ggg aat gat act ttt gct ctg ctg ggt aag gca caa	640
Gly Leu Gln Asp Gly Asn Asp Thr Phe Ala Leu Leu Gly Lys Ala Gln	
175 180 185	
tgc ctt gag atg cgc cag aat tat tca ggt gcc ctg gag act gtg aac	688
Cys Leu Glu Met Arg Gln Asn Tyr Ser Gly Ala Leu Glu Thr Val Asn	
190 195 200	
cag ata atc gtg aat ttt ccg agc ttc ctt cct gct ttt gtt aag aaa	736
Gln Ile Ile Val Asn Phe Pro Ser Phe Leu Pro Ala Phe Val Lys Lys	
205 210 215	
atg aaa tta caa cta gcc ttg cag gat tgg gac cag aca gtt gag aca	784
Met Lys Leu Gln Leu Ala Leu Gln Asp Trp Asp Gln Thr Val Glu Thr	
220 225 230	
gca aaa ggt tgc tgc tcc aag ata gcc aaa atg tgg aag cac tga gaa	832
Ala Lys Gly Cys Cys Ser Lys Ile Ala Lys Met Trp Lys His *	
235 240 245	
tgcaggcact ctactatgtg tgtagagagg gggatataga gaaggcttcc accaagctgg	892
aaaacttggg aaatgcattg gatgccatgg aaccacagaa tgctcaactt ttctataaca	952
ttacactcgc cttcagcaga acttgtggac gtagtcaact tattcttcaa aaaattcaaa	1012
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taccaatt	1080

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 <211> 2128
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (107)..(286)

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ttcaatattg tagttaattt tttggctttc aacagcagcc ctagta atg gtg gag	115
	Met Val Glu
	1

ttg tta att aat gtg tat att gta ctg aat ttc tgt cag tta agg ggt	163
Leu Leu Ile Asn Val Tyr Ile Val Leu Asn Phe Cys Gln Leu Arg Gly	
5 10 15	
tca ctg ctt tgg tgg aaa ttg gtg gaa att gct agc agg ttc cac gat	211
Ser Leu Leu Trp Trp Lys Leu Val Glu Ile Ala Ser Arg Phe His Asp	
20 25 30 35	
gtt tat ttt ttt ctc cat gtt gta tat cat tac cat ttc aca tac gcg	259
Val Tyr Phe Phe Leu His Val Val Tyr His Tyr His Phe Thr Tyr Ala	
40 45 50	
ttt cta ttt ttc ttc ctc tcc tcc tga tctcc ttaaaaatga atctagagtt	311
Phe Leu Phe Phe Phe Leu Ser Ser *	
55 60	
ggtaggctttt tccccctcct ctttggccag ttccacagtt cagttcttcc tgaaaacagg	371
gatgatgaac ttgtaggac aggacaaatg tgtgtttttc aaaaacttaa ggctgggtgt	431
gaaacacctt ctgtggacaa ggatttgtaa acttctctcc tccctccagc tgcggcccca	491
gcctaactga tagttacttg attcagtgtg ctagacactt aaatagcatc tatgtctctt	551
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agctgtgatt ttgttgga gcaagtatta tggccaaagc cagtttcttg gcatttcaaa	671
aataatgcaa taaaaactag ttgagggttag ctgaggctgg aatgccttt ttcattgtaa	731
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ttcatccctt gatcttaaat caaaacgtca gatcaatgaa ctatgaacta aagtattttt	851
cttaagccta ttgagtgatt aattttttta aaaatgttta aatgcatatg cttttctttc	911
agcacaacaa acagcaaaaa cttttgtaat aactaactta cttttgcatg tatgaagaac	971
tgagtcattt atttccctaa ctactcctc tttcaagtaa caggtggcag atcataaaat	1031
gaattcttta ttgtatctac aactccaca ttctttactg tgtcctacta ctgtatcttg	1091
gtccctgct gtattaaaca ccatcttaag cacttggtcc tgcaggactc cttcttgaca	1151
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tctctatcac accgaatact aagatttatt tcctctgatg gtacatagat ttctctctcc	1271
actaagaggg tcaactctcat agaggaatgt cttgtcagtt ttatacttgc tgaggctaga	1331
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aaacttgaaa ggtttgcaag gtttctccta tcctgttaa aattatcatt tattatctct	1511
ttgtcagtg tagtaaggta acccatgaca gaataatttg agtgatagtt catcatgcag	1571

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aggatatgat caagatatta cctaattggtt ttatcctgaa aaaggtgtat acttttaggg 1631
cactgttaac aatgcgagtg aaaccaagat ggtgcaagtt ccctttgcag atggcgtggg 1691
cacacttgat ttttattatg agtgaatgta atctttctgt attttaccag agttacagca 1751
attacctgaa aagtttccta acattttaat aatggttaggg atttcgtttt ggtttttagtt 1811
gtcctcaaga gacaacaggt tcacagtaat ttccatgatg ttgggtgtgg ctaagctggg 1871
gattggttct gttccccctg ctcccggtga gagaaaagct atatttatac tgcattcttt 1931
ctcaactttc aggtaaaaca aactatgatt taaaaaaga aaaaagaaaa gacaggtact 1991
tttacttcaa agagtgtctt gctacatttt tatttaaac aaaaatcaaa taaaataagg 2051
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attccaaaaa aaaaaaa 2128

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<210> 246
<211> 3373
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (146)..(2254)

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<400> 246

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tttccccaca ggggtgactta aatgtcccag gctggaaggt ggagcgagaa gtggatgccc 120
ccagggctct gggtcacact ccagg  atg act tct cgg aac cag ctg gtg cag 172
                               Met Thr Ser Arg Asn Gln Leu Val Gln
                               1             5

aag gtg ctg cag gag ctg cag gaa gca gtg gag tgc gaa ggc ctg gag 220
Lys Val Leu Gln Glu Leu Gln Glu Ala Val Glu Cys Glu Gly Leu Glu
 10             15             20             25

ggg ctc ata ggt gct tcc ttg gag gcc aag cag gtc ctg tct tcc ttc 268
Gly Leu Ile Gly Ala Ser Leu Glu Ala Lys Gln Val Leu Ser Ser Phe
             30             35             40

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Thr Leu Pro Thr Cys Arg Glu Gly Gly Pro Gly Leu Gln Val Leu Glu
             45             50             55

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Val Asp Ser Val Ala Leu Ser Leu Tyr Pro Glu Asp Ala Pro Arg Asn
 60             65             70

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Ala Ser Met Leu Leu Trp Gly Asp Ala Gly Leu Ser Leu Glu Leu Arg	
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Ala Arg Thr Val Val Glu Met Leu Leu His Arg His Tyr Tyr Leu Gln	
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Gly Met Ile Asp Ser Lys Val Met Leu Gln Ala Val Arg Tyr Ser Leu	
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Cys Ser Glu Glu Ser Pro Glu Met Thr Ser Leu Pro Pro Ala Thr Leu	
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Phe Ser Asn Val Trp His Leu Tyr Ala Leu Ala Ser Val Leu Gln Arg	
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Phe Asn Arg Val Ile Arg Pro Arg Arg Cys Asp His Val Pro Ser Thr	
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Leu His Ile Met Trp Ala Gly Gln Pro Leu Thr Ser His Phe Phe Arg	
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His Gln Tyr Phe Ala Pro Val Val Gly Leu Glu Glu Val Glu Ala Glu	
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Gly Ala Pro Gly Val Ala Pro Ala Leu Pro Ala Leu Ala Pro Leu Ser	
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Ser Pro Ala Lys Thr Leu Glu Leu Leu Asn Arg Glu Pro Gly Leu Ser	
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Tyr Ser His Leu Cys Glu Arg Tyr Ser Val Thr Lys Ser Thr Phe Tyr	
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Lys Ser Phe Pro Ser Tyr Lys Glu Phe Ser Ala Leu Phe Pro Leu Thr	
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Ala Arg Ser Thr Tyr Tyr Met Trp Lys Arg Ala Leu Tyr Asp Gly Leu	
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 Met Gly Ala Thr Gly Ala Ala Glu
 1 5
 ccg ctg caa tcc gtg ctg tgg gtg aag cag cag cgc tgc gcc gtg agc 161
 Pro Leu Gln Ser Val Leu Trp Val Lys Gln Gln Arg Cys Ala Val Ser
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 ctg gag ccc gcg cgg gct ctg ctg cgc tgg tgg cgg agc ccg ggg ccc 209
 Leu Glu Pro Ala Arg Ala Leu Leu Arg Trp Trp Arg Ser Pro Gly Pro
 25 30 35 40
 gga gcc ggc gcc ccc ggc gcg gat gcc tgc tct gtg cct gta tct gag 257
 Gly Ala Gly Ala Pro Gly Ala Asp Ala Cys Ser Val Pro Val Ser Glu

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gga aaa tgg cag aaa atg gaa aag cct tac gct ttt aca gtt cac tgt Gly Lys Trp Gln Lys Met Glu Lys Pro Tyr Ala Phe Thr Val His Cys 75 80 85			353
gta aag aga gca cga cgg cac cgc tgg aag tgg gcg cag gtg act ttc Val Lys Arg Ala Arg Arg His Arg Trp Lys Trp Ala Gln Val Thr Phe 90 95 100			401
tgg tgt cca gag gag cag ctg tgt cac ttg tgg ctg cag acc ctg cgg Trp Cys Pro Glu Glu Gln Leu Cys His Leu Trp Leu Gln Thr Leu Arg 105 110 115 120			449
gag atg ctg gag aag ctg acg tcc aga cca aag cat tta ctg gta ttt Glu Met Leu Glu Lys Leu Thr Ser Arg Pro Lys His Leu Leu Val Phe 125 130 135			497
atc aac ccg ttt gga gga aaa gga caa ggc aag cgg ata tat gaa aga Ile Asn Pro Phe Gly Gly Lys Gly Gln Gly Lys Arg Ile Tyr Glu Arg 140 145 150			545
aaa gtg gca cca ctg ttc acc tta gcc tcc atc acc act gac atc atc Lys Val Ala Pro Leu Phe Thr Leu Ala Ser Ile Thr Thr Asp Ile Ile 155 160 165			593
gtt act gaa cat gct aat cag gcc aag gag act ctg tat gag att aac Val Thr Glu His Ala Asn Gln Ala Lys Glu Thr Leu Tyr Glu Ile Asn 170 175 180			641
ata gac aaa tac gac ggg tga gt aagccgtctt tcatcgccat caagtccatt Ile Asp Lys Tyr Asp Gly * 185 190			694
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Phe	Thr	Asp	Pro	Asp	Leu	Leu	Leu	Asp	Leu	Val	Asp	Ala	Ala	Thr	Arg		
	165					170					175						
cgc	tgg	gta	cct	gtc	tac	ctg	ctc	ctg	gac	cgc	cag	cag	ctg	cct	gcc	1110	
Arg	Trp	Val	Pro	Val	Tyr	Leu	Leu	Leu	Asp	Arg	Gln	Gln	Leu	Pro	Ala		
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ttc	ctg	gaa	ctg	gcc	cag	cag	ctg	ggg	gtg	aac	ccc	tgg	aac	acg	gag	1158	
Phe	Leu	Glu	Leu	Ala	Gln	Gln	Leu	Gly	Val	Asn	Pro	Trp	Asn	Thr	Glu		
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aac	gtg	gat	gtc	cgt	gtc	gtg	cgg	ggc	tgc	agc	ttc	cag	agc	cgc	tgg	1206	
Asn	Val	Asp	Val	Arg	Val	Val	Arg	Gly	Cys	Ser	Phe	Gln	Ser	Arg	Trp		
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cga	cgg	cag	gtg	agc	ggc	acc	gtg	cgg	gag	aag	ttt	gtg	ctg	ctg	gac	1254	
Arg	Arg	Gln	Val	Ser	Gly	Thr	Val	Arg	Glu	Lys	Phe	Val	Leu	Leu	Asp		
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ggc	gag	agg	gtc	atc	tca	gga	tcc	tac	agc	ttc	acg	tgg	agt	gac	gca	1302	
Gly	Glu	Arg	Val	Ile	Ser	Gly	Ser	Tyr	Ser	Phe	Thr	Trp	Ser	Asp	Ala		
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cgc	ctg	cac	cga	ggc	ctg	gtg	acc	ctg	ctg	act	ggc	gaa	att	gtt	gac	1350	
Arg	Leu	His	Arg	Gly	Leu	Val	Thr	Leu	Leu	Thr	Gly	Glu	Ile	Val	Asp		
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gcc	ttc	agc	ctt	gag	ttc	cgg	acg	ctg	tac	gcg	gcc	tcc	tgc	ccg	ctc	1398	
Ala	Phe	Ser	Leu	Glu	Phe	Arg	Thr	Leu	Tyr	Ala	Ala	Ser	Cys	Pro	Leu		
				280					285					290			
cca	cct	gcg	ccc	ccc	cag	aaa	ccc	tcg	gtc	ata	ggc	ggc	ctg	cag	cgg	1446	
Pro	Pro	Ala	Pro	Pro	Gln	Lys	Pro	Ser	Val	Ile	Gly	Gly	Leu	Gln	Arg		
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Gly	Arg	Ser	Leu	His	Arg	Val	Ser	Arg	Arg	Arg	Ser	Val	Ala	Pro	Ala		
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Ser	Pro	Pro	Pro	Pro	Asp	Gly	Pro	Leu	Ala	His	Arg	Leu	Ala	Ala	Cys		
	325					330					335						
cgc	gtc	tcc	cct	gct	acc	ccg	ggg	ccg	gca	ctc	agt	gac	att	cta	agg	1590	
Arg	Val	Ser	Pro	Ala	Thr	Pro	Gly	Pro	Ala	Leu	Ser	Asp	Ile	Leu	Arg		
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agt	gtg	cag	cgc	gcc	cgg	acc	ccc	agc	ggc	ccc	ccg	gcc	cgg	ccc	agc	1638	
Ser	Val	Gln	Arg	Ala	Arg	Thr	Pro	Ser	Gly	Pro	Pro	Ala	Arg	Pro	Ser		
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cgc	tcc	atg	tgg	gac	cta	agc	cgc	ctg	tcc	cag	ctg	tct	ggc	tcc	agt	1686	
Arg	Ser	Met	Trp	Asp	Leu	Ser	Arg	Leu	Ser	Gln	Leu	Ser	Gly	Ser	Ser		

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Asp Gly Asp Asn Glu Leu Lys Lys Ser Trp Gly Ser Lys Asp Thr Pro			
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Ala Lys Ala Leu Met Arg Gln Arg Gly Thr Gly Gly Gly Pro Trp Gly			
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Glu Val Asp Ser Arg Pro Pro Trp Gly Gly Ala Leu Pro Leu Pro Pro			
420	425	430	435
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Ala His Arg Leu Arg Tyr Leu Ser Pro Ala Arg Arg Arg Phe Gly Gly			
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Asp Ala Thr Phe Lys Leu Gln Glu Pro Arg Gly Val Arg Pro Ser Asp			
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Trp Ala Pro Arg Ala Gly Leu Gly Gly Gln Pro *			
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Met Ala Pro Arg Pro
1 5
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Arg Ala Arg Pro Gly Val Ala Val Ala Cys Cys Trp Leu Leu Thr Val
10 15 20
gtt cta cgc tgc tgc gta tca ttc aat gtt gat gtg aaa aat tca atg 509
Val Leu Arg Cys Cys Val Ser Phe Asn Val Asp Val Lys Asn Ser Met
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Thr Phe Ser Gly Pro Val Glu Asp Met Phe Gly Tyr Thr Val Gln Gln
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tat gaa aat gaa gaa gga aaa tgg gtg ctt att ggt tct ccg tta gtt 605
Tyr Glu Asn Glu Glu Gly Lys Trp Val Leu Ile Gly Ser Pro Leu Val
55 60 65
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Gly Gln Pro Lys Asn Arg Thr Gly Asp Val Tyr Lys Cys Pro Val Gly
70 75 80 85
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Arg Gly Glu Ser Leu Pro Cys Val Lys Leu Asp Leu Pro Val Asn Thr
90 95 100
tca att ccc aat gtc aca gaa gta aag gag aac atg aca ttt gga tca 749
Ser Ile Pro Asn Val Thr Glu Val Lys Glu Asn Met Thr Phe Gly Ser
105 110 115
act tta gtc acc aac cca aat gga gga ttt ctg gct tgt ggg ccc tta 797
Thr Leu Val Thr Asn Pro Asn Gly Gly Phe Leu Ala Cys Gly Pro Leu
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Tyr Ala Tyr Arg Cys Gly His Leu His Tyr Thr Thr Gly Ile Cys Ser
135 140 145
gac gtc agc ccc aca ttt caa gtc gtg aat tcc att gcc cct gta caa 893
Asp Val Ser Pro Thr Phe Gln Val Val Asn Ser Ile Ala Pro Val Gln
150 155 160 165
gaa tgc agc act caa ctg gac ata gtc ata gtg ctg gat ggt tcc aac 941
Glu Cys Ser Thr Gln Leu Asp Ile Val Ile Val Leu Asp Gly Ser Asn
170 175 180

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Ser Ile Tyr Pro Trp Asp Ser Val Thr Ala Phe Leu Asn Asp Leu Leu	
185 190 195	
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Lys Arg Met Asp Ile Gly Pro Lys Gln Thr Gln Val Gly Ile Val Gln	
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Ile Val Thr Asp Gly Glu Ser His Asp Asn His Arg Leu Lys Lys Val	
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Val Ser Asp Glu Leu Ala Leu Val Thr Ile Val Lys Thr Leu Gly Glu	
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Arg Ile Phe Ala Leu Glu Ala Thr Ala Asp Gln Ser Ala Ala Ser Phe	
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Glu Met Glu Met Ser Gln Thr Gly Phe Ser Ala His Tyr Ser Gln Asp	
375 380 385	
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Trp Val Met Leu Gly Ala Val Gly Ala Tyr Asp Trp Asn Gly Thr Val	
390 395 400 405	

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aat gtt gag tct acc aaa aag aat gaa ccg ctt gct tct tat tta ggt Asn Val Glu Ser Thr Lys Lys Asn Glu Pro Leu Ala Ser Tyr Leu Gly 425 430 435	1709
tac act gta aac tct gct act gct tct tct gga gat gtg ctc tat att Tyr Thr Val Asn Ser Ala Thr Ala Ser Ser Gly Asp Val Leu Tyr Ile 440 445 450	1757
gct gga cag cct cgg tac aat cat aca ggc cag gtc att atc tac agg Ala Gly Gln Pro Arg Tyr Asn His Thr Gly Gln Val Ile Ile Tyr Arg 455 460 465	1805
atg gaa gat gga aac atc aaa att ctc cag acg ctc agt gga gaa cag Met Glu Asp Gly Asn Ile Lys Ile Leu Gln Thr Leu Ser Gly Glu Gln 470 475 480 485	1853
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ctg aaa ttt ttt ggc cag tct atc cac gga gaa atg gat tta aat ggt	2333

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gac	ggg	ctg	aca	gat	gtg	act	att	ggg	ggc	ctt	ggg	ggg	gct	gcc	ctc	2381	
Asp	Gly	Leu	Thr	Asp	Val	Thr	Ile	Gly	Gly	Leu	Gly	Gly	Ala	Ala	Leu		
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Phe	Trp	Ser	Arg	Asp	Val	Ala	Val	Val	Lys	Val	Thr	Met	Asn	Phe	Glu		
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Pro	Asn	Lys	Val	Asn	Ile	Gln	Lys	Lys	Asn	Cys	His	Met	Glu	Gly	Lys		
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Ser	Lys	Glu	Asp	Thr	Ile	Tyr	Glu	Ala	Asp	Leu	Gln	Tyr	Arg	Val	Thr		
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Leu	Asp	Ser	Leu	Arg	Gln	Ile	Ser	Arg	Ser	Phe	Phe	Ser	Gly	Thr	Gln		
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Glu	Arg	Lys	Val	Gln	Arg	Asn	Ile	Thr	Val	Arg	Lys	Ser	Glu	Cys	Thr		
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Lys	His	Ser	Phe	Tyr	Met	Leu	Asp	Lys	His	Asp	Phe	Gln	Asp	Ser	Val		
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Lys	Asp	Cys	Gly	Asn	Lys	Glu	Lys	Cys	Ile	Ser	Asp	Leu	Ser	Leu	His		
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gtc	gcc	acc	act	gaa	aag	gac	ctg	ctg	att	gtc	cga	tcc	cag	aat	gat	2909	
Val	Ala	Thr	Thr	Glu	Lys	Asp	Leu	Leu	Ile	Val	Arg	Ser	Gln	Asn	Asp		
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Lys	Phe	Asn	Val	Ser	Leu	Thr	Val	Lys	Asn	Thr	Lys	Asp	Ser	Ala	Tyr		
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Asn	Thr	Arg	Thr	Ile	Val	His	Tyr	Ser	Pro	Asn	Leu	Val	Phe	Ser	Gly		

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Ile Glu Ala Ile Gln Lys Asp Ser Cys Glu Ser Asn His Asn Ile Thr			
870	875	880	885
tgt aaa gtt gga tat ccc ttc ctg aga aga gga gag atg gta act ttc			3101
Cys Lys Val Gly Tyr Pro Phe Leu Arg Arg Gly Glu Met Val Thr Phe			
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aaa ata ttg ttt cag ttt aac aca tcc tat ctc atg gaa aat gtg acc			3149
Lys Ile Leu Phe Gln Phe Asn Thr Ser Tyr Leu Met Glu Asn Val Thr			
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att tat tta agt gca aca agt gac agc gaa gaa cct cct gaa acc ctt			3197
Ile Tyr Leu Ser Ala Thr Ser Asp Ser Glu Glu Pro Pro Glu Thr Leu			
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Ser Asp Asn Val Val Asn Ile Ser Ile Pro Val Lys Tyr Glu Val Gly			
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cta cag ttt tac agc tct gca agt gaa tac cac att tca att gct gcc			3293
Leu Gln Phe Tyr Ser Ser Ala Ser Glu Tyr His Ile Ser Ile Ala Ala			
	950	955	960
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Asn Glu Thr Val Pro Glu Val Ile Asn Ser Thr Glu Asp Ile Gly Asn			
	970	975	980
gaa att aat atc ttc tac ttg att aga aaa agt gga tct ttt cca atg			3389
Glu Ile Asn Ile Phe Tyr Leu Ile Arg Lys Ser Gly Ser Phe Pro Met			
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Pro Glu Leu Lys Leu Ser Ile Ser Phe Pro Asn Met Thr Ser Asn Gly			
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tac cct gtg ctg tac cca act gga ttg tca tct tct gag aat gca aac			3485
Tyr Pro Val Leu Tyr Pro Thr Gly Leu Ser Ser Glu Asn Ala Asn			
	1015	1020	1025
tgc aga ccc cat atc ttt gag gat cct ttc agt atc aac tct gga aag			3533
Cys Arg Pro His Ile Phe Glu Asp Pro Phe Ser Ile Asn Ser Gly Lys			
1030	1035	1040	1045
aaa atg act aca tca act gac cat ctc aaa cga ggc aca att ctg gac			3581
Lys Met Thr Thr Ser Thr Asp His Leu Lys Arg Gly Thr Ile Leu Asp			
	1050	1055	1060
tgc aat aca tgt aaa ttt gct acc atc aca tgt aat ctc act tct tct			3629
Cys Asn Thr Cys Lys Phe Ala Thr Ile Thr Cys Asn Leu Thr Ser Ser			
	1065	1070	1075
gac atc agc caa gtc aat gtt tcg ctt atc ttg tgg aaa cca act ttt			3677
Asp Ile Ser Gln Val Asn Val Ser Leu Ile Leu Trp Lys Pro Thr Phe			
	1080	1085	1090

ata aaa tca tat ttt tcc agc tta aat ctt act ata agg gga gaa ctt	3725
Ile Lys Ser Tyr Phe Ser Ser Leu Asn Leu Thr Ile Arg Gly Glu Leu	
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cgg agt gaa aat gca tct ctg gtt tta agt agc agc aat caa aaa aga	3773
Arg Ser Glu Asn Ala Ser Leu Val Leu Ser Ser Ser Asn Gln Lys Arg	
1110 1115 1120 1125	
gag ctt gct att caa ata tcc aaa gat ggg cta ccg ggc aga gtg cca	3821
Glu Leu Ala Ile Gln Ile Ser Lys Asp Gly Leu Pro Gly Arg Val Pro	
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Leu Trp Val Ile Leu Leu Ser Ala Phe Ala Gly Leu Leu Leu Leu Met	
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Leu Leu Ile Leu Ala Leu Trp Lys Ile Gly Phe Phe Lys Arg Pro Leu	
1160 1165 1170	
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Lys Lys Lys Met Glu Lys *	
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cagaaaa atg gtt cgt att gtt ctt aca aag aca aag aga gat gca gca 649
Met Val Arg Ile Val Leu Thr Lys Thr Lys Arg Asp Ala Ala
1 5 10
aat tgt tgg act tct cta cta gaa tct gaa tat gca gcg gat cct tgg 697
Asn Cys Trp Thr Ser Leu Leu Glu Ser Glu Tyr Ala Ala Asp Pro Trp
15 20 25 30
gtg caa gac caa atg cag aga aag ctt aca tta gag aga ttc caa aaa 745
Val Gln Asp Gln Met Gln Arg Lys Leu Thr Leu Glu Arg Phe Gln Lys
35 40 45
gaa aat cct ggt ttt gac ttc agt gga gca gaa atc tca gga aac tac 793
Glu Asn Pro Gly Phe Asp Phe Ser Gly Ala Glu Ile Ser Gly Asn Tyr
50 55 60
act aaa ggt gga cca gat ttc tca aac ctt gag aaa taa ctgctttttt 842
Thr Lys Gly Gly Pro Asp Phe Ser Asn Leu Glu Lys *
65 70 75
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Pro Trp Leu Leu Ser Trp Val Ser Ala Thr Ala Trp Arg Ala Ala Arg
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tca ccc ctt ctg tgt cat tct ctg agg aaa aca agt tct tct caa gga   149
Ser Pro Leu Leu Cys His Ser Leu Arg Lys Thr Ser Ser Ser Gln Gly
          25           30           35

gga aag tct gaa ctt gtc aaa cag tcc ctt aag aag ccg aag tta cca   197
Gly Lys Ser Glu Leu Val Lys Gln Ser Leu Lys Lys Pro Lys Leu Pro
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gaa ggt cgt ttt gat gca cca gag gat tcc cat tta gag aaa gaa cca   245
Glu Gly Arg Phe Asp Ala Pro Glu Asp Ser His Leu Glu Lys Glu Pro
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ctg gaa aaa ttt cca gat gat gtt aat cca gtg acc aaa gaa aaa ggt   293
Leu Glu Lys Phe Pro Asp Asp Val Asn Pro Val Thr Lys Glu Lys Gly
          75           80           85

gga ccc agg ggc cca gaa cct acc cga tat gga gat tgg gaa cga aaa   341
Gly Pro Arg Gly Pro Glu Pro Thr Arg Tyr Gly Asp Trp Glu Arg Lys
          90           95           100

gga cgc tgt att gat ttt taa gt cgcataattct ttaacttcaa tattgttttc   394
Gly Arg Cys Ile Asp Phe *
          105

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tcgtgtagtt tgtataatgt gtttaaatat atatatatat atatatatat atatatatat   514

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cacgcccagc ctagaaatga ttcttagagc tgtaggcctt tacttcatca tttttcagtt 874
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 Arg Gly Ala Gly Gly Arg Trp Asn Ser Thr Ser Trp Ser Thr Gly Cys
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aag ttg cca gcg tgc cca agg aga gta tcc cgc tgt tca cct acg ggc 151
 Lys Leu Pro Ala Ser Pro Arg Arg Val Ser Arg Cys Ser Pro Thr Gly
 25 30 35

ctg atc aaa ctt gcc ttc ctg ttc tcc aag acc agg tgc aag ttc ttc 199
 Leu Ile Lys Leu Ala Phe Leu Phe Ser Lys Thr Arg Cys Lys Phe Phe
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agt ctg act gag aca cca gag gat tac act atc att gtc gat gag gaa 247
 Ser Leu Thr Glu Thr Pro Glu Asp Tyr Thr Ile Ile Val Asp Glu Glu
 55 60 65

gga ttc cta gag ctg ccc tcc tca gag cac ctg agt gtg gcg gat gcc 295
 Gly Phe Leu Glu Leu Pro Ser Ser Glu His Leu Ser Val Ala Asp Ala
 70 75 80 85

acc tgg ctg gcc ctg aac gtg gtg tcc ggc ggt ggc agc ttc tcc agc 343
 Thr Trp Leu Ala Leu Asn Val Val Ser Gly Gly Gly Ser Phe Ser Ser
 90 95 100

tcc cag cct att ggc atg acc aag atc gcc aag tca gtc atc gcc cca 391
 Ser Gln Pro Ile Gly Met Thr Lys Ile Ala Lys Ser Val Ile Ala Pro
 105 110 115

ctg gct gac cag aac ata tcc gtg ttc atg ctg tcc acg tat cag aca 439
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 120 125 130

gac ttc atc ctg gtg ctc aag cgg gac ctg ccc ttt gtc acc cac acg 487
 Asp Phe Ile Leu Val Leu Lys Arg Asp Leu Pro Phe Val Thr His Thr

135	140	145	
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Leu Ser Ser Glu Phe Thr Ile Leu Trp Ser Val Ala Arg Leu *			
150	155	160	
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cctaagaggt tgatacgacc atgagtcctat tttcactgag gaaaaccgaa gaaaagaaat			180
tgtaaatggc cagagatgta tggctggtga	atg gcc ctg tgt gga ggc agg		231
	Met Ala Leu Cys Gly Gly Arg		
	1 5		
gcc aag gtg aat gct cct gct atg cag atg atg cag ccc aga gag ccg			279
Ala Lys Val Asn Ala Pro Ala Met Gln Met Met Gln Pro Arg Glu Pro			
10 15 20			

cag cca cct ctg cga gtc cca cag ctg gaa gga gca ccc agt cct ccc 327
Gln Pro Pro Leu Arg Val Pro Gln Leu Glu Gly Ala Pro Ser Pro Pro
25 30 35

aca cta gcc gga cag gcc cgc agc ctg cac tac tga gctg tcacggagga 377
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ggaggcctgg tgcactacac agctcctttg tgectccagg ccacctgccc aagctgggtgt 180

gcctcccttc taaggctctg tcccactggg cacaggaggc agatccagca gcgtggaatc 240

ccagataac atg tcc cac aga ctc tgg caa cgt cac aga tca cat gga 288
Met Ser His Arg Leu Trp Gln Arg His Arg Ser His Gly
1 5 10

gag gca agt gca ggc caa cga cat ccg cat ccg ggt cct aca gga gga 336
Glu Ala Ser Ala Gly Gln Arg His Pro His Pro Gly Pro Thr Gly Gly
15 20 25

gaa cgg gcg gct cca atc aat gct gtc caa aat ccg gga agt ggc cca 384
Glu Arg Ala Ala Pro Ile Asn Ala Val Gln Asn Pro Gly Ser Gly Pro
30 35 40 45

gca ggg tgg cct caa ggt ggg cct gag agg gcg ggc cct tgg gga cca 432
Ala Gly Trp Pro Gln Gly Gly Pro Glu Arg Ala Gly Pro Trp Gly Pro
50 55 60

gga gga agc ccc tat cca gca gca ggt ctt cag act ctg ccc cgg gaa 480
Gly Gly Ser Pro Tyr Pro Ala Ala Gly Leu Gln Thr Leu Pro Arg Glu
65 70 75

ctt gtg gag agc cca cct cat cac atg agg cct tag gctg tgcttttgtg 530
Leu Val Glu Ser Pro Pro His His Met Arg Pro *
80 85

aaacattttt cacatttcca gaaggcgtga ggatgttatg gattcgatgc cttccagttc 590

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636

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ggccctgccc acccaggggt ttccgagatc acccctggtg aggcggcgtg ccagtccctt      180
gctttcttac ttgttctgca gagcggggag ctgaggctgc atgaggaag actcccgtac      240
cccagcacgg tggaggggtg gatgggggtca cgcctgtgcg acccaggagg tggccagcag      300
aaggaaacag tagtgtccac catggtctgc gtctccccac cacggattgt cttgggtccg      360
gatttgagac atggcagggc cagatgagga caacttgatg acagtttaca gag   atg      416
                                   Met
                                   1

gag gca ggg tgc cag gaa gcc acg ggg gag ccc cca ggg cac tca gca      464
Glu Ala Gly Cys Gln Glu Ala Thr Gly Glu Pro Pro Gly His Ser Ala
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gtc cag gca ggg ctg ggc gtc ctg gca agg agc agg gac ctt ctg ccc      512
Val Gln Ala Gly Leu Gly Val Leu Ala Arg Ser Arg Asp Leu Leu Pro
      20                      25                      30

agg ggt gtg gcc agc ctg tgg gtg ctg tgt gca gga ccc cag gaa cca      560
Arg Gly Val Ala Ser Leu Trp Val Leu Cys Ala Gly Pro Gln Glu Pro
      35                      40                      45

agg ccg cag tct ctt ccc tcg ctc cag cat cct ccc aag gcc acc ctt      608
Arg Pro Gln Ser Leu Pro Ser Leu Gln His Pro Pro Lys Ala Thr Leu
      50                      55                      60                      65

ggc tgc act cag cca gag agc tgg ggc aca ggg acc cca cag gtt tcc      656
Gly Cys Thr Gln Pro Glu Ser Trp Gly Thr Gly Thr Pro Gln Val Ser
      70                      75                      80

ctg gag gct gtc agg ggc tcc ggt ggg ggc ggg ggg tga gcccgtggg      705
Leu Glu Ala Val Arg Gly Ser Gly Gly Gly Gly Gly *
      85                      90

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<210> 256
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 <213> Homo sapiens

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 cagtttccac atctgcacaa tgggggtgac catcctgcc ctgctggctg ccaggagcgg 180
 ctgtgagtct tcaggcgtgg atgcagcctg ggggaagcca tagggcgctt tcacaggcct 240
 ggccttcacc atg gcg gga ggg aga ccg cat ctg aag agg agt ttc tcc 289
 Met Ala Gly Gly Arg Pro His Leu Lys Arg Ser Phe Ser
 1 5 10
 atc atc ccc tgc ttt gtc ttc gtg gag tcg gtg ctg ctg ggc att gtg 337
 Ile Ile Pro Cys Phe Val Phe Val Glu Ser Val Leu Leu Gly Ile Val
 15 20 25
 atc ctg ctt gct tac cgc ctg gag ttc acg gac acc ttc cct gtg cac 385
 Ile Leu Leu Ala Tyr Arg Leu Glu Phe Thr Asp Thr Phe Pro Val His
 30 35 40 45
 acc cag gga ttc ttc tgc tat gac agt acc tac gcc aag ccc tac cca 433
 Thr Gln Gly Phe Phe Cys Tyr Asp Ser Thr Tyr Ala Lys Pro Tyr Pro
 50 55 60
 ggg cct gag gct gcc agc cga gtg cct cct gct ctt gtc tac gca ctg 481
 Gly Pro Glu Ala Ala Ser Arg Val Pro Pro Ala Leu Val Tyr Ala Leu
 65 70 75
 gtc act gcc ggg ccc acc ctg acg atc ctg ctg gga gag ctg gcg cgt 529
 Val Thr Ala Gly Pro Thr Leu Thr Ile Leu Leu Gly Glu Leu Ala Arg
 80 85 90
 gcc ttt ttc cct gca cca cct tca gcc gtc cca gtc atc ggg gag agc 577
 Ala Phe Phe Pro Ala Pro Pro Ser Ala Val Pro Val Ile Gly Glu Ser
 95 100 105
 acc atc gtg tct ggg gcc tgc tgc cgc ttc agc ccc cca gtg cgg agg 625
 Thr Ile Val Ser Gly Ala Cys Cys Arg Phe Ser Pro Pro Val Arg Arg
 110 115 120 125
 ctg gtc cgc ttc ctg ggg gtc tac tcc ttc ggc ctg ttc acc acg acc 673
 Leu Val Arg Phe Leu Gly Val Tyr Ser Phe Gly Leu Phe Thr Thr Thr
 130 135 140

atc ttc gcc aac gcg ggg cag gtg gtg acc ggc aat ccc acg cca cac Ile Phe Ala Asn Ala Gly Gln Val Val Thr Gly Asn Pro Thr Pro His 145 150 155	721
ttc ctg tcc gtg tgc cgc ccc aac tac acg gcc ctg ggc tgc ctg cca Phe Leu Ser Val Cys Arg Pro Asn Tyr Thr Ala Leu Gly Cys Leu Pro 160 165 170	769
cct tct ccg gat cgg cca ggt ccc gac cgc ttt gtc act gac cag ggt Pro Ser Pro Asp Arg Pro Gly Pro Asp Arg Phe Val Thr Asp Gln Gly 175 180 185	817
gcc tgc gct ggc agt ccc agc ctc gtg gcc gcc gcg cgc cgc gcc ttc Ala Cys Ala Gly Ser Pro Ser Leu Val Ala Ala Ala Arg Arg Ala Phe 190 195 200 205	865
ccc tgc aag gat gcg gcc ctc tgc gcc tac gcg gtc acc tac aca gcg Pro Cys Lys Asp Ala Ala Leu Cys Ala Tyr Ala Val Thr Tyr Thr Ala 210 215 220	913
atg tac gtg act ctc gtg ttc cgc gtg aag ggc tcc cgc ctg gtc aaa Met Tyr Val Thr Leu Val Phe Arg Val Lys Gly Ser Arg Leu Val Lys 225 230 235	961
ccc tcg ctc tgc ctg gcc ttg ctg tgc ccg gcc ttc ctg gtg ggc gtg Pro Ser Leu Cys Leu Ala Leu Leu Cys Pro Ala Phe Leu Val Gly Val 240 245 250	1009
gtc cgc gtg gcc gag tac cga aac cac tgg tcg gac gtg ctg gct ggc Val Arg Val Ala Glu Tyr Arg Asn His Trp Ser Asp Val Leu Ala Gly 255 260 265	1057
ttc ctg aca ggg gcg gcc atc gcc acc ttt ttg gtc acc tgc gtt gtg Phe Leu Thr Gly Ala Ala Ile Ala Thr Phe Leu Val Thr Cys Val Val 270 275 280 285	1105
cat aac ttt cag agc cgg cca ccc tct ggc cga agg ctc tct ccc tgg His Asn Phe Gln Ser Arg Pro Pro Ser Gly Arg Arg Leu Ser Pro Trp 290 295 300	1153
gag gac ctg ggc caa gcc ccc acc atg gat agc ccc ctc gaa aag tta Glu Asp Leu Gly Gln Ala Pro Thr Met Asp Ser Pro Leu Glu Lys Leu 305 310 315	1201
agt gtg gcg cag gaa ccc gag gtc tgc agg ccg cat tcg aca ccg gca Ser Val Ala Gln Glu Pro Glu Val Cys Arg Pro His Ser Thr Pro Ala 320 325 330	1249
cgg ctc acc cca tcc aag tcg cag aac tgc gcc cgc cgt ggc cac ctg Arg Leu Thr Pro Ser Lys Ser Gln Asn Cys Ala Arg Arg Gly His Leu 335 340 345	1297
atc ccc agc tgt gtc tcc tcc agg gcc cca gcc atg tgt tcg tcg ccc Ile Pro Ser Cys Val Ser Ser Arg Ala Pro Ala Met Cys Ser Ser Pro 350 355 360 365	1345
cgt gtg ccc cgt cct cga ttg agg tct gag ccg acg ccc ttg ccc ctg	1393

Arg Val Pro Arg Pro Arg Leu Arg Ser Glu Pro Thr Pro Leu Pro Leu	
370 375 380	
ccc cta ccc ctg cca gcg ccc acc ccc agc cag ggc ccc tcg cct tcc	1441
Pro Leu Pro Leu Pro Ala Pro Thr Pro Ser Gln Gly Pro Ser Pro Ser	
385 390 395	
tcc cct gga cct ggg ggg cca ggc ggg ggt ggt gga cgt ggc cgg aag	1489
Ser Pro Gly Pro Gly Gly Pro Gly Gly Gly Gly Gly Arg Gly Arg Lys	
400 405 410	
ctg ctg ctg ccc acg ccc ctg ctg cgg gac ctg tac acc ctg agt gga	1537
Leu Leu Leu Pro Thr Pro Leu Leu Arg Asp Leu Tyr Thr Leu Ser Gly	
415 420 425	
ctc tat ccc tcc ccc ttc cac cgg gac aac ttc agc cct tac ctg ttt	1585
Leu Tyr Pro Ser Pro Phe His Arg Asp Asn Phe Ser Pro Tyr Leu Phe	
430 435 440 445	
gcc agc cgt gac cac ctg ctg tga ggcccgacca cccacccaga atctgcccag	1639
Ala Ser Arg Asp His Leu Leu *	
450	
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 <212> DNA
 <213> Homo sapiens

<220>
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cggcctcgct gagtgccag cgcggggcg cccaggcctg gggcaccgcg agtgccgaac	360
cttcggctgg acaccaag atg cct ggc gaa cag cag gca gag gaa gag gag	411
Met Pro Gly Glu Gln Gln Ala Glu Glu Glu Glu	
1 5 10	

gag gaa gag atg cag gag gag atg gtg ctg ctg gtg aag ggt gag gag	459
Glu Glu Glu Met Gln Glu Glu Met Val Leu Leu Val Lys Gly Glu Glu	
15 20 25	
gat gag ggt gag gag aag tat gag gtg gtg aaa ctc aag atc ccc atg	507
Asp Glu Gly Glu Glu Lys Tyr Glu Val Val Lys Leu Lys Ile Pro Met	
30 35 40	
gac aac aag gag gtc ccg ggc gag gcg ccc gcg ccg tcc gcc gac ccg	555
Asp Asn Lys Glu Val Pro Gly Glu Ala Pro Ala Pro Ser Ala Asp Pro	
45 50 55	
gcg cgt ccc cac gcg tgc ccc gac tgc ggc cgc gcc ttc gcg cgc cgc	603
Ala Arg Pro His Ala Cys Pro Asp Cys Gly Arg Ala Phe Ala Arg Arg	
60 65 70 75	
tcc acg ctg gcg aag cac gcg cgc acg cac acg ggc gaa cgg ccc ttc	651
Ser Thr Leu Ala Lys His Ala Arg Thr His Thr Gly Glu Arg Pro Phe	
80 85 90	
ggg tgc acc gag tgc ggg cgg cgc ttc tca cag aag tcg gcg ctg acc	699
Gly Cys Thr Glu Cys Gly Arg Arg Phe Ser Gln Lys Ser Ala Leu Thr	
95 100 105	
aaa cac ggc cgc acg cac acg ggc gag cgg ccc tac gag tgc ccc gag	747
Lys His Gly Arg Thr His Thr Gly Glu Arg Pro Tyr Glu Cys Pro Glu	
110 115 120	
tgc gac aaa cgc ttc tcg gcc gcc tcg aac ctg cgg cag cac cgg cgg	795
Cys Asp Lys Arg Phe Ser Ala Ala Ser Asn Leu Arg Gln His Arg Arg	
125 130 135	
cgg cac acg ggc gag aag ccg tac gca tgc gcg cac tgc ggc cgc cgc	843
Arg His Thr Gly Glu Lys Pro Tyr Ala Cys Ala His Cys Gly Arg Arg	
140 145 150 155	
ttc gcg cag agc tcc aac tac gca cag cac ctg cgc gtg cac acg ggc	891
Phe Ala Gln Ser Ser Asn Tyr Ala Gln His Leu Arg Val His Thr Gly	
160 165 170	
gag aag ccg tac gcg tgc ccg gac tgc gga cgc gcc ttt ggc ggc agc	939
Glu Lys Pro Tyr Ala Cys Pro Asp Cys Gly Arg Ala Phe Gly Gly Ser	
175 180 185	
tcg tgc ctg gcg cgc cac cga cgc acg cac acg ggc gag cgg ccc tac	987
Ser Cys Leu Ala Arg His Arg Arg Thr His Thr Gly Glu Arg Pro Tyr	
190 195 200	
gct tgc gcc gac tgc ggc acg cgc ttc gct cag agc tcg gcg ctg gcc	1035
Ala Cys Ala Asp Cys Gly Thr Arg Phe Ala Gln Ser Ser Ala Leu Ala	
205 210 215	
aag cac cgg cgc gtg cac acg ggc gag aag ccg cac cgc tgc gct gtg	1083
Lys His Arg Arg Val His Thr Gly Glu Lys Pro His Arg Cys Ala Val	
220 225 230 235	

tgt ggc cgt cgc ttc ggc cac cgc tcc aac ctg gcg gag cac gcg cgc Cys Gly Arg Arg Phe Gly His Arg Ser Asn Leu Ala Glu His Ala Arg 240 245 250	1131
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ttc cgc cta agc tgc cac ttc att cgc cac cga cgc gcg cac atg cgg Phe Arg Leu Ser Ser His Phe Ile Arg His Arg Arg Ala His Met Arg 270 275 280	1227
cgc cgc ctg tat att tgc gcc ggc tgc ggc agg gac ttc aag ctg ccc Arg Arg Leu Tyr Ile Cys Ala Gly Cys Gly Arg Asp Phe Lys Leu Pro 285 290 295	1275
cct ggc gcc acg gcc gcc act gcc acc gag cgt tgc ccg gag tgt gag Pro Gly Ala Thr Ala Ala Thr Ala Thr Glu Arg Cys Pro Glu Cys Glu 300 305 310 315	1323
ggc agc tga gtcccg agggctgcgg aggggcgcgc tggggcttcg acctggctgc Gly Ser *	1379
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ccaaacaaaa ccaaaaaaat ctcaaagcga ttggacctag cagctcatgc ctgtaatctc	2279
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 <213> Homo sapiens

<220>
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 <222> (97)..(525)

<400> 258

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                                     Met Asn Lys Glu Arg Ala
                                     1               5

ttc agg cat ggc gac ccg cct gag cca cct cca ggg gca aga gat gag      162
Phe Arg His Gly Asp Pro Pro Glu Pro Pro Gly Ala Arg Asp Glu
                10                15                20

cag att tac ttt aga aag gac aac agc atc agc cac tgc cac agc ccc      210
Gln Ile Tyr Phe Arg Lys Asp Asn Ser Ile Ser His Cys His Ser Pro
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ccc cag atc atc tgt act ggc tgt cag aac agt cct gct gaa acg cca      258
Pro Gln Ile Ile Cys Thr Gly Cys Gln Asn Ser Pro Ala Glu Thr Pro
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atc aca cct gtc att cac tgc tct gcc cag gac tct tca gtg ggc tcc      306
Ile Thr Pro Val Ile His Cys Ser Ala Gln Asp Ser Ser Val Gly Ser
                55                60                65                70

cca gcg cta agc att tgg cct gac act cca ggc gcc atg tgc cct ggt      354
Pro Ala Leu Ser Ile Trp Pro Asp Thr Pro Gly Ala Met Cys Pro Gly
                75                80                85

ccc cac cta cct ctc cac tgc aaa ttc tgg cca tac acc cct gca ccc      402
Pro His Leu Pro Leu His Cys Lys Phe Trp Pro Tyr Thr Pro Ala Pro
                90                95                100

cca aac agt gca ctc cca tct cag tcc aca ttc tcc cct tac aac atg      450
Pro Asn Ser Ala Leu Pro Ser Gln Ser Thr Phe Ser Pro Tyr Asn Met
                105                110                115

att cat cca aga cca tgg att cgt ggc ctt aag ttt act tct ggt ctg      498
Ile His Pro Arg Pro Trp Ile Arg Gly Leu Lys Phe Thr Ser Gly Leu
                120                125                130

gac ttc tgt gtc agc tcc aga gta tag ttgtc tcaactgaccc cttcacttgg      550
Asp Phe Cys Val Ser Ser Arg Val *
135                140

gtgccagaga acactggata ttccagaccc c      581

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Variable	Mean	SD	Min	Max
Age	34.5	10.2	21	55
Gender	Male	0.75	0	1
Marital Status	Married	0.65	0	1
Education	High School	0.35	0	1
Occupation	Unemployed	0.45	0	1
Income	\$10,000	0.25	0	1
Health	Good	0.70	0	1
Stress	Low	0.30	0	1
Depression	None	0.10	0	1
Loneliness	Low	0.20	0	1
Life Satisfaction	High	0.60	0	1
Resilience	High	0.55	0	1
Optimism	High	0.65	0	1
Gratitude	High	0.70	0	1
Forgiveness	High	0.60	0	1
Empathy	High	0.65	0	1
Compassion	High	0.60	0	1
Kindness	High	0.65	0	1
Generosity	High	0.60	0	1
Patience	High	0.65	0	1
Self-control	High	0.60	0	1
Emotional Stability	High	0.65	0	1
Psychological Well-being	High	0.60	0	1
Life Purpose	High	0.65	0	1
Meaning in Life	High	0.60	0	1
Existential Well-being	High	0.65	0	1
Transcendental Well-being	High	0.60	0	1
Humanistic Well-being	High	0.65	0	1
Existential Well-being	High	0.60	0	1
Transcendental Well-being	High	0.65	0	1
Humanistic Well-being	High	0.60	0	1
Existential Well-being	High	0.65	0	1
Transcendental Well-being	High	0.60	0	1
Humanistic Well-being	High	0.65	0	1
Existential Well-being	High	0.60	0	1
Transcendental Well-being	High	0.65	0	1
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Transcendental Well-being	High	0.65	0	1
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Humanistic Well-being	High	0.60	0	1
Existential Well-being	High	0.65	0	1
Transcendental Well-being	High	0.60	0	1
Humanistic Well-being	High	0.65	0	1
Existential Well-being	High	0.60	0	1
Transcendental Well-being	High	0.65	0	1

Variable	Mean	SD	Min	Max
Age	34.5	10.2	21	55
Gender	Male	0.75	0	1
Marital Status	Married	0.65	0	1
Education	High School	0.35	0	1
Occupation	Unemployed	0.45	0	1
Income	\$10,000	0.25	0	1
Health	Good	0.70	0	1
Stress	Low	0.30	0	1
Depression	None	0.10	0	1
Loneliness	Low	0.20	0	1
Life Satisfaction	High	0.60	0	1
Resilience	High	0.55	0	1
Optimism	High	0.65	0	1
Gratitude	High	0.70	0	1
Forgiveness	High	0.60	0	1
Empathy	High	0.65	0	1
Compassion	High	0.60	0	1
Kindness	High	0.65	0	1
Generosity	High	0.60	0	1
Patience	High	0.65	0	1
Self-control	High	0.60	0	1
Perseverance	High	0.65	0	1
Discipline	High	0.60	0	1
Responsibility	High	0.65	0	1
Integrity	High	0.60	0	1
Honesty	High	0.65	0	1
Trustworthiness	High	0.60	0	1
Reliability	High	0.65	0	1
Consistency	High	0.60	0	1
Stability	High	0.65	0	1
Balance	High	0.60	0	1
Harmony	High	0.65	0	1
Peace	High	0.60	0	1
Love	High	0.65	0	1
Kindness	High	0.60	0	1
Generosity	High	0.65	0	1
Patience	High	0.60	0	1
Self-control	High	0.65	0	1
Perseverance	High	0.60	0	1
Discipline	High	0.65	0	1
Responsibility	High	0.60	0	1
Integrity	High	0.65	0	1
Honesty	High	0.60	0	1
Trustworthiness	High	0.65	0	1
Reliability	High	0.60	0	1
Consistency	High	0.65	0	1
Stability	High	0.60	0	1
Balance	High	0.65	0	1
Harmony	High	0.60	0	1
Peace	High	0.65	0	1
Love	High	0.60	0	1

Variable	Mean	SD	Min	Max
Age	34.5	10.5	20	55
Gender	Male	Female		
Marital Status	Married	Single		
Education	High School	College		
Occupation	Manager	Worker		
Income	\$10,000	\$20,000		
Health	Good	Poor		
Stress	Low	High		
Life Satisfaction	High	Low		
Work Satisfaction	High	Low		
Family Satisfaction	High	Low		
Community Satisfaction	High	Low		
Overall Satisfaction	High	Low		

<222> (1)...(1480)

<223> n = a,t,c or g

<400> 260

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acg	ccgc	ctt	tcg	tac	gcg	gaatt	ttg	cag	at	ctt	cc	ct	gg	ac	ct	cagg	cct	ct	cc	ggc	180		
tg	gag	tag	ggg	tg	gac	gttc	ac	ata	ag	ctt	ct	tg	gt	cg	act	tac	cc	ga	at	ct	cc	gag	238
atg	gcc	gcg	ctg	cgt	cga	atg	ctc	cac	ttg	ccg	agc	ctg	atg	atg	ggg	286							
Met	Ala	Ala	Leu	Arg	Arg	Met	Leu	His	Leu	Pro	Ser	Leu	Met	Met	Gly								
1				5					10						15								
acg	tgc	cgc	ccc	ttt	gcg	ggc	tca	ctg	gct	gat	agt	tgc	ctg	gcg	gac	334							
Thr	Cys	Arg	Pro	Phe	Ala	Gly	Ser	Leu	Ala	Asp	Ser	Cys	Leu	Ala	Asp								
			20					25						30									
cgc	tgt	ctc	tgg	gat	cgg	ctg	cat	gcc	cag	cct	cgt	ttg	ggc	act	gtc	382							
Arg	Cys	Leu	Trp	Asp	Arg	Leu	His	Ala	Gln	Pro	Arg	Leu	Gly	Thr	Val								
			35				40						45										
ccc	acc	ttc	gac	tgg	ttc	ttt	gga	tac	gac	gaa	gtc	cag	ggg	ctc	cta	430							
Pro	Thr	Phe	Asp	Trp	Phe	Phe	Gly	Tyr	Asp	Glu	Val	Gln	Gly	Leu	Leu								
			50				55					60											
ctg	cca	ttg	ctg	cag	gag	gca	cag	gct	gcc	agt	cct	ctg	cga	gtg	ctg	478							
Leu	Pro	Leu	Leu	Gln	Glu	Ala	Gln	Ala	Ala	Ser	Pro	Leu	Arg	Val	Leu								
			65			70				75					80								
gat	gtg	ggc	tgt	ggg	act	tcc	agc	cta	tgt	aca	ggc	ctc	tac	acc	aaa	526							
Asp	Val	Gly	Cys	Gly	Thr	Ser	Ser	Leu	Cys	Thr	Gly	Leu	Tyr	Thr	Lys								
				85					90					95									
tct	cca	cac	cca	gtg	gat	gtg	ctg	ggg	gtg	gac	ttt	tct	cct	gtg	gct	574							
Ser	Pro	His	Pro	Val	Asp	Val	Leu	Gly	Val	Asp	Phe	Ser	Pro	Val	Ala								
			100					105					110										
gtg	gcc	cac	atg	aat	agc	ctc	ctg	gag	ggt	ggc	cca	agc	caa	aca	cct	622							
Val	Ala	His	Met	Asn	Ser	Leu	Leu	Glu	Gly	Gly	Pro	Ser	Gln	Thr	Pro								
			115				120						125										
cta	tgc	cct	gga	cac	cct	gcc	tca	agc	ctc	cac	ttc	atg	cac	gcc	gat	670							
Leu	Cys	Pro	Gly	His	Pro	Ala	Ser	Ser	Leu	His	Phe	Met	His	Ala	Asp								
			130				135						140										
gct	cag	aac	ctg	ggg	gct	gtg	gct	tct	tca	ggc	tct	ttc	caa	cta	ctg	718							
Ala	Gln	Asn	Leu	Gly	Ala	Val	Ala	Ser	Ser	Gly	Ser	Phe	Gln	Leu	Leu								
			145			150				155					160								
ctg	gac	aaa	ggc	aca	tgg	gat	gct	gtt	gcc	cgg	gga	ggt	ctg	cct	agg	766							
Leu	Asp	Lys	Gly	Thr	Trp	Asp	Ala	Val	Ala	Arg	Gly	Gly	Leu	Pro	Arg								
				165					170					175									
gct	tac	cag	ctt	cta	tca	gaa	tgc	ttg	agg	gtt	cta	aac	cct	cag	ggg	814							
Ala	Tyr	Gln	Leu	Leu	Ser	Glu	Cys	Leu	Arg	Val	Leu	Asn	Pro	Gln	Gly								

180	185	190	
acc ctg att cag ttc tca gat gag gac cct gat	gtg cga ctg ccc tgc	862	
Thr Leu Ile Gln Phe Ser Asp Glu Asp Pro Asp	Val Arg Leu Pro Cys		
195	200	205	
ctg gaa caa ggg tcc tat ggc tgg act gtg act	gtg cag gag cta ggc	910	
Leu Glu Gln Gly Ser Tyr Gly Trp Thr Val Thr	Val Gln Glu Leu Gly		
210	215	220	
ccg ttc agg ggc atc acc tac ttt gct tac ttg	att caa ggc tct cat	958	
Pro Phe Arg Gly Ile Thr Tyr Phe Ala Tyr Leu	Ile Gln Gly Ser His		
225	230	235	
taa agac attttagtag tcctgaccct agtatttctg	tgggcaagga gagggctgaa	1015	
★			
gaactgtctt tgcaagctat ctggctgcaa agtgagaatt	tgagtcctgg cttccacatt	1075	
tactagctgg gtgccatatt gctgaatggt tctgttcccc	agtttactca tctgcagagt	1135	
gagaataact tggagttacg gagattacat acaatgatgt	gcgcaatatt tagcacaaaa	1195	
tgaatgctga aaagagaagg tacaattggg tcattcccc	gtttcaacta actggagctc	1255	
ctaaaagcag cagacaggaa ctgaatcaaa acccctgcgc	tgactgactt gtataatcta	1315	
gtggcctaac ctgtaagcct cattnttgtc acctgtaaaa	ggagattgta agaggatggg	1375	
tataacgagc ttcataaacc tcgatgagat atttgagggg	gaggggaacaa tacttaccct	1435	
caaagctatt aggaggccgg agatgggaat atttccacaa	gcccg	1480	
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<213> Homo sapiens			
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<221> CDS			
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ttgaagatcg tgacgtcttg taactagcag tgtgtgcaca	gaatcctact caaggaacgt	180	
cttggccccag cgatgcaaag aactgaagtt tcaagctgga	agagcctgta ttgtcctcac	240	
aatagtatag aagaattcaa gagaggagag agagacagca	ccgaatgaag actgtaaaag	300	


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agtaagaaat gggagtgtga ggagtgttca cctgctgcag ccacagacta catacctgaa 1097
aactcagggg acatcccttg ctgcagcagc accttccacc ctgaggaaca tttctgcaga 1157
gacaacacct tggaagagaa tccgggcctt tcttggactg attggccaga accttcctta 1217
ttagaaaagc cagagtcctc tcgtggcagg aggagctact cctggaggtc caaggggtgc 1277
agaatcacta acagctgcaa aaaatccaag taacaccttc tgagtagctg ctgtcccaca 1337
caatagggta tgaagctgcg ctccctccatc gggtttgggg agggagcact ctgggactgt 1397
gagacaagga agcagggcca gcagtgcagc tatgagccaa gcaaagagaa gtctcagtgg 1457
agcatgagga gggagcagtc cagatgccaa caaggaaatg cgtttatggc tacaagagtg 1517
cctctgcttt ctctctctct cctcccacca aggattcttc caccttaatc ttgttttcat 1577
atgcctcttc ttacttcacc catgtttgtt gttatgcaaa taaaggtttt ctctccaaaa 1637
aaaaaaaaa 1645

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<210> 262
<211> 694
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (166)..(672)

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<400> 262
gcggtggaat tcgtcaaaca aaatccctta ccctcttcat tccctggtaa aaagatcaca 60
atcagattag ctgctcctgt gtgttcttct aagactctgc aggctgaggt ccctttgtca 120
gactgtgtcc aaaaagcaag taaaccact tcaagcacac aaatc atg gtg aag 174
Met Val Lys
1
acc aac atg tat cat aat gaa aag gtg aac ttt cat gtt gaa tgt aaa 222
Thr Asn Met Tyr His Asn Glu Lys Val Asn Phe His Val Glu Cys Lys
5 10 15
gac tat gta aaa aag gca aag gta aag atc aac cca gtg caa cag agc 270
Asp Tyr Val Lys Lys Ala Lys Val Lys Ile Asn Pro Val Gln Gln Ser
20 25 30 35
cgg ccc ttg ttg agc cag att cac aca gat gca gca aag gag aac acc 318
Arg Pro Leu Leu Ser Gln Ile His Thr Asp Ala Ala Lys Glu Asn Thr
40 45 50
tgc tac tgt ggt gca gtg gca aag aga caa gag aaa aaa ggg atg gag 366

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Cys Tyr Cys Gly Ala Val Ala Lys Arg Gln Glu Lys Lys Gly Met Glu	
55 60 65	
cct ctt caa ggt cat gcc act ccc gct ttg cct ttt aaa gaa acc cag	414
Pro Leu Gln Gly His Ala Thr Pro Ala Leu Pro Phe Lys Glu Thr Gln	
70 75 80	
gaa cta tta cta agt ccc ctg ccc cag gaa ggt cct ggg tca ctt gca	462
Glu Leu Leu Leu Ser Pro Leu Pro Gln Glu Gly Pro Gly Ser Leu Ala	
85 90 95	
gca gga gag agc agc agt ctt tct gcc agt aca tca gtc tca gat tca	510
Ala Gly Glu Ser Ser Ser Leu Ser Ala Ser Thr Ser Val Ser Asp Ser	
100 105 110 115	
tcc cag aaa aaa gaa gag cac aat tat tct ctt ttt gtc tcc gac aac	558
Ser Gln Lys Lys Glu Glu His Asn Tyr Ser Leu Phe Val Ser Asp Asn	
120 125 130	
ttg ggt gaa cag cca act aaa tgc agt cct gaa gaa gat gag gag gac	606
Leu Gly Glu Gln Pro Thr Lys Cys Ser Pro Glu Glu Asp Glu Glu Asp	
135 140 145	
gag gag gat gtt gat gat gag gac cat gat gaa gga ttc ggc agt gag	654
Glu Glu Asp Val Asp Asp Glu Asp His Asp Glu Gly Phe Gly Ser Glu	
150 155 160	
cat tac atc att ata taa tgggtacttcc tcaagttgct gg	694
His Tyr Ile Ile Ile *	
165	

<210> 263
 <211> 1540
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1033)..(1188)

<400> 263	
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tccagatctc cactcttatg cgccagctgc agcagggttaa ggacagccag caggatgagc	120
tggatgacct cggtgagatg cgcagaaagg tcctggaatc cttgtctgac aagattcaga	180
agaagaagaa aaaaattctg agttctgtgg tggcggaaac ccagcgtccc tatgaagagg	240
ctctctaca gaagatgtgg gaaagccagg acttcctgaa atgcatgcaa aggttcagag	300
aagtgcgtgg gcaaggaagg tgggtggtccc tgtagggaag cagtggatgg gcagtcccca	360

cggcctgtgg	gaatgagtc	ggcttctcct	gatctggcgc	tcaggaggtc	tctgattctg	420
gtgttggcct	ccctccttgc	cgggtgccatt	actgtcactt	gtctttcatc	tgggaaggcg	480
attggcactg	acctaggcct	tgcctcatta	gccagcaatg	ctggctaata	accattttac	540
aaccatcacc	aaacatcacc	tattcagcca	ttaaccaccg	tgcattcttta	ccccttgatt	600
cttgttactg	cccaccaccc	attatcagtg	ttaatgaact	tcaccatcac	tgccttcttg	660
aattaatttt	cattatcttg	cctcttcact	ggtttttaaat	gtgcatgccc	ttcactatct	720
ctgccagcct	ccattcattc	ccacgattga	gcattccccg	ccactttgta	acctgtctcc	780
attctccatg	atccctcacc	tgtttcagca	ccactgaata	ttgtcactaa	cttggaagcc	840
agccgcaccc	tgcattggga	agtcacctct	ctggagtcca	gcaagtccca	gtgacagaac	900
ccataccatt	tccccagata	gctttgctcc	tcgttcattt	tggcctttct	ccctttgggt	960
ggggggccatt	tgcctctccc	ttctccctcg	ctgtgccttt	cctctcagtt	tattgaccag	1020
tttgaggaga	ac	atg cct gta tta	agg gcc gag gtg	gaa gag ctc caa		1068
		Met Pro Val Leu	Arg Ala Glu Val	Glu Glu Leu Gln		
		1	5	10		
gcc cag acc	cgg gaa ccc	cga gag gtc	ata ttt gag	gat gtt ctg	ctt	1116
Ala Gln Thr	Arg Glu Pro	Arg Glu Val	Ile Phe Glu	Asp Val Leu	Leu	
	15	20	25			
cgg aga ccc	aag tgc acc	cca gac atg	gat gtc atc	ctc aac att	cct	1164
Arg Arg Pro	Lys Cys Thr	Pro Asp Met	Asp Val Ile	Leu Asn Ile	Pro	
	30	35	40			
gtg gaa gag	cca cta ccc	ttc tag atg	gcagtg	catgggccc	gcccctcc	1218
Val Glu Glu	Pro Leu Pro	Phe *				
	45	50				
tgcctctctc	ccagcacctg	gagccttgga	tcatttactt	ccaggaccgg	atctccattc	1278
agaccctgat	ctacagtctc	cctgctccct	ctgcccttcc	tccctctttc	tttccctccc	1338
tccctccctc	ccttcttccc	cccttccctt	ccctcctcct	tccttccctc	tctccctccc	1398
tccctccctt	ccttcttccc	gtgggttttt	cctctcttct	tcccttcttt	ctgggttggtg	1458
ctgctggggc	aggtgggaat	ttctgattaa	atctgctatt	cctttttttac	caataaagct	1518
ggattttacat	ttaaaaaaaaa	aa				1540

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<210> 264
<211> 583
<212> DNA
<213> Homo sapiens
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<220>
 <221> CDS
 <222> (216)..(464)

<400> 264
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 aggtttaaca agtcatttcc ataacataaa agtacaaaagt gaagtagcaa ttgctgatgt 120
 ggaatctgca gcaagcattt ccagaatatc tagataaatg gcagaggttag ctctactaga 180
 gttttaacag agacaaaaca gccttacttc aggag atg cca ttt agg act ttc 233
 Met Pro Phe Arg Thr Phe
 1 5
 aca gct cta ggt aag cta ata tct gac ttc aaa gat tca aag gac ggg 281
 Thr Ala Leu Gly Lys Leu Ile Ser Asp Phe Lys Asp Ser Lys Asp Gly
 10 15 20
 ctg act ctt tac ttt gta gag aca gcg tca cgc tct gtt gtg ctg gct 329
 Leu Thr Leu Tyr Phe Val Glu Thr Ala Ser Arg Ser Val Leu Ala
 25 30 35
 ggt ctt gaa ctc ttg acc tca agt gat cct cca acc tca gcc tcc caa 377
 Gly Leu Glu Leu Leu Thr Ser Ser Asp Pro Pro Thr Ser Ala Ser Gln
 40 45 50
 agc act gga att aca ggt gta agc cac ttt tcc cag cct ggg ctg gct 425
 Ser Thr Gly Ile Thr Gly Val Ser His Phe Ser Gln Pro Gly Leu Ala
 55 60 65 70
 ttc ttg tta gag gtc aat gca gtt ggt gac ttt aaa tga atgctaatat 474
 Phe Leu Leu Glu Val Asn Ala Val Gly Asp Phe Lys *
 75 80
 tcaattacca ttccaaaaat ccaagagcca gttaagaatt atgctacatc ctctgtgccga 534
 attcattgcc tcgagggcca aattccctat agtgatcgta ttaaattca 583

<210> 265
 <211> 2077
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (154)..(834)

<400> 265
 cggcagcagg acagcataga ggaagtcaag gaagatagaa acaggcatcc tccagcaaac 60
 ctgcccactc cagccagtag ccggattctt agaaaatatt ccaatattcg aggaaagctc 120

agagcccagc aacgtttaat caagaatgag aaa atg gaa tgc cca gat gct ctg	174
Met Glu Cys Pro Asp Ala Leu	
1 5	
gct gtg gaa agt aag cca agt cgt aag agc gta tgc atc aac cct ctg	222
Ala Val Glu Ser Lys Pro Ser Arg Lys Ser Val Cys Ile Asn Pro Leu	
10 15 20	
atg tcc ccc aag ctt gcc ctg caa gtg gat gca gat ggg ttt cct gtt	270
Met Ser Pro Lys Leu Ala Leu Gln Val Asp Ala Asp Gly Phe Pro Val	
25 30 35	
aag ccc aag agt act gaa gga atg aag gga agg aag ggg aag cag gtg	318
Lys Pro Lys Ser Thr Glu Gly Met Lys Gly Arg Lys Gly Lys Gln Val	
40 45 50 55	
tct gaa atc ttg cct aaa gca gaa gtt cag agt aaa cgc aag aga aca	366
Ser Glu Ile Leu Pro Lys Ala Glu Val Gln Ser Lys Arg Lys Arg Thr	
60 65 70	
gaa ggc agc agc cct cca gat agt aag aac aag ggg cct acg gtg aaa	414
Glu Gly Ser Ser Pro Pro Asp Ser Lys Asn Lys Gly Pro Thr Val Lys	
75 80 85	
gcc agc aaa gaa aag cat gct gat gga gcc acc aaa acc cct gct gcc	462
Ala Ser Lys Glu Lys His Ala Asp Gly Ala Thr Lys Thr Pro Ala Ala	
90 95 100	
aag agg cca gct gca agg gac aga agc agc caa ccc ccc aaa aag acg	510
Lys Arg Pro Ala Ala Arg Asp Arg Ser Ser Gln Pro Pro Lys Lys Thr	
105 110 115	
tct ttg aaa gag aat aaa gtg aag atc cct aaa aag tcc gct ggg aag	558
Ser Leu Lys Glu Asn Lys Val Lys Ile Pro Lys Lys Ser Ala Gly Lys	
120 125 130 135	
agc tgc cct ccc tcc agg aaa gaa aaa gag aat aca aac aaa agg cct	606
Ser Cys Pro Pro Ser Arg Lys Glu Lys Glu Asn Thr Asn Lys Arg Pro	
140 145 150	
tcc cag tct att gcc tcg gaa aca ctg acg aaa cct gca aaa cag aag	654
Ser Gln Ser Ile Ala Ser Glu Thr Leu Thr Lys Pro Ala Lys Gln Lys	
155 160 165	
ggg gcc ggt gaa tcc tct tca agg cct cag aaa gcc acg aat agg aag	702
Gly Ala Gly Glu Ser Ser Ser Arg Pro Gln Lys Ala Thr Asn Arg Lys	
170 175 180	
cag agt agt gga aag act cgg gcc aga ccc tca acg aaa acc cca gag	750
Gln Ser Ser Gly Lys Thr Arg Ala Arg Pro Ser Thr Lys Thr Pro Glu	
185 190 195	
agc agt gca gct cag aga aag cga aag ctg aag gca aag ctg gac tgt	798
Ser Ser Ala Ala Gln Arg Lys Arg Lys Leu Lys Ala Lys Leu Asp Cys	
200 205 210 215	
tcg cac ggc aaa cgg agg cgg ctg gat gca aag tga ttgg aaagatggta	848

Ser His Gly Lys Arg Arg Arg Leu Asp Ala Lys *

220

225

gccaagagta aaactgttct atagaagtaa ccttttatct tgcattaact aaatctgctt 908
 ttataagctt atcaagcctt tcaaatttac agttaatgga gaacaccgta atttgagatg 968
 tcagaaaatg catctcagat ggagaaggga acttgcagag tccttctctg aggctaaggg 1028
 aagttatata ttatattctg gttgttcctt ggggttttaa cttggaacca agcagttttc 1088
 gtttttaaaa gtacagtgcc ttatttatcc tttttgtttt taaatttaca aaagctaaaa 1148
 agctgatcta tgtgattaaa ggcttgattt ttataactga tgcacaagca cttgtactgt 1208
 agccgagaag accaccatca tgcacataaa aggagctttt cagcagccac cctgcagcat 1268
 ctgcccacga acagatgccc ttctttgcaa accccagcag tgaacttccc tctctgtctt 1328
 gtttggttgt ttagatgatg tttgaaagct aaaccaaata attttatggg atgcagagga 1388
 ttataatta taaaagatta ctatttctgt taccctctt taaaaaagat catgttcatt 1448
 gttggctcct cctctcacct ttgatgtttt gtcatttgag agcatgtatt ctaaattatg 1508
 tgcccatggg acaagagata tgcacaagt gtttaattttt gtttacaac tctaaaaaat 1568
 catttgcac cccaaactgt attactaatt ctaccatct tcttcatttc tggctctgct 1628
 agcactcctg caaggcttcc atcctacttc gggaggaaaa agcctaggat tttttttttc 1688
 catcttgtag ctgtaatttg atgattagga tgaaaatgac tcttattttc tttcttacct 1748
 agagtacttc catattcaaa gaaagccgaa ctattatttc cagtaataga aaggtttaag 1808
 aatatgtatg tccatgtgtg tttgggtgca tttgcatgtg gttatcagcc acaaattgtct 1868
 cccaatccca attttacagt aaaatttttt ccctatgcag tgtgcttggg tgtccctgag 1928
 ttgagtaatt agcaaaggac agatggttta aaagtagccc agtgtctctg tgagcatccc 1988
 caataccact ttggtaccag actcagaaag atctaaaaca gcatggagtt atgtaaaggt 2048
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<210> 266
 <211> 1175
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (116)..(685)


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cctaacagga gtcactggct caggaccca gggagaaacg ctctccccac ccacgccatg      935
ctgaccagag gtcttgacgc cctgtggat gccccgcgcg aggtcccccg atccccgcac      995
ccggactgct gtcacctgcc cctcccttgc gggcccccca ggaagccagg tgacccagg      1055
tgggaggctg tgtgtggagg ccactctgga aggaagttaa gacctgcca ggtgtggagc      1115
gaggggcaca ggggcatcct aacctcagaa actgaaataa agcctttgaa aaaaaaaaaa      1175

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<210> 267
<211> 1094
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (116)..(604)

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cgcaggcagg actctgggac agacgcaggc cagctgcca gagcccagac caagc atg      118
                                         Met
                                         1

gac gcc gtg gat gcc acc atg gag aaa ctc cgg gca cag tgc ctg tcc      166
Asp Ala Val Asp Ala Thr Met Glu Lys Leu Arg Ala Gln Cys Leu Ser
          5                      10                      15

cgc ggg gcc tcg ggc atc cag ggc ctg gcc agg ttt ttc cgc caa cta      214
Arg Gly Ala Ser Gly Ile Gln Gly Leu Ala Arg Phe Phe Arg Gln Leu
          20                      25                      30

gac cgg gac ggg agc aga tcc ctg gac gct gat gag ttc cgg cag ggt      262
Asp Arg Asp Gly Ser Arg Ser Leu Asp Ala Asp Glu Phe Arg Gln Gly
          35                      40                      45

ctg gcc aaa ctc ggg ctg gtg ctg gac cag gcg gag gca gag ggt gtg      310
Leu Ala Lys Leu Gly Leu Val Leu Asp Gln Ala Glu Ala Glu Gly Val
          50                      55                      60                      65

tgc agg aag tgg gac cgc aat ggc agc ggg acg ctg gat ctg gag gag      358
Cys Arg Lys Trp Asp Arg Asn Gly Ser Gly Thr Leu Asp Leu Glu Glu
          70                      75                      80

ttc ctt cgg gcg ctg cgg ccc ccc atg tcc cag gcc cgg gag gct gtc      406
Phe Leu Arg Ala Leu Arg Pro Pro Met Ser Gln Ala Arg Glu Ala Val
          85                      90                      95

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CCDS: CDS: 1-387

atc gca gct gca ttt gcc aag ctg gac cgc agt ggg gac ggc gtc gtg Ile Ala Ala Ala Phe Ala Lys Leu Asp Arg Ser Gly Asp Gly Val Val 100 105 110	454
acg gtg gac gac ctc cgc ggg gtg tac agt ggc cgt gcc cac ccc aag Thr Val Asp Asp Leu Arg Gly Val Tyr Ser Gly Arg Ala His Pro Lys 115 120 125	502
gtc aca ctg gcg gaa ttc cag gac tac tac agc ggc gtg agt gcc tcc Val Thr Leu Ala Glu Phe Gln Asp Tyr Tyr Ser Gly Val Ser Ala Ser 130 135 140 145	550
atg aac acg gat gag gag ttc gtg gcc atg atg acc agt gcc tgg cag Met Asn Thr Asp Glu Glu Phe Val Ala Met Met Thr Ser Ala Trp Gln 150 155 160	598
ctg tga gcagctccgg ctcagccctg ctgccctggc ctgtcactcc ccacccctgc Leu *	654
cggagacctc ccttccttgg gccccttctc tcctgggcag ccacaccaca gagcgggggag	714
gggcaggttg gggaatggag gctgcaggac tggctagacc aggtccctgc cgggtccacca	774
ggcggaggtg ggacaaaggt cctaacagga gtcactggct caggacccca gggagaaacg	834
ctctccccac ccacgccatg ctgaccagag gtcttgacgc ccctgtggat gccccgcgcg	894
aggtcccccg atccccgcac ccggactgct gctccctgcc cctcccttgc ggggtcccca	954
ggaagccagg tgaccccagg tgggaggctg tgtgtggagg ccatcctgga aggaagttta	1014
gacctgcca ggtgtggagc gaggggcaca ggggcatcct aacctcagaa actgaaataa	1074
agcctttgaa aaaaaaaaaa	1094

<210> 268
<211> 485
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (169)..(387)

<400> 268 ccctcttcat agaggagccg gaagcatcgg gagccgcggt acccgcccat cttccggcca ggatgtgttg tcctggtgag cgattgtcct gtggcgccg ggaccgagtt tgtggcccag ggttatgtgt gcacttcaca cctctgactt ttttcagggt tcctattg atg gtt agg Met Val Arg 1	60 120 177
--	------------------

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agc agg att tcg ggg atg aag gcg gca gca gca aga gga ggc tgc gac 225
Ser Arg Ile Ser Gly Met Lys Ala Ala Ala Ala Arg Gly Gly Cys Asp
      5              10              15

tgc gga ccc cag att cgt ccc cct cca cca cac aca acg cca aga cgg 273
Cys Gly Pro Gln Ile Arg Pro Pro Pro Pro His Thr Thr Pro Arg Arg
      20              25              30              35

gcc cca gga ggg cgt gaa gag aag act tcc ttt cct ctc ctc tcg cct 321
Ala Pro Gly Gly Arg Glu Glu Lys Thr Ser Phe Pro Leu Leu Ser Pro
              40              45              50

cct ggc gct ggc cgt atg aag gtg tct ccc aga agc att agc aga gga 369
Pro Gly Ala Gly Arg Met Lys Val Ser Pro Arg Ser Ile Ser Arg Gly
              55              60              65

gcc ctg tgg gag aaa tga ggagtg acccaaaaga aacttgctca aggacagcct 423
Ala Leu Trp Glu Lys *
              70

ccttaaagca gacttccata taccccaacc tgcaaaagaa gactttacgt gaaatgttac 483

ag 485

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<210> 269
 <211> 1170
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (168)..(611)

 <220>
 <221> misc_feature
 <222> (1)...(1170)
 <223> n = a,t,c or g

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attcagccgc ctttttatgt caccgggccc cacatggacc cagccggccc gagcgcgccc 60

cgccgctgac cgcccgcgcc ccgggaagga agaacactcg ctcccggcca tacttgcggtg 120

tgagttctga cccctggagg agccactgtg gaagcagagc aatcgcc  atg gag ttt 176
                               Met Glu Phe
                               1

gtg atg aag cag gct cta gga ggg gcc acc aag gac atg ggg aag atg 224
Val Met Lys Gln Ala Leu Gly Gly Ala Thr Lys Asp Met Gly Lys Met
      5              10              15

ctg ggg ggt gac gag gag aag gac cca gac gcc gcc aag aag gag gag 272
Leu Gly Gly Asp Glu Glu Lys Asp Pro Asp Ala Ala Lys Lys Glu Glu
      20              25              30              35

```

gag cgg cag gag gcg ctg cgc cag gcg gag gag gag cgc aag gcc aag	320
Glu Arg Gln Glu Ala Leu Arg Gln Ala Glu Glu Glu Arg Lys Ala Lys	
40 45 50	
tac gcc aag atg gag gcg gag cgc gag gcc gtg cgc cag ggc atc cga	368
Tyr Ala Lys Met Glu Ala Glu Arg Glu Ala Val Arg Gln Gly Ile Arg	
55 60 65	
gac aag tac ggc atc aag aag aag gag gag cgc gag gcc gag gcc cag	416
Asp Lys Tyr Gly Ile Lys Lys Lys Glu Glu Arg Glu Ala Glu Ala Gln	
70 75 80	
gcc gcc atg gag gcc aac tcc gag ggg agc ttg acg cgg ccc aag aag	464
Ala Ala Met Glu Ala Asn Ser Glu Gly Ser Leu Thr Arg Pro Lys Lys	
85 90 95	
gcc atc ccg ccg ggc tgc ggg gac gag gtg gag gag gag gac gag agc	512
Ala Ile Pro Pro Gly Cys Gly Asp Glu Val Glu Glu Glu Asp Glu Ser	
100 105 110 115	
atc ctg gac acc gtc atc aag tac ctg ccc ggg ccg ctg cat gac atg	560
Ile Leu Asp Thr Val Ile Lys Tyr Leu Pro Gly Pro Leu His Asp Met	
120 125 130	
ctc aag atg tat ccc cgc gcg gga cag ctg ccc cgc gga gcc ggc cat	608
Leu Lys Met Tyr Pro Arg Ala Gly Gln Leu Pro Arg Gly Ala Gly His	
135 140 145	
tga acac tgcaccctcc acaggagccg cagaggccct gaggcaccgg actgcttgga	665
*	
gaccctgcgc ccctgccag cacctcctcc gtgggcagct cctcggtgtg gggcctgcgg	725
ggttccctgc ggcgagccg ggcgcggtgtg tggcctaadc cacctggtgg ccctgcgggg	785
cggcatccga gccctgttt ctctccatt catgtttatt ttgcatcaca atttggtgaa	845
tctcaggtag atgaggtctt tgcatttagt gagttttatc ttgacagggc gcgctcgccc	905
ccggtccctt tcgtccacat caaaaatgca tcacgtctcc acgtgtttcg ggccagggcg	965
gggcttgga ttgaccttca tgaccttaca tagctttaga gaagccataa cgcttgactg	1025
caatactaac gaccgacgcc cctccggaca gagaccaccg cgccctctg cgcccatcg	1085
acgctgtccg cggngacgtc gctgaccgcc ctgctcgccc tgagccctct cactgacttc	1145
tcccgggtcg tgtcttatta aaact	1170

<210> 270
 <211> 1116
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (497)..(766)

<400> 270

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gatgacctct ttcttccttc cgttttgcca gtgtcactct gtgatgatag gtgtaagttg      60
actgtgtgca ttgcccgctct gtgaccgttt tcgactcaca gaaatggcag tctgaagtgg      120
ctcggcctct tgcttgagag acagattgga gcagagtctt tgtggatgca aagccacctg      180
ggccactgcc gtgtgtgcca cctgaactt caagctgccc tgaaccgcgt gcgttttctca      240
gtgtcacgta cagctcggcc tgaccgtttg ccttttagtg ttctcttctt tctcgggtgtc      300
ctcctcctct tcctcactaa cattcatcca gagcctttca gtgcagaaat caggtagctg      360
ctgaactcgg cagctgcgtc ctttttccca tcattctctt tgtcctttgc tagctgtcat      420
ttcttccttc ttggcttcaa ctgcacatcc ctgggtttgt cctaataagg aatttttccc      480
acttgagtag acaagc      atg aga ata tca tta ttt tta tat gtt ata tgt      529
                        Met Arg Ile Ser Leu Phe Leu Tyr Val Ile Cys
                        1          5          10

tat att ttt agc aga gaa aaa agt gga aaa tgt gtg caa act tgc aga      577
Tyr Ile Phe Ser Arg Glu Lys Ser Gly Lys Cys Val Gln Thr Cys Arg
                        15          20          25

agg ccc ccc gga gga ggg tcg tcc ctg tgc cca tgc tgt cag gaa ggc      625
Arg Pro Pro Gly Gly Gly Ser Ser Leu Cys Pro Cys Cys Gln Glu Gly
                        30          35          40

ccc gga gga ggg tcg tcc ctg tgc cca tgc tgt cag gaa ggc ccc gga      673
Pro Gly Gly Gly Ser Ser Leu Cys Pro Cys Cys Gln Glu Gly Pro Gly
                        45          50          55

gga ggg tcg tcc ctg tgc cca tgc ggt cag aaa ggc ccc gga gga ggg      721
Gly Gly Ser Ser Leu Cys Pro Cys Gly Gln Lys Gly Pro Gly Gly Gly
                        60          65          70          75

tca tct ctg tgc cca tgc ggt cag gtt ggg gct gag gca ctt tga tca      769
Ser Ser Leu Cys Pro Cys Gly Gln Val Gly Ala Glu Ala Leu *
                        80          85          90

ttgctcctcc tcagagtgtt cttttcctgc cctctcagat tataataacg aggtagttac      829
agagtgagct ccagcctaga tcgtctgggt ttgaatccag ctccatgact gtggccgtgt      889
tgctaattct ctctgagtct cagcttctt ttctgtaaag tgggtataat agtagagtct      949
aactgtggg gctgtggtgg gattcattgt gttcacacgt gtgcagggct gagaacaggg      1009
cccaaacag ggtaggcaca atgaagcatg agtcagaata ataatacaga tgacagtttc      1069
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tctatcacta atttgaacat tgcagacagt gcaaagaaga aaattag

1116

<210> 271
 <211> 2569
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (15)..(596)

<400> 271

cgcgccccca ttga atg gat gct gtg gta ccg gac cgg aat tcc cgg gtc 50
 Met Asp Ala Val Val Pro Asp Arg Asn Ser Arg Val
 1 5 10

gac cca cgc gtc cgg ttt ccc agc gcg gtg ccc gcc cct cat cct cct 98
 Asp Pro Arg Val Arg Phe Pro Ser Ala Val Pro Ala Pro His Pro Pro
 15 20 25

cca gtc tcc ctc ccc tcg ccg act gcc gcc cca ggc tcc gcc atg ggg 146
 Pro Val Ser Leu Pro Ser Pro Thr Ala Ala Pro Gly Ser Ala Met Gly
 30 35 40

aat gtg cca tcc gcg gtg aag cac tgc ctc agc tac cag cag ctt ctc 194
 Asn Val Pro Ser Ala Val Lys His Cys Leu Ser Tyr Gln Gln Leu Leu
 45 50 55 60

cgg gag cat ctc tgg atc ggg gat tca gtg gca ggg gcg ctc gac ccc 242
 Arg Glu His Leu Trp Ile Gly Asp Ser Val Ala Gly Ala Leu Asp Pro
 65 70 75

gcg cag gaa aca tcc cag tta tct gga ctc cct gag ttt gtt aaa ata 290
 Ala Gln Glu Thr Ser Gln Leu Ser Gly Leu Pro Glu Phe Val Lys Ile
 80 85 90

gta gaa gtt ggg cct agg gat gga ttg cag aat gaa aag gtt ata gtt 338
 Val Glu Val Gly Pro Arg Asp Gly Leu Gln Asn Glu Lys Val Ile Val
 95 100 105

cct aca gat ata aaa att gaa ttt atc aat cga ctt tcc caa act ggc 386
 Pro Thr Asp Ile Lys Ile Glu Phe Ile Asn Arg Leu Ser Gln Thr Gly
 110 115 120

ttg tct gta ata gaa gtg act agc ttt gtg tct tcc aga tgg gta cca 434
 Leu Ser Val Ile Glu Val Thr Ser Phe Val Ser Ser Arg Trp Val Pro
 125 130 135 140

cag gtt gct gct gga gct act gag ata tca gtt ttt gga gct gca tct 482
 Gln Val Ala Ala Gly Ala Thr Glu Ile Ser Val Phe Gly Ala Ala Ser
 145 150 155

gaa tcc ttt agc aag aag aat att aac tgt tcc att gaa gaa agt atg 530
 Glu Ser Phe Ser Lys Lys Asn Ile Asn Cys Ser Ile Glu Glu Ser Met

160	165	170	
gga aaa ttt gag gag gtt gtt aag tct gca aga cac atg aat att cca			578
Gly Lys Phe Glu Glu Val Val Lys Ser Ala Arg His Met Asn Ile Pro			
175	180	185	
gca cga ggg tac tta tga aatccc acaaattctg ttttggttaat gtttattggt			632
Ala Arg Gly Tyr Leu *			
190			
aaagcttact caaaaattat ctagagattc ttatatcatt tataaaaata tacatagaat			692
atcatatttc tattttgttt aatcagggtg atcactatat agttacatct cattaacatc			752
actgctgatt attagtgagt atctagcttg tggaatgtgt catgcaattg aaatcagagg			812
tactagcatg caaatctggc attattaact attttattaa cactctagca cccaaatgca			872
gccctcttat ctcagcctac atgtgctgat aagttggtat aaactcaca cagcttttgg			932
aaaagaatca cctaattgtgg ttttcaaatt ttttttaaaa catgactttt tcttcaaaga			992
gtattttatg tagaacttca atagaataca gcagatataa aattgagctg ctctgggaaa			1052
tcattttatc cattctttct cccctcaat ggctgacttt tctacttct ctgggtgatc			1112
ccaaagcacc tccatagtat cttgcagaac actgtttaaa aatacttgat aaattgctta			1172
tagaagataa atataaactt tcagttctct actattttct attatatgtg atttctataa			1232
atthagagat atcagagata tcaatccctt tctcctcgcc ttgccttttt cttgtggaaa			1292
cttatcagct gttcattcta agagatgttg attacaggac atggaaaata aaaactgacc			1352
caagatccac aaacctaat ttctctctca ggagtttaga aatgggtatac caaacatggt			1412
tacttgtatt gaaagattat gtgattttgt cactgagttc actattttgg ggttcttagg			1472
atggagccac atgcaaacca gtgacaggac agagtagtag aaagcagaaa tggaaaaagg			1532
aggctcctag cggatgatgag aggtatgggg gagggaggag agggaaaaat ctgccttggt			1592
gcttgtctgc ttccaggacc aatagttgcc tcaagtatta taaccaggcc tatgtgctgt			1652
gaaacctata atgcattttt gtgtgtgttt gtttcttaag gaagaatttg tttctaagac			1712
attagctact ttttctatta attttataaa tatggagata tgatgaacac acatcttaac			1772
aagttaaagt gcatagcgat tggtaataga aggttgaaag ctgggggatgg atttgggtgc			1832
aggctgtact tcccttagtt gaggtgagca aagttcatgg tagcgggaaa gattcaacag			1892
ttaatgagaa agataagtga gtcaattgtg actgaaaata ttagtgaaat gattggaatt			1952
tcaatcaagg tgttttgggg gaacaattag agttagacta tacctagtaa aatattttgt			2012
tagtttgttt tctatttata tttttctgt cctccatagt aagtctacat gagtttctaa			2072

aatttgaaat tacttttgta attaagatag atgcatatca tgtaaggact atatgagaaa 2132
aatttaaaat ccaaggcaat gtacttccaa agacataaaa taaaggatat ttatttttca 2192
ggcaaaagtt acaaaaccac aatcaaaaag gagagatata ctattggttt ctcaattcga 2252
atataaataa gttgtctcaa ttttctttaa aataaagaga aagatgaaga ccctatttcta 2312
cttcaatatg tgtttaaagt gtggagtata agctttaaag taattctcat tgggaagtta 2372
aaaagtatgt gactataaga agtaaattgc ttatgtagct tgctcttcaa ataggaaggg 2432
tttttttagt gttgaaagat ggatgcaaata ataagttgta ggaagtaacc ttttattatc 2492
ttagctttct gttgtaaaat ggaatagtta atgtaactgg gctaataaaa atcttaaac 2552
ctcttaaaaa aaaaaaa 2569

<210> 272
<211> 1204
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (64)..(630)

<400> 272
tttcgtaaat agttgctccg tgggctttcc gcatttcacc ctgctccagg cagcgtggtc 60
tgt atg gct ccg ccc tgg gca gga gga gaa aga aga ggg cca ggc acc 108
Met Ala Pro Pro Trp Ala Gly Gly Glu Arg Arg Gly Pro Gly Thr
1 5 10 15
acg tgc ctg cac tct ccc tgg atg ctg gag gct gct ccg ccg tgg gca 156
Thr Cys Leu His Ser Pro Trp Met Leu Glu Ala Ala Pro Pro Trp Ala
20 25 30
gga gga gaa gga aga gaa ctg ggt gcc gcc tgc ctg cac tct ctc cgg 204
Gly Gly Glu Gly Arg Glu Leu Gly Ala Ala Cys Leu His Ser Leu Arg
35 40 45
atg ctg gag gct gga ggc agt gag gca gca aca gcg cga ggg cga ggc 252
Met Leu Glu Ala Gly Gly Ser Glu Ala Ala Thr Ala Arg Gly Arg Gly
50 55 60
gac ttt gga gct gcc tca tgc agc gac ctc gcc ttc cgc tgc gcc tcc 300
Asp Phe Gly Ala Ala Ser Cys Ser Asp Leu Ala Phe Arg Cys Ala Ser
65 70 75
tcc cag aac cca aga agc ctg gaa cct gtg gcg tcc agc cct gaa agg 348
Ser Gln Asn Pro Arg Ser Leu Glu Pro Val Ala Ser Ser Pro Glu Arg
80 85 90 95

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agg aga cgg caa ccc agc cgc gct ttt gcc tgc act ctc cct gga tgc      396
Arg Arg Arg Gln Pro Ser Arg Ala Phe Ala Cys Thr Leu Pro Gly Cys
                100                105                110

tgg agg ctg gag gca gtg acg cag caa cag cgc gag gcg act ttg gag      444
Trp Arg Leu Glu Ala Val Thr Gln Gln Gln Arg Glu Ala Thr Leu Glu
                115                120                125

cgg cct cat ata gcg acc tcg cct tcc gct gcg cgt cct ccc aga gcc      492
Arg Pro His Ile Ala Thr Ser Pro Ser Ala Ala Arg Pro Pro Arg Ala
                130                135                140

caa gaa gcc cgg aac ctg tgg cat cca tct ctg aaa gga gaa gac ggc      540
Gln Glu Ala Arg Asn Leu Trp His Pro Ser Leu Lys Gly Glu Asp Gly
                145                150                155

aac cca gcc gag gca cta ctg ggt tgg ggt ctc cac gac cga gct ggt      588
Asn Pro Ala Glu Ala Leu Leu Gly Trp Gly Leu His Asp Arg Ala Gly
                160                165                170                175

ctc atc aag tgg cgt cca aca agg ggc tca aac ccg ggt tga ggggttg      637
Leu Ile Lys Trp Arg Pro Thr Arg Gly Ser Asn Pro Gly *
                180                185

ctggagcgcac ggagaacgtg gaactacact ggaggacacc agagtactct taagcaatcc      697

cttggccaaa accagcaact gatttgata ccatcaagac acctgaaatc ttgtcatgag      757

ccagatactg aggaagagat tttgggaaga acccaaggac cccccagttg cagccatgtc      817

aagactgaca ataaggaaga catcagtccc agcaagcaac attcatcggg cacagccacc      877

catgtggggc cagatcaaga agttgacaca gacggcggaa gaaaatctga agaaagcgga      937

tgaccagcta caatgagtaa tctaattgta gctatgatgg ctgtgctcac cattgccatg      997

agtattcccc cagcacctgc tgaaacaaaa aacattatac ttattgggca tatattcctt     1057

ttccaccagt ttcattggcca gtgacatggt tagaccccc agtggaggta tacactaatg     1117

atagcttttg gatacctggt tctacagatg atagaggccc atctcacccc caaaaggagg     1177

gaacattatg aatatttcgt tgggatt                                           1204

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<210> 273
 <211> 943
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (356)..(610)

<400> 273
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tgccaccctc tcctcagggc cacctcccc tggagccaga ggcaccgtag tcaagagaca 120
acacgaggag cctccactcc gggcagctgt tcgggttcgt ctcagttgcc aaacggaata 180
atttcacact ctgataacct gattgttttt taagccttgt ggtattctta attgcccggt 240
gttagataaa ctgtgattta aagagcacia acccagatag cagacacaca aaacactggc 300
ttgggaatag caaggagtga cttatttact ttagcaaagc cttttataag gtttt atg 358
Met
1
gct gca cta tca gag tgt cac cca gaa gtc act ctg gga ggt gaa cgc 406
Ala Ala Leu Ser Glu Cys His Pro Glu Val Thr Leu Gly Gly Glu Arg
5 10 15
aca ggg cag gac caa ggt agc acc agg cag aca caa gcc tcc ctg tgg 454
Thr Gly Gln Asp Gln Gly Ser Thr Arg Gln Thr Gln Ala Ser Leu Trp
20 25 30
gga gcc tct ctc atc tgt cgg ggg cct gcg ggc agg gga gag gag gtg 502
Gly Ala Ser Leu Ile Cys Arg Gly Pro Ala Gly Arg Gly Glu Glu Val
35 40 45
ccc cta cag gca agc ctg tgg ggg cgg cac cca gac ctc tgg aga cca 550
Pro Leu Gln Ala Ser Leu Trp Gly Arg His Pro Asp Leu Trp Arg Pro
50 55 60 65
agc acc act gcc acc cag tgc tgg gga gaa ggg atg gag aga atc aaa 598
Ser Thr Thr Ala Thr Gln Cys Trp Gly Glu Gly Met Glu Arg Ile Lys
70 75 80
agc cag cac tag gaa ggctgttgc tctgcatgac ccatggcggg gcaggtggag 653
Ser Gln His *
85
gggaagccgg acacaggaga gctcctgggg ccagacacgc cacctctgcc aggtgagccc 713
acgtcctgag ctgcagcctc aggaaccag ggttcttcca agaactccct tcacccaca 773
tggtcacttc ccagcctcct gaccacact caggccagc tcttccag actgtcatcc 833
tctttctaga aggaaacagg gacccctgg ggtccgggat ggccctgagc tcccctgtgt 893
gccccacacc ctggcgggtct ttgcccccat gtgccctgag tctgatgcct 943

<210> 274
<211> 803
<212> DNA
<213> Homo sapiens

<220>
 <221> CDS
 <222> (27) .. (488)

<400> 274

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Met Thr Ser His Ala Arg Val Arg Lys	
1 5	
ctt gga tcc tct aga gcg gcc gct gtc gtt gtt ctg agg aga aac ctt	101
Leu Gly Ser Ser Arg Ala Ala Val Val Val Leu Arg Arg Asn Leu	
10 15 20 25	
aca agt gta ata aat gtg cga agg ttt tta atc aaa aag gaa tcc ttg	149
Thr Ser Val Ile Asn Val Arg Arg Phe Leu Ile Lys Lys Glu Ser Leu	
30 35 40	
cac aac atc aga gag ttc ata ctg gag aga aac ctt aca agt gta atg	197
His Asn Ile Arg Glu Phe Ile Leu Glu Arg Asn Leu Thr Ser Val Met	
45 50 55	
aat gtg gca agg ttt tta atc aaa aag caa gcc ttg caa aac atc aga	245
Asn Val Ala Arg Phe Leu Ile Lys Lys Gln Ala Leu Gln Asn Ile Arg	
60 65 70	
gag ttc ata ctg cag aga aac ctt aca agt gta atg agt gtg gca aag	293
Glu Phe Ile Leu Gln Arg Asn Leu Thr Ser Val Met Ser Val Ala Lys	
75 80 85	
cct tta ctg gac agt caa cac tta ttc acc atc aag caa tcc atg ggt	341
Pro Leu Leu Asp Ser Gln His Leu Phe Thr Ile Lys Gln Ser Met Gly	
90 95 100 105	
gta ggg aaa ctt tac aaa tgt aat gat tgt cac aaa gtc ttc agt aat	389
Val Gly Lys Leu Tyr Lys Cys Asn Asp Cys His Lys Val Phe Ser Asn	
110 115 120	
gct aca acc att gca aat cat tac aga atc cat att gaa gag aga tct	437
Ala Thr Thr Ile Ala Asn His Tyr Arg Ile His Ile Glu Glu Arg Ser	
125 130 135	
aca agt gta ata aat gtg gca aat ttt tca gac gtc att cat aac ttg	485
Thr Ser Val Ile Asn Val Ala Asn Phe Ser Asp Val Ile His Asn Leu	
140 145 150	
tag ttca tcagtgaact catactggag agaaacctta caaatatcat gactgtgaca	542
*	
aggtcttcag tcaagcttca tcctatgcaa aacatagaat tcatacagga gagaaacctc	602
acaagtgtga tgattgtggc aaagccttta cttcatgttc acacctcatt agacatcaga	662
gaattcatac tggacagatg ccttacaaat gtaaggggtgg caaggtcttc actctgtggg	722
cattccatgc agaacatcag aaaattcatt tttgagataa ttgttcctaaa taaaatgaat	782

<210> 275
 <211> 1078
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (357)..(713)

<220>
 <221> misc_feature
 <222> (1)...(1078)
 <223> n = a,t,c or g

<400> 275

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acgccccccc actgagacta cagtccagng ncggcgaant cgagaaaaca cagcaacgag      60
gtgaatgaca tgggagacag acctgggggtc ttttagggac ggaaagcctc agccaagacc      120
cagactccca gggatcatcaa cctcctcggg tcactaacc tccccagtgt ctgtctaccc      180
ctaagtccag agaacacgtc ctctctaggg tcgagccgga atcaatatag gctacaaggg      240
catcagttca ggctgcgcgg aggagagaag gaagtgctga tgtggagtcc tccctcccc      300

ttctccttca cccccaagtg tctcccacga ctgccctccc cgacctctag ctgacc      356
atg gca tca gag gca gaa aaa aca ttc cat cgg ttt gct gcg ttt gga      404
Met Ala Ser Glu Ala Glu Lys Thr Phe His Arg Phe Ala Ala Phe Gly
  1             5             10             15

gaa tca tca agc agt ggc act gaa atg aac aac aag aac ttc tcc aag      452
Glu Ser Ser Ser Ser Gly Thr Glu Met Asn Asn Lys Asn Phe Ser Lys
          20             25             30

ctg tgc aaa gac tgt ggc atc atg gat ggc aag aca gtc acc tcc acg      500
Leu Cys Lys Asp Cys Gly Ile Met Asp Gly Lys Thr Val Thr Ser Thr
          35             40             45

gac gtg gac atc gtg ttc agc aaa gtc aag gcc aag aac gcc cga acc      548
Asp Val Asp Ile Val Phe Ser Lys Val Lys Ala Lys Asn Ala Arg Thr
          50             55             60

atc acg ttt caa cag ttc aaa gag gca gtg aag gaa ctg ggc cag aag      596
Ile Thr Phe Gln Gln Phe Lys Glu Ala Val Lys Glu Leu Gly Gln Lys
          65             70             75             80

cgc ttc aaa ggg aag agt cca gat gaa gtc ctg gag aac att tat gga      644
Arg Phe Lys Gly Lys Ser Pro Asp Glu Val Leu Glu Asn Ile Tyr Gly
          85             90             95

ctc atg gag ggc aaa gac cca gcc acc act ggc gct act ttt ccc tgg      692
Leu Met Glu Gly Lys Asp Pro Ala Thr Thr Gly Ala Thr Phe Pro Trp

```

100	105	110	
tta cct atg caa gaa acc tga aa gtgacccctag acccctccac ctccccaatc			745
Leu Pro Met Gln Glu Thr *			
115			
ccagctacgg ggaggcgggc ctgcatgggtg gttaagatca aggcttttga gtgaaacaga			805
ccaggaattg aatcctgcct ctgcagctta caaactgcac accatctatc tgtttacgaa			865
accactgaaa gcttccttgt ttcattctgtt catgaggata gtatttttta ctcacggcag			925
tatgaggatc cattaagatg tatatcaaga gtttttagac cagtgcccg cacaatgtgga			985
tgctctcgtc tcgcctggac agcacacaca ctccaactcc agtaagactc aactcaaata			1045
tatctcttat acaacttcaa gaaaaaaaaa aaa			1078

<210> 276
 <211> 724
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (74)..(223)

<400> 276		
aaaaatgaaa catttaccct agtgtctaag tgtctaataa ggaagaactt aaaatgtggg		60
cacctatgta aaa atg tca aaa ttg aaa atg cgg agg ggg cat ctg gaa		109
Met Ser Lys Leu Lys Met Arg Arg Gly His Leu Glu		
1 5 10		
tca aac tgg tgg cct ctc ggt ctg cag tct tat gct cta acc ctg agc		157
Ser Asn Trp Trp Pro Leu Gly Leu Gln Ser Tyr Ala Leu Thr Leu Ser		
15 20 25		
tat acc cct tcc tgc tgc tgt ggg ggt caa tta atg cct ttg act tgt		205
Tyr Thr Pro Ser Cys Cys Cys Gly Gly Gln Leu Met Pro Leu Thr Cys		
30 35 40		
gcg gtc aca ccc aga tga ccagtc acctgtgtgt tgccacttca caatggaagc		259
Ala Val Thr Pro Arg *		
45 50		
tcctaggagc tgccaggtct acctcagtga aaactcattg accttgtgca tagcaagagg		319
cagtccccgc tcctcagata acccccgtgc ctgtgtcttc cctgccttga gtccttagtt		379
atgggcagca ggctggaaaa gcactgccag cagccactag aatggccttg agagtcatcc		439
tcacagtaact gtttatgggtg ggcacatata agagaaactt tgtgtgactg aggtgtctgt		499

tctaaaacac ttaatgacag agttgggcct ggctctcctg gtccagtgtt ccattcaggg 559
cagattcagc acaactgcag tctaggacaa aagatgattc tttcaacttt tactttttca 619
gttaatacaa atgaagaatg ttagagaagg agcaactcca agaaatagtg agaagtgtgt 679
agctgagtag atttcccaaa agcattaata gggccagtgt tacca 724

<210> 277
<211> 1007
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (119)..(682)

<400> 277
tttcgtcagt tcgcggcagt tcgcgcggga gcggggcgcc tgggtggatg ggcgcttggg 60
cgctgggct gccggacggt gggaacggaa gtcgctgtgg gacgctgagg aagccagg 118
atg gcg act ccg agc aag aag acg tca act cca agc ccc cag cct tcc 166
Met Ala Thr Pro Ser Lys Lys Thr Ser Thr Pro Ser Pro Gln Pro Ser
1 5 10 15
aag aga gct ctc ccg aga gac cct tcg tcg gag gtc ccg agc aag agg 214
Lys Arg Ala Leu Pro Arg Asp Pro Ser Ser Glu Val Pro Ser Lys Arg
20 25 30
aag aat tcg gcc ccg cag ctg ccg ctg ttg cag tcg tcc ggg cct ttc 262
Lys Asn Ser Ala Pro Gln Leu Pro Leu Leu Gln Ser Ser Gly Pro Phe
35 40 45
gtg gaa ggc tct atc gtc cgc atc tcg atg gag aac ttc cta aca tat 310
Val Glu Gly Ser Ile Val Arg Ile Ser Met Glu Asn Phe Leu Thr Tyr
50 55 60
gat att tgt gaa gta tct cct gga ccc cac ttg aat atg atc gtt gga 358
Asp Ile Cys Glu Val Ser Pro Gly Pro His Leu Asn Met Ile Val Gly
65 70 75 80
gcc aat gga aca ggg aag tcg agc att gtg tgt gcc att tgc ctt ggt 406
Ala Asn Gly Thr Gly Lys Ser Ser Ile Val Cys Ala Ile Cys Leu Gly
85 90 95
tta gct gga aaa cct gct ttc atg gga cga gca gat aag gtt ggg ttt 454
Leu Ala Gly Lys Pro Ala Phe Met Gly Arg Ala Asp Lys Val Gly Phe
100 105 110
ttt gtg aag aga gga tgt tct aga ggc atg gtt gaa att gaa ttg ttc 502
Phe Val Lys Arg Gly Cys Ser Arg Gly Met Val Glu Ile Glu Leu Phe
115 120 125
agg gct tct gga aat ctt gta atc acc cgt gag att gat gtg gca aaa 550

Arg Ala Ser Gly Asn Leu Val Ile Thr Arg Glu Ile Asp Val Ala Lys
130 135 140

aat cag tcc ttt tgg ttc atc aac aaa aaa tct aca acc cag aaa ata 598
Asn Gln Ser Phe Trp Phe Ile Asn Lys Lys Ser Thr Thr Gln Lys Ile
145 150 155 160

gtg gaa gag aaa gtt gca gcc tta aat att cag tgg gga atc ttt gcc 646
Val Glu Glu Lys Val Ala Ala Leu Asn Ile Gln Trp Gly Ile Phe Ala
165 170 175

agt ttc tcc tca gga caa gtt gga gga att tgc taa actc agcaaattgg 696
Ser Phe Ser Ser Gly Gln Val Gly Gly Ile Cys *
180 185

actcctcgaa gcaactggaaa gttcaatggg ccccagaaa ttgcgcaata tcctgtgtac 756

tccaaactgt ggagaagaag aacagtcccg acccctgcgc agagaaactg ctgtctctcg 816

cgaaatggtg tgcccgttc gaggattata ccccgggtgg gagggcttct agcagggccg 876

cacatattcg agctgccacc cacagcacgc tggacaaaag ctgcgcctc agagacatat 936

tgacgcgag cgcatcacag gcaactccact catgcacagg agccctgcgg cgcggaacgg 996

cgcacacacc g 1007

<210> 278
<211> 439
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (18)..(131)

<400> 278

cgacgatttc gtccaaa atg gcg gca gcg atg gat gtg gat acc ccg agc 50
Met Ala Ala Ala Met Asp Val Asp Thr Pro Ser
1 5 10

ggc acc aac agc ggc gcg ggc aag aag cgc ttt gaa gtg aaa aag gtt 98
Gly Thr Asn Ser Gly Ala Gly Lys Lys Arg Phe Glu Val Lys Lys Val
15 20 25

ggg tct cgc cag cgc ctt cct cag gga agc tag agaggcgc ggatctggct 149
Gly Ser Arg Gln Arg Leu Pro Gln Gly Ser *
30 35

ggcaggcccg aggatggtcg aggcgcggag taaagggttt catttcaggg cgttcctggg 209

accgggtacc acgaaaggaa gccggggggc gggctctaga gttgatcggc gtgacggcgg 269

cccactgttg ggggaagtgt tggtttcgct gtgaggctaa ggggccaatc acagagctgc 329

ttattgagat acgcgggggtt gcgacttggc ggcgggagcc aagcgcttga gctgtcactg 389
gagtgggttga gaggtggggg aaggacaggg tatggtggag tgggggtgggt 439

<210> 279
<211> 1771
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (24)..(1049)

<400> 279
tttcgtcacg ggccttggtc acc atg tcg gtg ctg gat gcg ctt tgg gag 50
Met Ser Val Leu Asp Ala Leu Trp Glu
1 5

gat cgg gat gtc cgt ttc gac ctg tcc gcg cag caa atg aaa aca aga 98
Asp Arg Asp Val Arg Phe Asp Leu Ser Ala Gln Gln Met Lys Thr Arg
10 15 20 25

cct gga gaa gtc ctt att gat tgt tta gat tcc att gaa gac acc aaa 146
Pro Gly Glu Val Leu Ile Asp Cys Leu Asp Ser Ile Glu Asp Thr Lys
30 35 40

gga aat aat gga gat aga ggt aga ctc ttg gta aca aat tta aga att 194
Gly Asn Asn Gly Asp Arg Gly Arg Leu Leu Val Thr Asn Leu Arg Ile
45 50 55

ctc tgg cac tct ttg gca tta tca aga gtc aat gtt tct gtc ggt tac 242
Leu Trp His Ser Leu Ala Leu Ser Arg Val Asn Val Ser Val Gly Tyr
60 65 70

aat tgc ata ttg aat att aca aca agg act gct aac tct aaa tta cga 290
Asn Cys Ile Leu Asn Ile Thr Thr Arg Thr Ala Asn Ser Lys Leu Arg
75 80 85

ggc caa act gaa gct ctc tat ata cta aca aaa tgt aac agt act cgt 338
Gly Gln Thr Glu Ala Leu Tyr Ile Leu Thr Lys Cys Asn Ser Thr Arg
90 95 100 105

ttt gaa ttt ata ttt aca aat ttg gtt cct gga agc cct aga ctt ttt 386
Phe Glu Phe Ile Phe Thr Asn Leu Val Pro Gly Ser Pro Arg Leu Phe
110 115 120

act tct gtg atg gca gta cac aga gct tat gaa act tct aaa atg tat 434
Thr Ser Val Met Ala Val His Arg Ala Tyr Glu Thr Ser Lys Met Tyr
125 130 135

cgt gat ttt aaa tta aga agt gca cta att cag aac aag caa cta aga 482
Arg Asp Phe Lys Leu Arg Ser Ala Leu Ile Gln Asn Lys Gln Leu Arg
140 145 150

ctg ttg cca caa gaa cat gta tat gat aaa ata aat gga gtt tgg aat	530
Leu Leu Pro Gln Glu His Val Tyr Asp Lys Ile Asn Gly Val Trp Asn	
155 160 165	
tta tcc agt gat cag ggc aat tta gga acc ttt ttt att acc aat gtg	578
Leu Ser Ser Asp Gln Gly Asn Leu Gly Thr Phe Phe Ile Thr Asn Val	
170 175 180 185	
aga att gtg tgg cat gca aat atg aat gat agt ttt aat gtc agt ata	626
Arg Ile Val Trp His Ala Asn Met Asn Asp Ser Phe Asn Val Ser Ile	
190 195 200	
cca tat ctg caa att cgt tca ata aag att aga gat tca aaa ttt ggt	674
Pro Tyr Leu Gln Ile Arg Ser Ile Lys Ile Arg Asp Ser Lys Phe Gly	
205 210 215	
tta gct ctt gtc ata gaa agc tct cag cag agt ggt gga tat gtt ctt	722
Leu Ala Leu Val Ile Glu Ser Ser Gln Gln Ser Gly Gly Tyr Val Leu	
220 225 230	
ggc ttt aaa ata gat cct gtg gaa aaa cta caa gaa tca gtt aag gaa	770
Gly Phe Lys Ile Asp Pro Val Glu Lys Leu Gln Glu Ser Val Lys Glu	
235 240 245	
atc aat tca ctt cac aaa gtc tat tct gcc agt ccc ata ttt gga gtt	818
Ile Asn Ser Leu His Lys Val Tyr Ser Ala Ser Pro Ile Phe Gly Val	
250 255 260 265	
gat tat gag atg gaa gaa aag ccc cag ccg ctc gaa gct ctg aca gtc	866
Asp Tyr Glu Met Glu Glu Lys Pro Gln Pro Leu Glu Ala Leu Thr Val	
270 275 280	
gaa caa att caa gat gat gta gaa ata gac tct gat ggt cac acg gat	914
Glu Gln Ile Gln Asp Asp Val Glu Ile Asp Ser Asp Gly His Thr Asp	
285 290 295	
gct ttt gtg gct tat ttt gct gat ggc aat aag caa caa gat cgt gaa	962
Ala Phe Val Ala Tyr Phe Ala Asp Gly Asn Lys Gln Gln Asp Arg Glu	
300 305 310	
cct gta ttt tca gaa gaa ctg ggg ctt gca ata gag aaa ttg aag gat	1010
Pro Val Phe Ser Glu Glu Leu Gly Leu Ala Ile Glu Lys Leu Lys Asp	
315 320 325	
gga ttc acc cta cag gga ctt tgg gaa gta atg agt tga ttgaccttga	1059
Gly Phe Thr Leu Gln Gly Leu Trp Glu Val Met Ser *	
330 335 340	
gttgagatgg atttctatta aagatatctc tagttttaaag atactagtca cctgccataa	1119
gtcatggaat agttttttata ttacagctt ttatatattaa aacttgtaag agttttttta	1179
atgattgagg aaaaagtcac ttagaaaact tcagtttttcg gccagcgcgt cgagggaggg	1239
gccagcgaca catggcctag taaccgtccg gccgcggcgc tggcttaagc catggctgag	1299

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ggtagccgga ttcctcaggc cggggcgctc ctacagcagt gcctgcacgc cgggctgcaa 1359
attcgcccag ccgatgggga cgtcgcggcc cagtgggtgg aggtccaaag aggactggtg 1419
atctacgtgt gctttttcaa gggagctgat aaagaacttc ttcccaaat ggatctacga 1479
ctctggctcc actgattacc ttaaccatat tacatggaat gatgtaaggg agaaacagaa 1539
gactcttggt gaacagctcc tgtctttggt gaacagctcc ccagggcctc ctaccgcaa 1599
actgcttgct aagaatctag ccatacttta tagtattgga gacacattct ccgttcatga 1659
agcaatcgat aaatgtaatg atcttattcg tagcaaagat gattctccaa gttatcttcc 1719
cactaagctg taagtgaaac attaaaacag aacagaaaac aaaaaaaaaa aa 1771

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<210> 280
<211> 1109
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (162)..(1064)

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<400> 280
gtttgggccc tttggggtgg tacggaacac aacatcgggg ttgccatata ccggaattcc 60
cgggtcgacg atttcgttgc gcgttccgga actggtttcc cggaaggatt atgtctgcgc 120
cctcgatccg accggaagtt gcacgctgag ccgcggacac c      atg cag tcg gat 173
                                   Met Gln Ser Asp
                                   1

gat gtt atc tgg gat aca cta gga aac aag caa ttt tgt tcc ttc aaa 221
Asp Val Ile Trp Asp Thr Leu Gly Asn Lys Gln Phe Cys Ser Phe Lys
  5              10              15              20

ata aga acc aag act cag agc ttc tgc cga aat gaa tat agc ctg act 269
Ile Arg Thr Lys Thr Gln Ser Phe Cys Arg Asn Glu Tyr Ser Leu Thr
              25              30              35

gga ctg tgt aat cgg tca tcc tgt ccc ctg gca aat agt cag tat gcc 317
Gly Leu Cys Asn Arg Ser Ser Cys Pro Leu Ala Asn Ser Gln Tyr Ala
              40              45              50

act att aaa gaa gag aaa gga cag tgc tac ttg tat atg aag gtt ata 365
Thr Ile Lys Glu Glu Lys Gly Gln Cys Tyr Leu Tyr Met Lys Val Ile
              55              60              65

gaa cga gcg gct ttt cct cgg cgt ctc tgg gaa cgg gtc cgg ctt agt 413
Glu Arg Ala Ala Phe Pro Arg Arg Leu Trp Glu Arg Val Arg Leu Ser
              70              75              80

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aaa aac tat gag aaa gca ctg gag caa ata gat gaa aat ctg att tac	461
Lys Asn Tyr Glu Lys Ala Leu Glu Gln Ile Asp Glu Asn Leu Ile Tyr	
85 90 95 100	
tggtgg ccc cgt ttc att cga cac aaa tgt aag cag aga ttc acc aag atc	509
Trp Pro Arg Phe Ile Arg His Lys Cys Lys Gln Arg Phe Thr Lys Ile	
105 110 115	
acc caa tac cta att cga att aga aaa ctt aca cta aag cga cag agg	557
Thr Gln Tyr Leu Ile Arg Ile Arg Lys Leu Thr Leu Lys Arg Gln Arg	
120 125 130	
aaa ctt gtt cct ttg agt aag aag gtg gag cgt agg gag aaa aga aga	605
Lys Leu Val Pro Leu Ser Lys Lys Val Glu Arg Arg Glu Lys Arg Arg	
135 140 145	
gag gaa aag gca tta ata gct gct cag ctg gac aat gcc att gag aag	653
Glu Glu Lys Ala Leu Ile Ala Ala Gln Leu Asp Asn Ala Ile Glu Lys	
150 155 160	
gaa tta ctg gag aga ctg aaa caa gat acg tat ggc gac atc tac aac	701
Glu Leu Leu Glu Arg Leu Lys Gln Asp Thr Tyr Gly Asp Ile Tyr Asn	
165 170 175 180	
ttc ccc att cat gcc ttc gac aaa gcc ctg gaa caa cag gag gca gag	749
Phe Pro Ile His Ala Phe Asp Lys Ala Leu Glu Gln Gln Glu Ala Glu	
185 190 195	
agt gac tct tca gat act gag gaa aaa gat gat gat gat gat gat gag	797
Ser Asp Ser Ser Asp Thr Glu Glu Lys Asp Asp Asp Asp Asp Asp Glu	
200 205 210	
gaa gat gtg ggg aaa aga gaa ttt gtc gaa gat ggt gag gta gat gag	845
Glu Asp Val Gly Lys Arg Glu Phe Val Glu Asp Gly Glu Val Asp Glu	
215 220 225	
agt gac ata agt gat ttt gag gat atg gat aaa ctg gat gcc agc agt	893
Ser Asp Ile Ser Asp Phe Glu Asp Met Asp Lys Leu Asp Ala Ser Ser	
230 235 240	
gat gaa gat cag gat ggt aaa tcc tcc agt gag gag gag gaa gaa aag	941
Asp Glu Asp Gln Asp Gly Lys Ser Ser Ser Glu Glu Glu Glu Glu Lys	
245 250 255 260	
gcc ctt agt gcg aaa cac aaa ggc aaa atg ccc ttg aga gga cca ctg	989
Ala Leu Ser Ala Lys His Lys Gly Lys Met Pro Leu Arg Gly Pro Leu	
265 270 275	
cag aga aaa cga gcc tat gtg gaa ata gaa tac gag cag gag aca gag	1037
Gln Arg Lys Arg Ala Tyr Val Glu Ile Glu Tyr Glu Gln Glu Thr Glu	
280 285 290	
ccc gtg gcc aaa gcc aaa acc acg tga tttcc ctttcagtca tttataccca	1089
Pro Val Ala Lys Ala Lys Thr Thr *	
295 300	
ggactgaaca tgcagaactg	1109

<210> 281
 <211> 2018
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (36)..(1520)

<220>
 <221> misc_feature
 <222> (1)...(2018)
 <223> n = a,t,c or g

<400> 281
 acagctccca agccacaggc agaagcccca cagag atg gag cag aag gaa ggg 53
 Met Glu Gln Lys Glu Gly
 1 5

aag ctc tct gag gat ggg acc acc gtc tcc cca gct gcg gac aac cct 101
 Lys Leu Ser Glu Asp Gly Thr Thr Val Ser Pro Ala Ala Asp Asn Pro
 10 15 20

gag atg tca gga ggt gga gcc cct gca gag gag acc aaa ggc aca gct 149
 Glu Met Ser Gly Gly Gly Ala Pro Ala Glu Glu Thr Lys Gly Thr Ala
 25 30 35

gga aag gcc atc aat gag ggg cct ccc act gag tca gga aag cag gaa 197
 Gly Lys Ala Ile Asn Glu Gly Pro Pro Thr Glu Ser Gly Lys Gln Glu
 40 45 50

aag gca cca gcc gag gac ggc atg tca gca gaa ctc cag ggg gaa gca 245
 Lys Ala Pro Ala Glu Asp Gly Met Ser Ala Glu Leu Gln Gly Glu Ala
 55 60 65 70

aat gga tta gat gag gtc aaa gtg gaa tct cag agg gag gct ggt ggg 293
 Asn Gly Leu Asp Glu Val Lys Val Glu Ser Gln Arg Glu Ala Gly Gly
 75 80 85

aaa gag gat gct gag gct gaa ctt aaa aag gag gat ggt gag aag gaa 341
 Lys Glu Asp Ala Glu Ala Glu Leu Lys Lys Glu Asp Gly Glu Lys Glu
 90 95 100

gag acc act gtg ggt tct cag gag atg act ggc agg aaa gaa gag acc 389
 Glu Thr Thr Val Gly Ser Gln Glu Met Thr Gly Arg Lys Glu Glu Thr
 105 110 115

aaa tct gaa ccc aaa gag gct gag gaa aag gag agc acg ctg gcc tct 437
 Lys Ser Glu Pro Lys Glu Ala Glu Glu Lys Glu Ser Thr Leu Ala Ser
 120 125 130

gag aag cag aag gct gag gag aaa gag gcc aaa cct gaa tct ggg cag 485
 Glu Lys Gln Lys Ala Glu Glu Lys Glu Ala Lys Pro Glu Ser Gly Gln

135	140	145	150	
aaa gcc gat gcc aat gac aga gac aag cct gaa cct aag gca aca gtt				533
Lys Ala Asp Ala Asn Asp Arg Asp Lys Pro Glu Pro Lys Ala Thr Val	155	160	165	
gag gag gag gac gcc aag aca gcc tct cag gag gag aca ggc cag agg				581
Glu Glu Glu Asp Ala Lys Thr Ala Ser Gln Glu Glu Thr Gly Gln Arg	170	175	180	
aaa gag tgc agc act gaa ccc aag gag aag gct act gat gaa gag gcc				629
Lys Glu Cys Ser Thr Glu Pro Lys Glu Lys Ala Thr Asp Glu Glu Ala	185	190	195	
aag gct gaa tcg cag aag gct gtt gtg gag gat gag gct aag gct gaa				677
Lys Ala Glu Ser Gln Lys Ala Val Val Glu Asp Glu Ala Lys Ala Glu	200	205	210	
ccc aag gag ccc gat ggg aaa gag gag gcc aaa cat ggt gca aaa gag				725
Pro Lys Glu Pro Asp Gly Lys Glu Glu Ala Lys His Gly Ala Lys Glu	215	220	225	230
gag gct gat gca aaa gag gag gcg gag gat gca gag gag gca gag cca				773
Glu Ala Asp Ala Lys Glu Glu Ala Glu Asp Ala Glu Glu Ala Glu Pro	235	240	245	
ggc agt ccc agc gaa gag cag gag cag gac gtg gaa aaa gag cca gag				821
Gly Ser Pro Ser Glu Glu Gln Glu Gln Asp Val Glu Lys Glu Pro Glu	250	255	260	
gga ggg gca ggg gtg att ccc agc tcc cca gag gag tgg cct gag agc				869
Gly Gly Ala Gly Val Ile Pro Ser Ser Pro Glu Glu Trp Pro Glu Ser	265	270	275	
ccc act ggg gag ggg cac aac ctc agc aca gat ggg ctg ggt cca gac				917
Pro Thr Gly Glu Gly His Asn Leu Ser Thr Asp Gly Leu Gly Pro Asp	280	285	290	
tgt gta gct tcc gga cag acc agt cct tca gcc agt gag tct tca ccc				965
Cys Val Ala Ser Gly Gln Thr Ser Pro Ser Ala Ser Glu Ser Ser Pro	295	300	305	310
agc gac gtg ccc cag agt ccc cct gag tcc cct tcc tca ggg gag aag				1013
Ser Asp Val Pro Gln Ser Pro Pro Glu Ser Pro Ser Ser Gly Glu Lys	315	320	325	
aag gag aag gca cca gag cgc agg gta tca gcc cct gct cgg ccc cgg				1061
Lys Glu Lys Ala Pro Glu Arg Arg Val Ser Ala Pro Ala Arg Pro Arg	330	335	340	
ggg ccc ggg gca cag aac cgc aaa gcc atc gtg gac aag ttt ggc ggg				1109
Gly Pro Gly Ala Gln Asn Arg Lys Ala Ile Val Asp Lys Phe Gly Gly	345	350	355	
gca gct tcc ggc ccc acg gcc ttg ttc cgc aac act aag gca gcc ggg				1157
Ala Ala Ser Gly Pro Thr Ala Leu Phe Arg Asn Thr Lys Ala Ala Gly	360	365	370	

gca gcc att ggt ggt gtc aag aac atg ctc ttg gag tgg tgc cga gcc	1205
Ala Ala Ile Gly Gly Val Lys Asn Met Leu Leu Glu Trp Cys Arg Ala	
375 380 385 390	
atg aca aaa aaa tac gag cat gtg gac atc cag aac ttc tcc tcc agc	1253
Met Thr Lys Lys Tyr Glu His Val Asp Ile Gln Asn Phe Ser Ser Ser	
395 400 405	
tgg agc agt ggt atg gcc ttc tgt gcc ctc atc cac aag ttc ttc cct	1301
Trp Ser Ser Gly Met Ala Phe Cys Ala Leu Ile His Lys Phe Phe Pro	
410 415 420	
gac gcc ttt gac tac gca gag ctg gat ccc gca aag cgc cgg cac aac	1349
Asp Ala Phe Asp Tyr Ala Glu Leu Asp Pro Ala Lys Arg Arg His Asn	
425 430 435	
ttc acc ctg gcc ttc tcc aca gca gag aaa ctg gct gac tgt gct cag	1397
Phe Thr Leu Ala Phe Ser Thr Ala Glu Lys Leu Ala Asp Cys Ala Gln	
440 445 450	
ctg ctg gac gtg gat gac atg gtg cgg ttg gct gtg ccc gac tcc aag	1445
Leu Leu Asp Val Asp Asp Met Val Arg Leu Ala Val Pro Asp Ser Lys	
455 460 465 470	
tgc gtc tac aca tac atc cag gaa ctg tac cgc agc ctt gtg cag aaa	1493
Cys Val Tyr Thr Tyr Ile Gln Glu Leu Tyr Arg Ser Leu Val Gln Lys	
475 480 485	
gga ctg gtg aag acc aag aag aag tga ggagg tgactggctc tgtgggcaga	1545
Gly Leu Val Lys Thr Lys Lys Lys *	
490 495	
gatgggcagg gtgcccagct cagcagccac ggcccggggg ttcccttctg ctccatggag	1605
gcaccagagc caggggctta ggcaagggtg tgtggcgttg gttttaactg cattaaggt	1665
acttttgtaa aatcctgtct ggccccctca gtgctctctc ccatacttgg ncccaggaac	1725
ctctgcactc tgggataata aactctggcc cataggggat tcctcacctg ctgaggtctc	1785
aataactgcg caaggtgttt gggaaaggac aatggcctgg tcccaccact aaccagctgt	1845
gtgacacata cagttaacct ctctgggccc cagtttacag tctgaaaggg gataatgaga	1905
gttccaacct tatgaagggtg ttgcaagagt taaacgagat aatgaaatgg gcaaaaagct	1965
ttgcccagtc ctgccactca agtgttcagt aagtggctgc caaaaataaa aaa	2018

<210> 282
 <211> 706
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (39) .. (377)

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<400> 282
cgccctccccg ctgaccccg gatctgaggc tgtcagag      atg act ctg gtt ctg      53
                                         Met Thr Leu Val Leu
                                           1              5

tcc atg aat aga ttc tgc gag ccc att gtc tcg gaa gga gct gct gaa      101
Ser Met Asn Arg Phe Cys Glu Pro Ile Val Ser Glu Gly Ala Ala Glu
                    10                      15                      20

att gct ggg tac caa aca cta tgg gag gct gac agc tac gga ggc cca      149
Ile Ala Gly Tyr Gln Thr Leu Trp Glu Ala Asp Ser Tyr Gly Gly Pro
                    25                      30                      35

agc ccc cca ggg cca gca caa gct cct ttg cag gga gac cgg gga gct      197
Ser Pro Pro Gly Pro Ala Gln Ala Pro Leu Gln Gly Asp Arg Gly Ala
                    40                      45                      50

ggt ccc cca ctg gca gct cca ctt ggt gac ttc ctt tct gtg tat cag      245
Gly Pro Pro Leu Ala Ala Pro Leu Gly Asp Phe Leu Ser Val Tyr Gln
                    55                      60                      65

gag cag agc aga gga caa ctt gta gaa gac atg acc att aag aga cat      293
Glu Gln Ser Arg Gly Gln Leu Val Glu Asp Met Thr Ile Lys Arg His
                    70                      75                      80                      85

caa ctt cgc aac aaa tat aag aca agg ata caa gga ttc cta tgt gat      341
Gln Leu Arg Asn Lys Tyr Lys Thr Arg Ile Gln Gly Phe Leu Cys Asp
                    90                      95                      100

gca gct agg ttt tta tat cct tct aac aaa tgg tga gcag gagacttttt      391
Ala Ala Arg Phe Leu Tyr Pro Ser Asn Lys Trp *
                    105                      110

tggaataat tagttgtgaa attccatttt tctgacagcc ccttaaattt gaagttattt      451

catttgtagt taaggttatc acatccctgc caattttact agattttttc agagacaagc      511

attcagcatg gcattagtaa tgatgggtta aactaggtgc agaactgtcc catgaagaga      571

agaatgatat cagtatttaa ataataaaag aagagacaat gtatgggtta tagtgattca      631

ttttaagatt gctgtatttt gattttgtgg tttaaaataa atgcattaag gatcttttaa      691

gttaaaaaaa aaaaaa                                                    706

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<210> 283
 <211> 758
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (539) .. (697)

<400> 283
 agattatgtg tcatcatttc ttgcttctta gacatagtgc gtataagaac agtggaaatc 60
 aaagtagaaa atttcacact aggatgaaca tactgtattc tctactaggt agcgaagctg 120
 agtagctgac ctgtgatatc attaggagtt gagctgaaac tacttaaaac tgctctagcc 180
 ccaaccacgc tcaactccta atgatatcac aggtcagcta ctcagcttcg ctacctagta 240
 gagaatacag tatgttcatc ctagtgtgaa attttctact ttgatttcca ctgttcttat 300
 acgcattatg tctaagaagc aagaaatgat gacacataat ctaaagaaga aacaatcgat 360
 agaaaaagac cttatggatc acccaagtgt tggaatttag acaaagactt taaaattcca 420
 tgaaaaattht tctttatgtht aaagaaaaac gagaggcaga atgattgaga gaatagaaaa 480
 tttgagcaga gaaaaaaagt aacaaaaatag aaaatctaga actgaaaata tatccgaa 538
 atg aat aaa ttg ttt tat ttg tta ttt att ttt gta gaa aca gga tct 586
 Met Asn Lys Leu Phe Tyr Leu Leu Phe Ile Phe Val Glu Thr Gly Ser
 1 5 10 15
 cat ggt gtt gcc cag gtt ggt ctt gaa ctc ctg agc tca aga gat cct 634
 His Gly Val Ala Gln Val Gly Leu Glu Leu Leu Ser Ser Arg Asp Pro
 20 25 30
 cct gcc tct gcc tcc caa gct gct ggg att aca ggc atg aac cac tgt 682
 Pro Ala Ser Ala Ser Gln Ala Ala Gly Ile Thr Gly Met Asn His Cys
 35 40 45
 gcc cag ctg aaa tga ataaattgga taggcttaac aaaatggata caacaaaatg 737
 Ala Gln Leu Lys *
 50
 gatacaacag aaaaaaaaaa a 758

<210> 284
 <211> 1482
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (939) .. (1475)

<400> 284
 ccagcctgcc ctcttagtcc ctgacagctg cagtgcagc atctgtgatt gcaaagcatg 60
 acaatttata tctctcattt catcacacca tctatcagca gacagtcagg ctttaaaaat 120

caatcccaca ctgactcagt ccccagcaga gatggcctct gacaacagta tccacactgc	180
aggctggaca agggccctat taattttgag actcagccaa atttccttct gaccctaagc	240
tggatgaatcc ctgctccttt gcttttggttg gggttggtgt gagctaaggc tgtgatccca	300
tttgctccta tggcctccag gtggcctggg cctccatgaa tgggccacat ggtcatactg	360
aatgcttgat tacactcaga cctagcagtc gtctggggcg agctgggttta tggatcactt	420
tgtcacaatg ttccatcctt ccagggtcccc atccccgcgg tgggaaaaca ttgcttttagg	480
cagtgtctaga ggacttcagc aggcattggc agcttctgga ttcaggatta gaacaaagaa	540
ggaggagtca cagcaaagat aggaacagaa ggcagagaga acagacagat ggggggtgttt	600
gagaaggagg gcctttgaga cctcagggag tgggagacac tggctcgaga ataataataa	660
tggcaatttc tctcatctgt gttttcaggg catggactgg aactcccaat acccctgaca	720
tgggctgagt caacgtggtc atgaacatgt gacaggaggc agcagaagtt gcagagaaga	780
gtgaggcacg tttgaaaaag gctgaaaaat gtttctgtcc aggcaagggt gtgtgctgaa	840
tgactcaagg attttttggg gcattgaatg aacagcggga cattggacac ctgctgatcc	900
atcaccccg gcccgggcag gcccgtggat gaagagag atg gag aag acc agg	953
	Met Glu Lys Thr Arg
	1 5
cat gag act gtg gag aag cca cac cac cag aaa ccc ctg ccc cat gcg	1001
His Glu Thr Val Glu Lys Pro His His Gln Lys Pro Leu Pro His Ala	
	10 15 20
ccg tcc agc cca cac ctg tgg atg cac ggg gga ttg cag gca ggg ctc	1049
Pro Ser Ser Pro His Leu Trp Met His Gly Gly Leu Gln Ala Gly Leu	
	25 30 35
cca ccg tgg act cag gaa cag gca ggg aag ctg ctg cct cac cag gcg	1097
Pro Pro Trp Thr Gln Glu Gln Ala Gly Lys Leu Leu Pro His Gln Ala	
	40 45 50
aag ggg cca gga ggg gga ggc gga gag gcc cgt cta gcc cct gcg gct	1145
Lys Gly Pro Gly Gly Gly Gly Gly Glu Ala Arg Leu Ala Pro Ala Ala	
	55 60 65
gtc acc gtg gtg cct cct cac tgg cca gtg cgg tcg cgc ctc agc ttc	1193
Val Thr Val Val Pro Pro His Trp Pro Val Arg Ser Arg Leu Ser Phe	
	70 75 80 85
gtt aat agg gga ggg ggc cta aga gtt ttc acg tcc agg ctc ggg cag	1241
Val Asn Arg Gly Gly Gly Leu Arg Val Phe Thr Ser Arg Leu Gly Gln	
	90 95 100
tgg gga ggc agg cag gag tgg ccg ctg gtt ttt cag acc tcc cag gga	1289
Trp Gly Gly Arg Gln Glu Trp Pro Leu Val Phe Gln Thr Ser Gln Gly	
	105 110 115

ggc cga gga aat ggc ccg tcc tgg agt ggg cgt ggt tct gtc ttc aga 1337
 Gly Arg Gly Asn Gly Pro Ser Trp Ser Gly Arg Gly Ser Val Phe Arg
 120 125 130
 tgg atg ctg gag ggt tgg gct gcg tgg gac cct ggg ccc tgc tgc ttc 1385
 Trp Met Leu Glu Gly Trp Ala Ala Trp Asp Pro Gly Pro Cys Cys Phe
 135 140 145
 ccg gag gat gcg ctg tcc ggg gct gca cag gtt ggc tgt gtt ttt tgg 1433
 Pro Glu Asp Ala Leu Ser Gly Ala Ala Gln Val Gly Cys Val Phe Trp
 150 155 160 165
 atg ctt gtt att ttt ttt ttt ctt ctc ttc act ctg tca tga aactggc 1482
 Met Leu Val Ile Phe Phe Phe Leu Leu Phe Thr Leu Ser *
 170 175

<210> 285
 <211> 3504
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (392)..(1120)

<400> 285
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 cctttttgact taggagctga agttgccctc ctataaaggc cagtccccctc agttaagtct 120
 cagacgggtat tttgccgact tgattgccat tgtgagcaat cgcttcacac tctgcccttc 180
 tgcccgccat cttgctgtct atttactgga cctgtttatg gaccgctatg acatctctat 240
 ccagcagctg catttagttg cgctttcctg cctgcttcta gcaagtaaatttgaagaaaa 300
 agaagacagt gtgcctaagc tggagcagct caacagcctg gggtgtatga ctaatatgaa 360
 tctagtatta acaaaacaaa atttgctaca t atg gaa cta tta tta tta gaa 412
 Met Glu Leu Leu Leu Leu Glu
 1 5
 acc ttt cag tgg aac ctc tgc ctt cca aca gcc gcc cat ttc att gag 460
 Thr Phe Gln Trp Asn Leu Cys Leu Pro Thr Ala Ala His Phe Ile Glu
 10 15 20
 tat tat ctc tct gaa gca gta cac gaa aca gat ctt cat gac ggc tgg 508
 Tyr Tyr Leu Ser Glu Ala Val His Glu Thr Asp Leu His Asp Gly Trp
 25 30 35
 cca atg att tgc ttg gaa aag act aaa ctc tac atg gcc aaa tat gca 556
 Pro Met Ile Cys Leu Glu Lys Thr Lys Leu Tyr Met Ala Lys Tyr Ala

40	45	50	55	
gat tac ttc ctg gaa gta tct ttg caa gct gct gca tgt gtg gct tct				604
Asp Tyr Phe Leu Glu Val Ser Leu Gln Ala Ala Cys Val Ala Ser	60	65	70	
tcg agg att ata ctt cgt ctt tct cca acg tgg cct aca aga cta cat				652
Ser Arg Ile Ile Leu Arg Leu Ser Pro Thr Trp Pro Thr Arg Leu His	75	80	85	
cgt ctt act gcc tac tct tgg gat ttc tta gtg cag tgt att gaa cga				700
Arg Leu Thr Ala Tyr Ser Trp Asp Phe Leu Val Gln Cys Ile Glu Arg	90	95	100	
ctg ttg atc gct cat gat aat gat gtg aaa gaa gca aac aaa cag aga				748
Leu Leu Ile Ala His Asp Asn Asp Val Lys Glu Ala Asn Lys Gln Arg	105	110	115	
ggg caa gca gga cct cag tca gcg caa cta agt gta ttc cag aca gcc				796
Gly Gln Ala Gly Pro Gln Ser Ala Gln Leu Ser Val Phe Gln Thr Ala	120	125	130	135
tcc cag cca tca cgg cca gtt cac ttt cag caa cct cag tat ctc cat				844
Ser Gln Pro Ser Arg Pro Val His Phe Gln Gln Pro Gln Tyr Leu His	140	145	150	
cag aca cat cag acc tca ctg cag tat cgc cat cct acg tca gaa caa				892
Gln Thr His Gln Thr Ser Leu Gln Tyr Arg His Pro Thr Ser Glu Gln	155	160	165	
cca agc tgt cag cag att gta tcg acc aca cac acc tca tct tac aca				940
Pro Ser Cys Gln Gln Ile Val Ser Thr Thr His Thr Ser Ser Tyr Thr	170	175	180	
cta cag aca tgt cct gct ggc ttc caa act agt gtt cag ggc ctt ggg				988
Leu Gln Thr Cys Pro Ala Gly Phe Gln Thr Ser Val Gln Gly Leu Gly	185	190	195	
cac atg cag act ggt gtt ggg atg tca ctg gca ata cca gta gaa gtt				1036
His Met Gln Thr Gly Val Gly Met Ser Leu Ala Ile Pro Val Glu Val	200	205	210	215
aag ccc tgt ctg agt gtt tct tac aac cgg agt tat cag ata aat gaa				1084
Lys Pro Cys Leu Ser Val Ser Tyr Asn Arg Ser Tyr Gln Ile Asn Glu	220	225	230	
cat tac cct tgt att act cca tgt ttt gaa agg tga ttat ttgtgaagct				1134
His Tyr Pro Cys Ile Thr Pro Cys Phe Glu Arg *	235	240		
gataaccgac ccagactgct ttgtgacatg aagctatggg taagcggtttt gttaaacttct				1194
gttcaaaagg aaagggatct aaatgacatc agaactcttc aggtaccagc accaggaaga				1254
ctgaatatcc tttttaatgc accatgaatc ctgggagact aagcaaatta acagtatgtc				1314
aaattctgtt acaacaaatc cctgtatgac aaaaatgttc aagtcctggc tgatggtcca				1374

aatatttcaa	aaatattcag	tacaacagaa	aatttggaca	gacttcaatt	tgccattttg	1434
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ggaaacactt	aactgtaatg	caacatgcct	tggaatggt	atagtgtgaa	ctacctttat	1914
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gaatgaagtg	gtagttcctg	tgattcataa	tacatatgta	ggttttgcat	atctcagtgc	2034
aatccatgat	ttatactcag	aatcgacatt	cttaaaaagt	tatttcaagg	gatggcataa	2094
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tcagtagcta	ctttcattgg	attgacccta	caactgccct	gggacatttc	actgtaccag	2334
tattaactgc	aaacagcaat	aattgtcatt	acagcaaggg	cagtttgggg	gtaaagcatt	2394
ttggaggaat	aaccttaaaa	agttaaaaag	tcattgtaat	aactgataaa	ctgtatacat	2454
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gtaagggtgtg	tcttttttgt	ttttttaaga	tagcacttga	atagaaggga	aaactgcatg	2574
gcagatacgt	gactgccaca	atatgcatcg	aagacaaact	tactataaag	atgttgtggg	2634
tatgcagcag	gagtctcagt	aatcaagcca	atggcctttg	tcaggaaggg	aaggggctca	2694
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gtacataggg	catgatgtgg	atttattagt	ctggtagata	aatgaaaaa	ccactcaggt	2874
aagaacactc	actcatggca	gtttttaagc	atgaaaattg	ttttctgaaa	gtatcatcac	2934
ttttcctttt	taaagaaggc	tgctaattgg	attttggtag	ttcttacctc	aagaaaactt	2994
gaattatttg	ggggaaagta	ggctcaaaag	agaatatatc	tttcacattc	acattcagaa	3054

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cccagcaacc tggagtccaa ttttcagtat ttttaactacc tcaataatgc tatgaatgta 3114
agatattggg atagagatcc caacttgaaa caacagccag tgcctgtggt aacttaatgt 3174
cttgtcaaat acttttattg attgggtttat atgccattct tgttatagaa gaatatgcct 3234
tttaaaaaag cttattaata acactttccc aatttatatt ttaaaaagct aaagaacact 3294
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gggtgggatg ggggtggttg agaaccagaa ctatttttaa aacattaggt ttcaatataa 3414
atacaactca caactgctag ctttgggggg tgggggaaca ttgtttgggt tttgttttgt 3474
ttaatttatt gattagtctt taaagtaggc 3504

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<210> 286
<211> 650
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (217)..(510)

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<400> 286
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gaagagccca ggtccctgcc ccagttctac cacagctctc atgccacag ccctgtctgt 180
ctggacacat tactaggcac agactgctga cagggg atg tcc tgg gcg gtt gac 234
Met Ser Trp Ala Val Asp
1 5

ctg cct gtg tgt caa agg aca cct cac tgc agg gtc caa gac aga gtg 282
Leu Pro Val Cys Gln Arg Thr Pro His Cys Arg Val Gln Asp Arg Val
10 15 20

ctc cac tgt ggc ttc ctg gga agc ccg ctg gtg gga gct cct ggg agc 330
Leu His Cys Gly Phe Leu Gly Ser Pro Leu Val Gly Ala Pro Gly Ser
25 30 35

agg aga cag ctg tgc tct ccc cac tcc tcc ctc cgg cct cag cac cca 378
Arg Arg Gln Leu Cys Ser Pro His Ser Ser Leu Arg Pro Gln His Pro
40 45 50

cag gtg gcc tct gct ctc ttg gag gcg aag ctg ctc ccc tct cct cca 426
Gln Val Ala Ser Ala Leu Leu Glu Ala Lys Leu Leu Pro Ser Pro Pro
55 60 65 70

acc tca ttc tct gcc tgc ttc atc cgg ccc cac aca cac acc ggt aat 474
Thr Ser Phe Ser Ala Cys Phe Ile Arg Pro His Thr His Thr Gly Asn

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75	80	85	
ctg tgt tcc ttt ctg cca tta atc ctc ctc atg taa atat tcccaatact			524
Leu Cys Ser Phe Leu Pro Leu Ile Leu Leu Met *			
90	95		
ctttcagtc ccaaagccat aggccacat ctgcttgtgg atcagaaaca tgctggcaga			584
gcgcggtggg actgctgccc cctggccctt aggagtgggg tctggggcgc cctcagaaca			644
acgaca			650

<210> 287
 <211> 1619
 <212> DNA
 <213> Homo sapiens

<220>
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gcggcctcct tgcccgggct tggggcgccg cgctggggaa agccgggggc ccggacacat	60
tggcgtgaga cctgggagta cgttgtgcc aatcattgcc acttgccaca tgagtgtaa	119
atg atg gcg gat gcc aag tat gtc ctc tgc cga tgg gaa aag cga tta	167
Met Met Ala Asp Ala Lys Tyr Val Leu Cys Arg Trp Glu Lys Arg Leu	
1 5 10 15	
tgg cct gcg aag gtt ttg gcc cga acc gcg act tca aca aaa aat aag	215
Trp Pro Ala Lys Val Leu Ala Arg Thr Ala Thr Ser Thr Lys Asn Lys	
20 25 30	
aga aga aag gaa tat ttt cta gct gtg caa atc ctc tcc cta gag gaa	263
Arg Arg Lys Glu Tyr Phe Leu Ala Val Gln Ile Leu Ser Leu Glu Glu	
35 40 45	
aaa att aag gtg aaa agc act gaa gtt gag atc cta gag aag tct caa	311
Lys Ile Lys Val Lys Ser Thr Glu Val Glu Ile Leu Glu Lys Ser Gln	
50 55 60	
att gaa gcc att gct tcc tcg tta gcc tca cag aat gag gtt cct gcg	359
Ile Glu Ala Ile Ala Ser Ser Leu Ala Ser Gln Asn Glu Val Pro Ala	
65 70 75 80	
gca ccc ctg gaa gaa ctg gcc tac aga cgg tcg ctt cgc gtg gct ctg	407
Ala Pro Leu Glu Glu Leu Ala Tyr Arg Arg Ser Leu Arg Val Ala Leu	
85 90 95	
gac gtt ctg agc gag ggc tcg att tgg agt caa gaa agc tct gca ggg	455
Asp Val Leu Ser Glu Gly Ser Ile Trp Ser Gln Glu Ser Ser Ala Gly	
100 105 110	
aca ggt aga gct gac cgg tct ctg cga ggg aag ccc atg gag cat gtc	503

Thr	Gly	Arg	Ala	Asp	Arg	Ser	Leu	Arg	Gly	Lys	Pro	Met	Glu	His	Val	
	115						120					125				
tcc	tcg	ccc	tgt	gat	tcg	aac	tcc	tca	tct	ctt	ccc	cgc	gga	gac	gtg	551
Ser	Ser	Pro	Cys	Asp	Ser	Asn	Ser	Ser	Ser	Leu	Pro	Arg	Gly	Asp	Val	
	130						135					140				
ttg	ggc	agt	tcc	aga	cct	cac	agg	agg	agg	cca	tgt	gtg	caa	caa	agc	599
Leu	Gly	Ser	Ser	Arg	Pro	His	Arg	Arg	Arg	Pro	Cys	Val	Gln	Gln	Ser	
	145					150				155					160	
ctg	tca	agt	tcg	ttc	act	tgt	gaa	aag	gac	ccc	gag	tgc	aaa	gtg	gac	647
Leu	Ser	Ser	Ser	Phe	Thr	Cys	Glu	Lys	Asp	Pro	Glu	Cys	Lys	Val	Asp	
				165					170					175		
cac	aag	aag	ggg	ctc	agg	aaa	agt	gaa	aac	cca	aga	ggc	ccg	ttg	gtc	695
His	Lys	Lys	Gly	Leu	Arg	Lys	Ser	Glu	Asn	Pro	Arg	Gly	Pro	Leu	Val	
			180					185					190			
ctc	cca	gct	gga	ggt	ggt	gcc	caa	gat	gag	agt	ggg	tcc	aga	atc	cac	743
Leu	Pro	Ala	Gly	Gly	Gly	Ala	Gln	Asp	Glu	Ser	Gly	Ser	Arg	Ile	His	
			195				200					205				
cac	aaa	aat	tgg	act	ctt	gca	agt	aag	agg	gga	aga	aac	tca	gcg	cag	791
His	Lys	Asn	Trp	Thr	Leu	Ala	Ser	Lys	Arg	Gly	Arg	Asn	Ser	Ala	Gln	
	210					215					220					
aag	gct	agc	ttg	tgc	ctg	aat	gga	tct	tcc	ctt	tca	gag	gac	gac	acg	839
Lys	Ala	Ser	Leu	Cys	Leu	Asn	Gly	Ser	Ser	Leu	Ser	Glu	Asp	Asp	Thr	
	225				230					235					240	
gag	aga	gac	atg	ggg	agc	aaa	gga	ggc	agc	tgg	gca	gcc	ccg	tcc	ttg	887
Glu	Arg	Asp	Met	Gly	Ser	Lys	Gly	Gly	Ser	Trp	Ala	Ala	Pro	Ser	Leu	
				245					250					255		
ccc	tcc	ggg	gtc	agg	gag	gac	gat	ccc	tgt	gcc	aac	gct	gag	gga	cac	935
Pro	Ser	Gly	Val	Arg	Glu	Asp	Asp	Pro	Cys	Ala	Asn	Ala	Glu	Gly	His	
			260					265					270			
gac	ccc	ggt	ctg	ccg	ttg	ggc	agc	ctc	act	gcg	ccc	cca	gcc	cct	gag	983
Asp	Pro	Gly	Leu	Pro	Leu	Gly	Ser	Leu	Thr	Ala	Pro	Pro	Ala	Pro	Glu	
		275					280					285				
ccc	tcg	gcc	tgc	tca	gag	cct	gga	gaa	tgc	cct	gcg	aaa	aag	agg	ccg	1031
Pro	Ser	Ala	Cys	Ser	Glu	Pro	Gly	Glu	Cys	Pro	Ala	Lys	Lys	Arg	Pro	
	290					295					300					
cgc	ctg	gat	ggc	agc	caa	agg	ccg	cct	gcc	gtg	cag	ctg	gag	ccc	atg	1079
Arg	Leu	Asp	Gly	Ser	Gln	Arg	Pro	Pro	Ala	Val	Gln	Leu	Glu	Pro	Met	
	305				310				315						320	
gca	gca	ggg	gcc	gca	cca	tcc	ccc	ggg	ccg	ggg	cca	ggg	ccc	aga	gag	1127
Ala	Ala	Gly	Ala	Ala	Pro	Ser	Pro	Gly	Pro	Gly	Pro	Gly	Pro	Arg	Glu	
				325				330						335		
tct	gtg	acc	ccg	cgc	agc	acc	gcc	agg	ctg	ggc	ccg	cct	ccc	tcc	cac	1175
Ser	Val	Thr	Pro	Arg	Ser	Thr	Ala	Arg	Leu	Gly	Pro	Pro	Pro	Ser	His	

340	345	350	
gcc tct gcg gat gca acc aga tgt ctt cct tgc ccg gat tcc cag aag			1223
Ala Ser Ala Asp Ala Thr Arg Cys Leu Pro Cys Pro Asp Ser Gln Lys			
355	360	365	
ctg gag aaa gag tgc cag tct tcc gaa gag tcc atg ggg tct aat tcc			1271
Leu Glu Lys Glu Cys Gln Ser Ser Glu Glu Ser Met Gly Ser Asn Ser			
370	375	380	
atg cgt tct atc ctg gag gaa gac gag gaa gac gag gag cca cca aga			1319
Met Arg Ser Ile Leu Glu Glu Asp Glu Glu Asp Glu Glu Pro Pro Arg			
385	390	395	400
gtc ctt tta tac cac gaa cca cgt tcg ttt gaa gta gga atg cta gtc			1367
Val Leu Leu Tyr His Glu Pro Arg Ser Phe Glu Val Gly Met Leu Val			
	405	410	415
tgg cat aaa cat aaa aaa tac ccc ttc tgg cca gca gtg gtc aaa agc			1415
Trp His Lys His Lys Lys Tyr Pro Phe Trp Pro Ala Val Val Lys Ser			
	420	425	430
gtc agg cag aga gat aag aaa gca agt gtg cta tac atc gaa gga cac			1463
Val Arg Gln Arg Asp Lys Lys Ala Ser Val Leu Tyr Ile Glu Gly His			
	435	440	445
atg aac ccg aaa atg aaa ggt ttc aca gtg tct ctt aaa agt tta aag			1511
Met Asn Pro Lys Met Lys Gly Phe Thr Val Ser Leu Lys Ser Leu Lys			
	450	455	460
cac ttt gat tgt aaa gag aaa cag acg ctt ctg aat caa gcc agg gag			1559
His Phe Asp Cys Lys Glu Lys Gln Thr Leu Leu Asn Gln Ala Arg Glu			
465	470	475	480
gac ttc aac cag gac atc ggc tgg tgt gct ccc tca tca ccg act aca			1607
Asp Phe Asn Gln Asp Ile Gly Trp Cys Ala Pro Ser Ser Pro Thr Thr			
	485	490	495
ggg tcc ggt tag			1619
Gly Ser Gly *			
500			

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 <211> 713
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<220>
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 <222> (202)..(435)

<400> 288
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atggaaaata tggacataag aatttacagt taagaaaagg ctgtaaaagt gtggatgagt	300
gtaagggaca ccaaggaggt tataatggac ttaaccaatg tttgaaaatt accacaagca	360
aaatattttca atgtaataaaa tatgtaaaag tc atg cat aaa ttt tca aat tca	413
Met His Lys Phe Ser Asn Ser	
1 5	
aat aga cac aag ata aga cat act gaa aat aaa cat ttc aga tgt aaa	461
Asn Arg His Lys Ile Arg His Thr Glu Asn Lys His Phe Arg Cys Lys	
10 15 20	
gaa tgt gac aaa tca ctt tgc atg ctt tca cgc cta act caa cat aaa	509
Glu Cys Asp Lys Ser Leu Cys Met Leu Ser Arg Leu Thr Gln His Lys	
25 30 35	
aaa att cat act aga gag aat ttc tac aaa tgt gaa gag tgt gga aaa	557
Lys Ile His Thr Arg Glu Asn Phe Tyr Lys Cys Glu Glu Cys Gly Lys	
40 45 50 55	
acc ttt aac tgg tcc aca aac ctt tct aaa cct aag aaa att cat act	605
Thr Phe Asn Trp Ser Thr Asn Leu Ser Lys Pro Lys Lys Ile His Thr	
60 65 70	
gga gaa aaa ccc tac aaa tgt gaa gta tgt gga aaa gcc ttt cac caa	653
Gly Glu Lys Pro Tyr Lys Cys Glu Val Cys Gly Lys Ala Phe His Gln	
75 80 85	
tcc tca atc ctt act aaa cat aag ata att cgt act gga gaa aaa ccc	701
Ser Ser Ile Leu Thr Lys His Lys Ile Ile Arg Thr Gly Glu Lys Pro	
90 95 100	
tat aaa tgt gca cac tgt ggc aaa gcc ttt aaa cag tcc tca cac ctt	749
Tyr Lys Cys Ala His Cys Gly Lys Ala Phe Lys Gln Ser Ser His Leu	
105 110 115	
act aga cat aag ata att cat act gaa gag aaa ccc tac aaa tgt gaa	797
Thr Arg His Lys Ile Ile His Thr Glu Glu Lys Pro Tyr Lys Cys Glu	
120 125 130 135	
caa tgt ggc aag gtc ttt aag cag tcc cca acc ctt act aaa cat cag	845
Gln Cys Gly Lys Val Phe Lys Gln Ser Pro Thr Leu Thr Lys His Gln	
140 145 150	
ata att tat act gga ggt cga cgc gac cgc gaa ttc gga tcc tcg aga	893
Ile Ile Tyr Thr Gly Gly Arg Arg Asp Arg Glu Phe Gly Ser Ser Arg	
155 160 165	
gat ctc ttt ttt tgg gtt tgg tgg ggt atc ttc gtc atg taa tagggcg	942
Asp Leu Phe Phe Trp Val Trp Trp Gly Ile Phe Val Met *	
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gcacg      atg gcc tcg tct cag ggg aaa aac gag ctg aaa tta gcc gac      167
            Met Ala Ser Ser Gln Gly Lys Asn Glu Leu Lys Leu Ala Asp
              1              5              10

tgg atg gca act ctg ccg gag agc atg cac agc atc ccc ctc acc aat      215
Trp Met Ala Thr Leu Pro Glu Ser Met His Ser Ile Pro Leu Thr Asn
  15              20              25              30

tta gcc att cca ggg tct cat gat tcc ttc agc ttc tac att gat gaa      263
Leu Ala Ile Pro Gly Ser His Asp Ser Phe Ser Phe Tyr Ile Asp Glu
              35              40              45

gcc tct cca gta ggt cct gag cag cca gaa act gtc cag aat ttt gtc      311
Ala Ser Pro Val Gly Pro Glu Gln Pro Glu Thr Val Gln Asn Phe Val
              50              55              60

tct gtg ttt gga act gtg gcc aaa aag ctc atg cgg aaa tgg tta gcc      359
Ser Val Phe Gly Thr Val Ala Lys Lys Leu Met Arg Lys Trp Leu Ala
              65              70              75

act cag aca atg aat ttt act ggc cag cta gga gct gga att cgt tat      407
Thr Gln Thr Met Asn Phe Thr Gly Gln Leu Gly Ala Gly Ile Arg Tyr
              80              85              90

ttt gat ctt cga att tcc acc aag ccc aga gac ccc gac aat gaa ctc      455
Phe Asp Leu Arg Ile Ser Thr Lys Pro Arg Asp Pro Asp Asn Glu Leu
              95              100              105              110

tat ttt gct cat ggt ttg ttc agt gcc aaa gtc aat gaa ggc ctt gag      503
Tyr Phe Ala His Gly Leu Phe Ser Ala Lys Val Asn Glu Gly Leu Glu
              115              120              125

gag atc aat gca ttc ctc aca gat cac cat aag gag gta gtg ttc ttg      551
Glu Ile Asn Ala Phe Leu Thr Asp His His Lys Glu Val Val Phe Leu
              130              135              140

gac ttc aac cac ttc tat ggg atg cag aaa tat cac cat gaa aaa ctg      599
Asp Phe Asn His Phe Tyr Gly Met Gln Lys Tyr His His Glu Lys Leu
              145              150              155

gtc caa atg ctg aaa gac atc tat gga aat aaa atg tgc cca gcg att      647
Val Gln Met Leu Lys Asp Ile Tyr Gly Asn Lys Met Cys Pro Ala Ile
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160	165	170	
ttt gcc cag gaa gtt agt tta aag tac ctg tgg gag aag gac tat caa			695
Phe Ala Gln Glu Val Ser Leu Lys Tyr Leu Trp Glu Lys Asp Tyr Gln			
175	180	185	190
gtg ctg gtc ttc tac cat agt cca gtg gct ctg gaa gtg ccc ttt ctc			743
Val Leu Val Phe Tyr His Ser Pro Val Ala Leu Glu Val Pro Phe Leu			
	195	200	205
tgg cct ggg cag atg atg cca gca ccc tgg gcc aac acc aca gac ccc			791
Trp Pro Gly Gln Met Met Pro Ala Pro Trp Ala Asn Thr Thr Asp Pro			
	210	215	220
gag aaa ctg atc cag ttt ctt caa gca tcc atc act gag aga aga aag			839
Glu Lys Leu Ile Gln Phe Leu Gln Ala Ser Ile Thr Glu Arg Arg Lys			
	225	230	235
aag gga tcg ttt ttt ata tct cag gtg gtg ctg acc ccc aaa gct agc			887
Lys Gly Ser Phe Phe Ile Ser Gln Val Val Leu Thr Pro Lys Ala Ser			
	240	245	250
act gtg gtc aaa ggg gtg gca agt ggc ctc aga gaa aca atc aca gaa			935
Thr Val Val Lys Gly Val Ala Ser Gly Leu Arg Glu Thr Ile Thr Glu			
	255	260	265
aga gct ctt cct gcc atg atg cag tgg gtc cgc acg cag aag cca gga			983
Arg Ala Leu Pro Ala Met Met Gln Trp Val Arg Thr Gln Lys Pro Gly			
	275	280	285
gag agt ggc atc aat att gtc act gcc gat ttt gta gaa ctt ggt gac			1031
Glu Ser Gly Ile Asn Ile Val Thr Ala Asp Phe Val Glu Leu Gly Asp			
	290	295	300
ttt atc agc act gtc ata aag ctc aac tat gtc ttt gat gaa gga gaa			1079
Phe Ile Ser Thr Val Ile Lys Leu Asn Tyr Val Phe Asp Glu Gly Glu			
	305	310	315
gcc aac act tga tag cactacttgg agtttccatg aataagatgg agaaagctca			1134
Ala Asn Thr *			
	320		
ttgtattagg gcatactatc tgtaaact ctgatcttcc tattccactg agtctctgaa			1194
gggaataggg ctggtagtgg gtgggaaaag gggaaaaaact gtttcttcag tgattacaat			1254
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tggttaggaat aaaaaaaaaa aa			1336

<210> 291
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Lys Leu Lys Leu Leu Ser Leu Ser Gln Ser Phe Ser Ser Thr Ala Pro	
185 190 195 200	
tct gac aca gac ctc ggg gag agc tta ggg gcc aac gtg gcc acc aca	795
Ser Asp Thr Asp Leu Gly Glu Ser Leu Gly Ala Asn Val Ala Thr Thr	
205 210 215	
gac tcg gat gag aga gat gat gca tct gtg tgc agt gga ggt gac tcc	843
Asp Ser Asp Glu Arg Asp Asp Ala Ser Val Cys Ser Gly Gly Asp Ser	
220 225 230	
act gat gac ggt ggc tac agg agc agc atg tgg gac cag ggc gac atc	891
Thr Asp Asp Gly Gly Tyr Arg Ser Ser Met Trp Asp Gln Gly Asp Ile	
235 240 245	
ctg gag tct ggg tca ggc act tcc ttg gag gag gca ttg gag gcc cca	939
Leu Glu Ser Gly Ser Gly Thr Ser Leu Glu Glu Ala Leu Glu Ala Pro	
250 255 260	
gcc aca gac ctg gcc agg cct gag ttc tgt tac gag gct gag agc cct	987
Ala Thr Asp Leu Ala Arg Pro Glu Phe Cys Tyr Glu Ala Glu Ser Pro	
265 270 275 280	
gat gag gcc gcc ctg gtg cac gct gcc cat gcc tac agc ttc aca cta	1035
Asp Glu Ala Ala Leu Val His Ala Ala His Ala Tyr Ser Phe Thr Leu	
285 290 295	
gtg tcc cgg aca cct gag cag gtg act gtg cgc ctg ccc cag ggc acc	1083
Val Ser Arg Thr Pro Glu Gln Val Thr Val Arg Leu Pro Gln Gly Thr	
300 305 310	
tgc ctc acc ttc agc ctc ctc tgc acc ctg ggc ttt gac tct gtc agg	1131
Cys Leu Thr Phe Ser Leu Leu Cys Thr Leu Gly Phe Asp Ser Val Arg	
315 320 325	
aag aga atg tct gtg gtt gtg agg cac cca ctg act ggc gag att gtt	1179
Lys Arg Met Ser Val Val Arg His Pro Leu Thr Gly Glu Ile Val	
330 335 340	
gtc tac acc aag ggt gct gac tcg gtc atc atg gac ctg ctg gaa gac	1227
Val Tyr Thr Lys Gly Ala Asp Ser Val Ile Met Asp Leu Leu Glu Asp	
345 350 355 360	
cca gcc tgc gta cct gac att aat atg gaa aag aag ctg aga aaa atc	1275
Pro Ala Cys Val Pro Asp Ile Asn Met Glu Lys Lys Leu Arg Lys Ile	
365 370 375	
cga gcc cgg acc caa aag cat cta gac ttg tat gca aga gat ggc ctg	1323
Arg Ala Arg Thr Gln Lys His Leu Asp Leu Tyr Ala Arg Asp Gly Leu	
380 385 390	
cgc aca cta tgc att gcc aag aag gtt gta agc gaa gag gac ttc cgg	1371
Arg Thr Leu Cys Ile Ala Lys Lys Val Val Ser Glu Glu Asp Phe Arg	
395 400 405	

aga tgg gcc agt ttc cgg cgt gag gct gag gca tcc ctc gac aac cga	1419
Arg Trp Ala Ser Phe Arg Arg Glu Ala Glu Ala Ser Leu Asp Asn Arg	
410 415 420	
gat gag ctt ctc atg gaa act gca cag cat ctg gag aat caa ctc acc	1467
Asp Glu Leu Leu Met Glu Thr Ala Gln His Leu Glu Asn Gln Leu Thr	
425 430 435 440	
tta ctt gga gcc act ggg atc gaa gac cgg ctg cag gaa gga gtt cca	1515
Leu Leu Gly Ala Thr Gly Ile Glu Asp Arg Leu Gln Glu Gly Val Pro	
445 450 455	
gat acg att gcc act ctg cgg gag gct ggg atc cag ctc tgg gtc ctg	1563
Asp Thr Ile Ala Thr Leu Arg Glu Ala Gly Ile Gln Leu Trp Val Leu	
460 465 470	
act gga gat aag cag gag aca gcg gtc aac att gcc cat tcc tgc aga	1611
Thr Gly Asp Lys Gln Glu Thr Ala Val Asn Ile Ala His Ser Cys Arg	
475 480 485	
ctg tta aat cag acc gac act gtt tat acc atc aat aca gag aat cag	1659
Leu Leu Asn Gln Thr Asp Thr Val Tyr Thr Ile Asn Thr Glu Asn Gln	
490 495 500	
gag acc tgt gaa tcc atc ctc aat tgt gca ttg gaa gag cta aag caa	1707
Glu Thr Cys Glu Ser Ile Leu Asn Cys Ala Leu Glu Glu Leu Lys Gln	
505 510 515 520	
ttt cgt gaa cta cag aag cca gac cgc aag ctc ttt gga ttc cgc tta	1755
Phe Arg Glu Leu Gln Lys Pro Asp Arg Lys Leu Phe Gly Phe Arg Leu	
525 530 535	
cct tcc aag aca cca tcc atc acc tca gaa gct gtg gtt cca gaa gct	1803
Pro Ser Lys Thr Pro Ser Ile Thr Ser Glu Ala Val Val Pro Glu Ala	
540 545 550	
gga ttg gtc atc gat ggg aag aca ttg aat gcc atc ttc cag gga aag	1851
Gly Leu Val Ile Asp Gly Lys Thr Leu Asn Ala Ile Phe Gln Gly Lys	
555 560 565	
cta gag aag aag ttt ctg gaa ttg acc cag tat tgt cgg tcc gtc ctg	1899
Leu Glu Lys Lys Phe Leu Glu Leu Thr Gln Tyr Cys Arg Ser Val Leu	
570 575 580	
tgc tgc cgc tcc acg cca ctc cag aag agt atg ata gtc aag ctg gtg	1947
Cys Cys Arg Ser Thr Pro Leu Gln Lys Ser Met Ile Val Lys Leu Val	
585 590 595 600	
cga gac aag ttg cgc gtc atg acc ctt tcc ata ggt gat gga gca aat	1995
Arg Asp Lys Leu Arg Val Met Thr Leu Ser Ile Gly Asp Gly Ala Asn	
605 610 615	
gat gta agc atg att caa gct gct gat att gga att gga ata tct gga	2043
Asp Val Ser Met Ile Gln Ala Ala Asp Ile Gly Ile Gly Ile Ser Gly	
620 625 630	
cag gaa ggc atg cag gct gtc atg tcc agc gac ttt gcc atc acc cgc	2091

Gln	Glu	Gly	Met	Gln	Ala	Val	Met	Ser	Ser	Asp	Phe	Ala	Ile	Thr	Arg	
		635					640					645				
ttt	aag	cat	ctc	aag	aag	ttg	ctg	ctc	gtg	cat	ggc	cac	tgg	tgt	tac	2139
Phe	Lys	His	Leu	Lys	Lys	Leu	Leu	Leu	Val	His	Gly	His	Trp	Cys	Tyr	
	650					655					660					
tcg	cgc	ctg	gcc	agg	atg	gtg	gtg	tac	tac	ctc	tac	aag	aac	gtg	tgc	2187
Ser	Arg	Leu	Ala	Arg	Met	Val	Val	Tyr	Tyr	Leu	Tyr	Lys	Asn	Val	Cys	
	665				670					675					680	
tac	gtc	aac	ctg	ctc	ttc	tgg	tat	cag	ttc	ttc	tgt	ggc	ttc	tcc	agc	2235
Tyr	Val	Asn	Leu	Leu	Phe	Trp	Tyr	Gln	Phe	Phe	Cys	Gly	Phe	Ser	Ser	
				685					690					695		
tcc	acc	atg	att	gat	tac	tgg	cag	atg	ata	ttc	ttc	aat	ctc	ttc	ttt	2283
Ser	Thr	Met	Ile	Asp	Tyr	Trp	Gln	Met	Ile	Phe	Phe	Asn	Leu	Phe	Phe	
			700					705					710			
acc	tcc	ttg	cct	cct	ctt	gtc	ttt	gga	gtc	ctt	gac	aaa	gac	atc	tct	2331
Thr	Ser	Leu	Pro	Pro	Leu	Val	Phe	Gly	Val	Leu	Asp	Lys	Asp	Ile	Ser	
		715					720					725				
gca	gaa	aca	ctc	ctg	gca	ttg	cct	gag	cta	tac	aag	agt	ggc	cag	aac	2379
Ala	Glu	Thr	Leu	Leu	Ala	Leu	Pro	Glu	Leu	Tyr	Lys	Ser	Gly	Gln	Asn	
	730					735					740					
tct	gag	tgc	tat	aac	ctg	tcg	act	ttc	tgg	att	tct	atg	gtg	gat	gca	2427
Ser	Glu	Cys	Tyr	Asn	Leu	Ser	Thr	Phe	Trp	Ile	Ser	Met	Val	Asp	Ala	
	745				750					755					760	
ttc	tac	cag	agc	ctc	atc	tgt	ttc	ttt	atc	cct	tac	ctg	gcc	tat	aag	2475
Phe	Tyr	Gln	Ser	Leu	Ile	Cys	Phe	Phe	Ile	Pro	Tyr	Leu	Ala	Tyr	Lys	
				765					770					775		
ggc	tct	gat	ata	gat	gtc	ttt	acc	ttt	ggg	aca	cca	atc	aac	acc	atc	2523
Gly	Ser	Asp	Ile	Asp	Val	Phe	Thr	Phe	Gly	Thr	Pro	Ile	Asn	Thr	Ile	
			780					785					790			
tcc	ctc	acc	aca	atc	ctt	ttg	cac	cag	gca	atg	gaa	atg	aag	aca	tgg	2571
Ser	Leu	Thr	Thr	Ile	Leu	Leu	His	Gln	Ala	Met	Glu	Met	Lys	Thr	Trp	
		795					800					805				
acc	att	ttc	cac	gga	gtc	gtg	ctc	ctc	ggc	agc	ttc	ctg	atg	tac	ttt	2619
Thr	Ile	Phe	His	Gly	Val	Val	Leu	Leu	Gly	Ser	Phe	Leu	Met	Tyr	Phe	
	810					815					820					
ctg	gta	tcc	ctc	ctg	tac	aat	gcc	acc	tgc	gtc	atc	tgc	aac	agc	ccc	2667
Leu	Val	Ser	Leu	Leu	Tyr	Asn	Ala	Thr	Cys	Val	Ile	Cys	Asn	Ser	Pro	
	825				830					835					840	
acc	aat	ccc	tat	tgg	gtg	atg	gaa	ggc	cag	ctc	tca	aac	ccc	act	ttc	2715
Thr	Asn	Pro	Tyr	Trp	Val	Met	Glu	Gly	Gln	Leu	Ser	Asn	Pro	Thr	Phe	
				845					850					855		
tac	ctc	gtc	tgc	ttt	ctc	aca	cca	gtt	gtt	gct	ctt	ctc	cca	aga	tac	2763
Tyr	Leu	Val	Cys	Phe	Leu	Thr	Pro	Val	Val	Ala	Leu	Leu	Pro	Arg	Tyr	

860	865	870	
ttt ttc ctg tct ctg caa gga act tgt ggg aag tct cta atc tca aaa			2811
Phe Phe Leu Ser Leu Gln Gly Thr Cys Gly Lys Ser Leu Ile Ser Lys			
875	880	885	
gct cag aaa att gac aaa ctc ccc cca gac aaa aga aac ctg gaa atc			2859
Ala Gln Lys Ile Asp Lys Leu Pro Pro Asp Lys Arg Asn Leu Glu Ile			
890	895	900	
cag agt tgg aga agc aga cag agg cct gcc cct gtc ccc gaa gtg gct			2907
Gln Ser Trp Arg Ser Arg Gln Arg Pro Ala Pro Val Pro Glu Val Ala			
905	910	915	920
cga cca act cac cac cca gtg tca tct atc aca gga cag gac ttc agt			2955
Arg Pro Thr His His Pro Val Ser Ser Ile Thr Gly Gln Asp Phe Ser			
	925	930	935
gcc agc acc cca aag agc tct aac cct ccc aag agg aag cat gtg gaa			3003
Ala Ser Thr Pro Lys Ser Ser Asn Pro Pro Lys Arg Lys His Val Glu			
	940	945	950
gag tca gta ctc cac gaa cag aga tgt ggc acg gag tgc atg agg gat			3051
Glu Ser Val Leu His Glu Gln Arg Cys Gly Thr Glu Cys Met Arg Asp			
	955	960	965
gac tca tgc tca ggg gac tcc tca gct caa ctc tca tcc ggg gag cac			3099
Asp Ser Cys Ser Gly Asp Ser Ser Ala Gln Leu Ser Ser Gly Glu His			
	970	975	980
ctg ctg gga cct aac agg ata atg gcc tac tca aga gga cag act gat			3147
Leu Leu Gly Pro Asn Arg Ile Met Ala Tyr Ser Arg Gly Gln Thr Asp			
985	990	995	1000
atg tgc cgg tgc tca aag agg agc agc cat cgc cga tcc cag agt tca			3195
Met Cys Arg Cys Ser Lys Arg Ser Ser His Arg Arg Ser Gln Ser Ser			
	1005	1010	1015
ctg acc ata tga gga gctgcagaaa tctgtacaaa ctcaacagag gccacctagt			3250
Leu Thr Ile *			
	1020		
cactgggtcca cataaccctt gacccttct tcttcataga ggaaacaatg tgccagtctt			3310
attctttttct tcaacaacct tgacttccat ggaggaagtg ctggccccaa ggggtctgac			3370
acaaagacgg gaaaccctagt cggcctctag ttttctgctg ctctcaggca gcacatcttg			3430
caaacagttt ggagaaggag gctgtttttg ttgaatcgag ttctcaaadc ggttttagacc			3490
aaagccattc ttctgaccct ctagataagc gtagcctaca acccagtgcc gtaagtttcc			3550
aagattcaag aagtgtatca acccaggcaa tatctcagga tatggaagtt tctgggttta			3610
tttacccttc agtgcccaga gttaaagttt cagaagagac ttgtgcacat aagggttca			3670
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ttggttctgc tttttgctg taagccaaag aaaa

3764

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<211> 614
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (361)..(462)

<400> 292

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gtccaatggc aatttgttca cctctaattt ttataatcat agtttagggg tgtgggctaaa	180
agcacaaact ctggaactag actgctagat atataatctt gggtatgctg tttgattgct	240
ctgggtactct gtacctcaat tttcaccagt taaatgcaga tttaggggtgg gtagttgtga	300
ggattaaaaat gtatgggtat accttagaaa ggtgccaaat atggctgggt gtggtggctc	360
atg tct gta atc cca acc cct tgg aag gcc gag gcg ggt ggc tca caa	408
Met Ser Val Ile Pro Thr Pro Trp Lys Ala Glu Ala Gly Gly Ser Gln	
1 5 10 15	
ggt cag gag atc aag acc act ctg gcc aac acg gtg aaa cac cgt ctc	456
Gly Gln Glu Ile Lys Thr Thr Leu Ala Asn Thr Val Lys His Arg Leu	
20 25 30	
cac taa aaatacaaaa tacaataaat tacaataata caaagtacaa aaaatacaaa	512
His *	
aaatacaaaa tactgaaaat actaaaaatt agccgggcat agtggcacgt gcctatagtc	572
ccagctactt gggaatctgc ggacgcgtgg gtcgacccgg gt	614

<210> 293
<211> 830
<212> DNA
<213> Homo sapiens

<220>
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<222> (219)..(467)

<400> 293

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cgaagcaggg ttccgagtc attcgaactg ccatctgatc cgctcttatc aatgaagcag      120
ccgatcatgg cggatggggc ccggtgcaag aggcgcaaac aagccaatcc caggaggaaa      180
aacgccttgg agtcagaaat gagcactcgg agcggggag      atg ccc tgc tgc tgc      233
                               Met Pro Cys Cys Cys
                               1                               5

ttg cca ccg gtg cgg ccc gtt tgt aac ttg caa agt ttg ttg ctt ttg      281
Leu Pro Pro Val Arg Pro Val Cys Asn Leu Gln Ser Leu Leu Leu Leu
                               10                               15                               20

ccc ctg att cgg gca gcg ggt cct ggg atg ctc ctg ctt ccc tcc tgc      329
Pro Leu Ile Arg Ala Ala Gly Pro Gly Met Leu Leu Leu Pro Ser Cys
                               25                               30                               35

ctc cca cgg agc ccg gga aga ggg tct gcc tcc cca tcc cgc cac ctt      377
Leu Pro Arg Ser Pro Gly Arg Gly Ser Ala Ser Pro Ser Arg His Leu
                               40                               45                               50

cca gca tca gcc tct gaa aaa tct cac aga gac atg cac gtt gta gca      425
Pro Ala Ser Ala Ser Glu Lys Ser His Arg Asp Met His Val Val Ala
                               55                               60                               65

aaa atc aaa tcc gga aac tgc ttg ttt cag aga aag aaa tga agttgtc      474
Lys Ile Lys Ser Gly Asn Cys Leu Phe Gln Arg Lys Lys *
                               70                               75                               80

ttttaaagaa aaactgaatt aggaggagag aaaagggaaa taggagaaga aaggaaaagt      534
taaatttgat ttttctccag agtttccact aaagggttgg ggacagtgtg aaggagaagg      594
ggagcttttt acaaatacct ttggtctctg aacttcagtg gcaaagaaca gggatcaagt      654
tgaatgttct cagggctttg gacccatagag gagaaacaat cagaagagca gaaatggtta      714
tccctgttta aaataagccc tcactcttta ccacttcctt aaaggagtgg aggtgctggt      774
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<210> 294
 <211> 757
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (493)..(735)

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<400> 294
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acgaggcaac ctcgaggaaa ccacccttat aatggccaag aacaggattg acgattacaa 120
tctcagctgg cctgtcatat aaaacatact gtcattgagc ttaagctccg cttgttctga 180
ggtttcacct ccatgtgttt cattgggtgca aaagtggatc tcttagttgg tcacttaatt 240
ctttcttttt cagaaagata ggatgttcac tggatatattt ggtcactctt agaaccttcc 300
ttcacattgt tttttatggg acccatgaat ggtagcctt tcttttctat tgtagaagga 360
aataaatagg agtaaaaaga ccattgtagt aaataagttc aaggggaact tgggaccaga 420
aaccactggt atgtacaaaa aaatggcaaa ttcaataaac tcaaatttaa aataattttt 480
aaattaacag tt      atg ata aat ttt ata ttt tat aca aat aga ttg ctt 528
                   Met Ile Asn Phe Ile Phe Tyr Thr Asn Arg Leu Leu
                   1             5             10

aga atg gtt ctc aag aat tat aag aga aat gaa ctc aca gta caa aaa 576
Arg Met Val Leu Lys Asn Tyr Lys Arg Asn Glu Leu Thr Val Gln Lys
      15             20             25

ttt tat aat tac tat act tgt gtt ttg ttt ggg ggc tgg gaa atg tat 624
Phe Tyr Asn Tyr Tyr Thr Cys Val Leu Phe Gly Gly Trp Glu Met Tyr
      30             35             40

ttt tac att gta gcc aat cat ttt ata ttt gtc aat tta aat ctt atg 672
Phe Tyr Ile Val Ala Asn His Phe Ile Phe Val Asn Leu Asn Leu Met
      45             50             55             60

ggg ctt ttt ttt tta tct ctc ttg atg tca gat ttt ata gtc ttt tta 720
Gly Leu Phe Phe Leu Ser Leu Leu Met Ser Asp Phe Ile Val Phe Leu
      65             70             75

aat aaa tcc att taa ttaaaacggt aaaaaaaaaa aa 757
Asn Lys Ser Ile *
      80

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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (125)..(1258)

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caagcaactg gattgaacac cctaagaaga aagattcaca ctgcaccagg agacatcaga 120
aaga atg aaa act ctg ccg ctg ttt gtg tgc atc tgt gca ctg agt gct 169

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Met	Lys	Thr	Leu	Pro	Leu	Phe	Val	Cys	Ile	Cys	Ala	Leu	Ser	Ala		
1				5					10					15		
tgc	ttc	tcg	ttc	agt	gaa	ggt	cga	gaa	agg	gat	cat	gaa	cta	cgt	cac	217
Cys	Phe	Ser	Phe	Ser	Glu	Gly	Arg	Glu	Arg	Asp	His	Glu	Leu	Arg	His	
				20					25					30		
aga	agg	cat	cat	cac	caa	tca	ccc	aaa	tct	cac	ttt	gaa	tta	cca	cat	265
Arg	Arg	His	His	His	Gln	Ser	Pro	Lys	Ser	His	Phe	Glu	Leu	Pro	His	
				35					40					45		
tat	cct	gga	ctg	cta	gct	cac	cag	aag	ccg	ttc	att	aga	aag	tcc	tat	313
Tyr	Pro	Gly	Leu	Leu	Ala	His	Gln	Lys	Pro	Phe	Ile	Arg	Lys	Ser	Tyr	
		50					55					60				
aaa	tgt	ctg	cac	aaa	cgc	tgt	agg	cct	aag	ctt	cca	cct	tca	cct	aat	361
Lys	Cys	Leu	His	Lys	Arg	Cys	Arg	Pro	Lys	Leu	Pro	Pro	Ser	Pro	Asn	
	65					70					75					
aac	ccc	ccc	aaa	ttc	cca	aat	cct	cac	cag	cca	cct	aaa	cat	cca	gat	409
Asn	Pro	Pro	Lys	Phe	Pro	Asn	Pro	His	Gln	Pro	Pro	Lys	His	Pro	Asp	
	80					85				90					95	
aaa	aat	agc	agt	gtg	gtc	aac	cct	acc	tta	gtg	gct	aca	acc	caa	att	457
Lys	Asn	Ser	Ser	Val	Val	Asn	Pro	Thr	Leu	Val	Ala	Thr	Thr	Gln	Ile	
				100					105					110		
cca	tct	gtg	act	ttc	cca	tca	gct	tcc	acc	aaa	att	act	acc	ctt	cca	505
Pro	Ser	Val	Thr	Phe	Pro	Ser	Ala	Ser	Thr	Lys	Ile	Thr	Thr	Leu	Pro	
			115					120					125			
aat	gtg	act	ttt	ctt	ccc	cag	aat	gcc	acc	acc	ata	tct	tca	aga	gaa	553
Asn	Val	Thr	Phe	Leu	Pro	Gln	Asn	Ala	Thr	Thr	Ile	Ser	Ser	Arg	Glu	
		130					135					140				
aat	gtt	aac	aca	agc	tct	tct	gta	gct	aca	tta	gca	cca	gtg	aat	tcc	601
Asn	Val	Asn	Thr	Ser	Ser	Ser	Val	Ala	Thr	Leu	Ala	Pro	Val	Asn	Ser	
	145					150					155					
cca	gct	cca	caa	gac	acc	aca	gct	gcc	cca	ccc	aca	cct	tct	gca	act	649
Pro	Ala	Pro	Gln	Asp	Thr	Thr	Ala	Ala	Pro	Pro	Thr	Pro	Ser	Ala	Thr	
	160				165					170					175	
aca	cca	gct	cca	cca	tct	tcc	tca	gct	cca	cca	gag	acc	aca	gct	gcc	697
Thr	Pro	Ala	Pro	Pro	Ser	Ser	Ser	Ala	Pro	Pro	Glu	Thr	Thr	Ala	Ala	
				180					185					190		
cca	ccc	aca	cct	tct	gca	act	aca	caa	gct	cca	cca	tct	tcc	tca	gct	745
Pro	Pro	Thr	Pro	Ser	Ala	Thr	Thr	Gln	Ala	Pro	Pro	Ser	Ser	Ser	Ala	
			195					200					205			
cca	cca	gag	acc	aca	gct	gcc	cca	ccc	aca	cct	cct	gca	act	aca	caa	793
Pro	Pro	Glu	Thr	Thr	Ala	Ala	Pro	Pro	Thr	Pro	Pro	Ala	Thr	Thr	Gln	
		210					215					220				
gct	cca	cca	tct	tcc	tca	gct	cca	cca	gag	acc	aca	gct	gcc	cca	ccc	841
Ala	Pro	Pro	Ser	Ser	Ser	Ala	Pro	Pro	Glu	Thr	Thr	Ala	Ala	Pro	Pro	

225	230	235	
aca cct cct gca act	aca cca gct cca cca tct tcc tca gct cca cca		889
Thr Pro Pro Ala Thr	Thr Pro Ala Pro Pro Ser Ser Ser Ala Pro Pro		
240	245	250	255
gag acc aca gct gtc cca ccc aca cct tct gca act acc cta gac cca			937
Glu Thr Thr Ala Val	Pro Pro Thr Pro Ser Ala Thr Thr Leu Asp Pro		
260	265		270
tca tcc gcc tca gct cca cca gag acc aca gct gcc cca ccc aca cct			985
Ser Ser Ala Ser Ala	Pro Pro Glu Thr Thr Ala Ala Pro Pro Thr Pro		
275	280		285
tct gca act aca cca gct cca ccg tct tcc cca gct cca caa gag acc			1033
Ser Ala Thr Thr	Pro Ala Pro Ser Ser Pro Ala Pro Gln Glu Thr		
290	295		300
aca gct gcc cca att acc aca cct aat tct tcc cca act act ctt gca			1081
Thr Ala Ala Pro Ile Thr	Thr Pro Asn Ser Ser Pro Thr Thr Leu Ala		
305	310		315
cct gac act tct gaa act tca gct gca ccc aca cac cag act act act			1129
Pro Asp Thr Ser Glu Thr	Ser Ala Ala Pro Thr His Gln Thr Thr Thr		
320	325		330
tcg gtc act act caa act act act act aaa caa cca act tca gct cct			1177
Ser Val Thr Thr Gln Thr Thr Thr Thr Lys Gln Pro Thr Ser Ala Pro			
340	345		350
ggc caa aat aaa att tct cga ttt ctt tta tat atg aag aat cta cta			1225
Gly Gln Asn Lys Ile Ser Arg Phe Leu Leu Tyr Met Lys Asn Leu Leu			
355	360		365
aac aga att att gac gac atg gtg gag caa tag tatattgt atgttgtaaa			1276
Asn Arg Ile Ile Asp Asp Met Val Glu Gln *			
370	375		
gtgttctgtc atttacaaga tgtgattcat gagtgcagaa ctaccacctt tcttttagca			1336
ccaatcccaa catgaaatta tattactcag atttaaagca ctatcattaa tctttcaatc			1396
taattattca ccaccacaag acctattaac aagacaaaat gcctctatcc cacaagccag			1456
atgcaggtct ggggttcaaa ataactcttt ggatcctaca gagatagcct actgagggca			1516
gagaaagtcc ttagataaag agagaatatt gtatgggcca tcaaccattt acttttccct			1576
gaatgttaga aactacaaaa ccactacctt gtaccccat caaaatccca cctgaaccat			1636
ctaatectat aaacataaag gggtaaaatt ggaactctcc agatgaacaa agacatctaa			1696
atatctgtag atagaaacat ttatctatct aaatatattg atagacctgt cattgtattg			1756
attaatgaca aaacccttta gataattatc ttccatttta aataaaattt tatttcacaa			1816
atatgagcca agaaagagga aagttgattt gaagtgagga ttagaagtga atgacaataa			1876

Lys Val Thr His His Ile Gly Pro Ser Ile Leu Ala Leu Tyr Gln Asn
70 75 80

gtg gat aag cat cca gac tat gct tga caaat acaaatagca tccaatatta 469
Val Asp Lys His Pro Asp Tyr Ala *
85 90

acacagaatt tccatggttt acaatagcag tggtaatccc aaatcatcct gtgaacgtct 529
cctggaatga ctccatagcc acacagaacc acatatggct tcagatagcc atggccctat 589
ttcacttttg tgctgcacca gctgagacct cagctgtagc aaccctcctc tgtccaccta 649
atgccgttta aagcccagcc cctggatttg tgaaccaaat cacatctact atcacagatg 709
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ctccagaacc cccatcctct gggctctttt taggccccta gattggcctg cagctgggag 180
cagagtggca agcatgcagg caggcagttg agaaagagga agtcgaggtg ctattgggtc 240
attctgtggt tatcccaggc tctaccagc cagcggttcc cttgggccag ctcgaaacgc 300
tggccgtagg tcatgggagc tgcaggagct gttagccagg ctagggtgcct gcaggttgaa 360
gaactgagct ctatctggct ctgagcccaa gtcattgtgc cagccttttg actctggagc 420
tgtggcttca gccaccaaga gcagcagtg atcctggaaa cctgagaacc cagacttctt 480
ctctgccatg gggg atg atc agg agg atg att ttc cca ggc ggc tca gcg 530
Met Ile Arg Arg Met Ile Phe Pro Gly Gly Ser Ala
1 5 10

aga gta tgg agg acc tca gcc tgg att tgg ggg ccc ttc agg gca gcg 578
Arg Val Trp Arg Thr Ser Ala Trp Ile Trp Gly Pro Phe Arg Ala Ala
15 20 25

agt atc tgc agg acc tgg gcc ttg ggg ccc ctt ccc aca gcc agc ctg 626

Ser Ile Cys Arg Thr Trp Ala Leu Gly Pro Leu Pro Thr Ala Ser Leu	
30 35 40	
ggg aga ccc cag aca gcc gcc cca ccg gtg aag aac cag gaa gag att	674
Gly Arg Pro Gln Thr Ala Ala Pro Pro Val Lys Asn Gln Glu Glu Ile	
45 50 55 60	
ctc ttt tct cca gct tgg cag ggt ccc aag acc tgt caa ggc ggc gca	722
Leu Phe Ser Pro Ala Trp Gln Gly Pro Lys Thr Cys Gln Gly Gly Ala	
65 70 75	
act ggg aaa ggt cgc gga gct gct cac aga gct ggc gga ggc tca acc	770
Thr Gly Lys Gly Arg Gly Ala Ala His Arg Ala Gly Gly Gly Ser Thr	
80 85 90	
tcg atg cct cag ctg tgg atg agg aac cct gtc tcc ccc gaa cac tgg	818
Ser Met Pro Gln Leu Trp Met Arg Asn Pro Val Ser Pro Glu His Trp	
95 100 105	
cca gcc ttg ctt tga acctgccagg aggagggctg aagacctgga ctcaaggggtg	873
Pro Ala Leu Leu *	
110	
tctctctggg	883
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tgg gac gga aac agc caa gta gga att gga gac tac aga att cct aag	98
Trp Asp Gly Asn Ser Gln Val Gly Ile Gly Asp Tyr Arg Ile Pro Lys	
15 20 25	
gcg atg ctc aca ttc ttg aat gga agt aga att cct gtc act gag aaa	146
Ala Met Leu Thr Phe Leu Asn Gly Ser Arg Ile Pro Val Thr Glu Lys	
30 35 40	
gca cct cat aaa gga att att aga gat tca acc tgt aag tac ctt cca	194
Ala Pro His Lys Gly Ile Ile Arg Asp Ser Thr Cys Lys Tyr Leu Pro	
45 50 55 60	
gag tgg cag agc tat cag tgc ttt ggg atg gaa tat gca atg atg gtt	242
Glu Trp Gln Ser Tyr Gln Cys Phe Gly Met Glu Tyr Ala Met Met Val	
65 70 75	

att gaa agt ctg gat cct gac aca gaa act cga aga ctt tcc cca gtg Ile Glu Ser Leu Asp Pro Asp Thr Glu Thr Arg Arg Leu Ser Pro Val 80 85 90	290
gct ata atg ggc aac ggt tat gtt gat ctt att aat ggc cca cag gat Ala Ile Met Gly Asn Gly Tyr Val Asp Leu Ile Asn Gly Pro Gln Asp 95 100 105	338
cat ggc tgg tgt gct gga tat aca tgc cag aga agg ctg tcc ctg ttt His Gly Trp Cys Ala Gly Tyr Thr Cys Gln Arg Arg Leu Ser Leu Phe 110 115 120	386
cac agc att gtg gct ctg aac aaa tct tat gaa gtt tac ttc act ggc His Ser Ile Val Ala Leu Asn Lys Ser Tyr Glu Val Tyr Phe Thr Gly 125 130 135 140	434
acc agt cct cag aat ctt cga ctg atg ttg ctt aat gtt gat cat aac Thr Ser Pro Gln Asn Leu Arg Leu Met Leu Leu Asn Val Asp His Asn 145 150 155	482
aag gct gtt cta gta gga att ttc ttt tcc aca ctt caa cgt ttg gat Lys Ala Val Leu Val Gly Ile Phe Phe Ser Thr Leu Gln Arg Leu Asp 160 165 170	530
gtc tat gtg aac aac tta ttg gtc tgt cca aaa act aca ata tgg aat Val Tyr Val Asn Asn Leu Leu Val Cys Pro Lys Thr Thr Ile Trp Asn 175 180 185	578
gcc cag cag aaa cac tgt gaa ctt aat aac cat ctg tac aaa gac caa Ala Gln Gln Lys His Cys Glu Leu Asn Asn His Leu Tyr Lys Asp Gln 190 195 200	626
ttc ctt cct aac ctg gat tcc act gtc ctt ggt gaa aac tac ttt gat Phe Leu Pro Asn Leu Asp Ser Thr Val Leu Gly Glu Asn Tyr Phe Asp 205 210 215 220	674
gga acc tac cag atg ctt tat ctt ttg gtt aaa gga act ata cct gtt Gly Thr Tyr Gln Met Leu Tyr Leu Leu Val Lys Gly Thr Ile Pro Val 225 230 235	722
gaa att cac act gcc aca gtg ata ttt gtt tct ttc caa tta tct gtt Glu Ile His Thr Ala Thr Val Ile Phe Val Ser Phe Gln Leu Ser Val 240 245 250	770
gca aca gaa gat gac ttt tat acc tct cac aat ctg gtt aaa aat ctt Ala Thr Glu Asp Asp Phe Tyr Thr Ser His Asn Leu Val Lys Asn Leu 255 260 265	818
gcc ttg ttc cta aag ata cca agt gac aaa atc cgt atc agc aaa ata Ala Leu Phe Leu Lys Ile Pro Ser Asp Lys Ile Arg Ile Ser Lys Ile 270 275 280	866
aga ggg aag agt ctg agg agg aag aga tcc atg gga ttc ata att gaa Arg Gly Lys Ser Leu Arg Arg Lys Arg Ser Met Gly Phe Ile Ile Glu 285 290 295 300	914

ata Ile	gag Glu	att Ile	gga Gly	gac Asp 305	cct Pro	cct Pro	att Ile	cag Gln	ttc Phe 310	ata Ile	agc Ser	aat Asn	ggc Gly	acc Thr 315	aca Thr	962
ggt Gly	cag Gln	atg Met	cag Gln 320	tta Leu	tct Ser	gaa Glu	ctc Leu	cag Gln 325	gaa Glu	att Ile	gct Ala	ggt Gly	tct Ser 330	ctt Leu	gga Gly	1010
caa Gln	gct Ala	gta Val 335	att Ile	tta Leu	gga Gly	aac Asn	atc Ile 340	agt Ser	agt Ser	atc Ile	ctt Leu	gga Gly 345	ttt Phe	aac Asn	att Ile	1058
tcg Ser	tcc Ser	atg Met 350	tct Ser	att Ile	act Thr	aat Asn 355	ccc Pro	ctc Leu	ccc Pro	agc Ser	cca Pro 360	agt Ser	gac Asp	tct Ser	ggg Gly	1106
tgg Trp 365	att Ile	aat Asn	gtg Val	act Thr 370	gcc Ala	cag Gln	cca Pro	gtt Val	gaa Glu	agg Arg 375	tct Ser	gca Ala	ttt Phe	cct Pro	gtt Val 380	1154
cat His	cac His	gtg Val	gcc Ala	ttc Phe 385	gtg Val	tcc Ser	tca Ser	ctc Leu	tta Leu 390	gtg Val	atc Ile	act Thr	cag Gln	ccg Pro 395	gtg Val	1202
gca Ala	gca Ala	cag Gln	cca Pro 400	gga Gly	cag Gln	cca Pro	ttt Phe	cct Pro 405	cag Gln	cag Gln	cct Pro	tcg Ser	gta Val 410	aag Lys	gca Ala	1250
aca Thr	gat Asp	tct Ser 415	gac Asp	ggg Gly	aac Asn	tgt Cys	gta Val 420	tca Ser	gtt Val	gga Gly	att Ile	act Thr 425	gca Ala	cta Leu	act Thr	1298
ttg Leu	agg Arg 430	gcc Ala	ata Ile	ctc Leu	aag Lys	gac Asp 435	tcc Ser	aat Asn	aat Asn	aac Asn	caa Gln 440	gtc Val	aat Asn	ggc Gly	ctt Leu	1346
agt Ser 445	gga Gly	aat Asn	aca Thr	aca Thr 450	att Ile	ccg Pro	ttt Phe	agc Ser	agc Ser	tgt Cys 455	tgg Trp	gcc Ala	aac Asn	tac Tyr	aca Thr 460	1394
gac Asp	ctt Leu	act Thr	ccc Pro	ctt Leu 465	aga Arg	aca Thr	gga Gly	aaa Lys	aat Asn 470	tat Tyr	aag Lys	att Ile	gaa Glu	ttt Phe 475	ata Ile	1442
ctg Leu	gat Asp	aat Asn	gtt Val 480	gtt Val	ggg Gly	gta Val	gaa Glu	tcc Ser 485	aga Arg	act Thr	ttc Phe	agc Ser	ctg Leu 490	ctg Leu	gca Ala	1490
gag Glu	tct Ser	gtc Val 495	tct Ser	agc Ser	agt Ser	ggc Gly	agc Ser 500	agc Ser	agc Ser	agc Ser	agc Ser	aac Asn 505	agc Ser	aaa Lys	gca Ala	1538
tca Ser	act Thr 510	gtg Val	ggt Gly	aca Thr	tat Tyr	gcc Ala 515	cag Gln	ata Ile	atg Met	act Thr 520	gta Val	gta Val	att Ile	agc Ser	tgt Cys	1586
ctg	gtt	gga	aga	atg	tgg	ctc	ttg	gaa	ata	ttt	atg	gct	gca	gtt	tca	1634

Leu Val Gly Arg Met Trp Leu Leu Glu Ile Phe Met Ala Ala Val Ser
525 530 535 540

act ttg aat ata act tta aga agc tac taa a gtgctgttcc gaagaatagg 1685
Thr Leu Asn Ile Thr Leu Arg Ser Tyr *
545 550

ctgaaacaaa aatataagaa ttattagcta ctttggtggg caataggcaa aagtctatag 1745
cattttcatg aaaatataact aaaaatattt ttatgatata taaaatgtac taattagctt 1805
taaacactaa aatcagattt cttcaaaata taaatttgtt ttgattcttt atatttatat 1865
gtttttattt catttcaata aacttccaga aatttgtcat ttgaaaaaaaa aaaaa 1920

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<212> DNA
<213> Homo sapiens

<220>
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<222> (191)..(379)

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ggtgaggcca tcacttcatc cagtgactag caccacctct ggcaatgtca gccccacact 180
cgcccgcgcc atg gcc tcc atc tcc gag ctt gcc tgt gtc tac ttg gcc 229
Met Ala Ser Ile Ser Glu Leu Ala Cys Val Tyr Leu Ala
1 5 10

ctc att ctg cac gat gac gag gtg atc atc atg gag gtt aat atc aat 277
Leu Ile Leu His Asp Asp Glu Val Ile Ile Met Glu Val Asn Ile Asn
15 20 25

acc ctc att aaa gca gcc agt gta aat gtt gaa cct ttt ggc ctg gct 325
Thr Leu Ile Lys Ala Ala Ser Val Asn Val Glu Pro Phe Gly Leu Ala
30 35 40 45

tgt ttg gaa agg ccc tgg cca acg tca aca ttg gaa gcc tca tct gca 373
Cys Leu Glu Arg Pro Trp Pro Thr Ser Thr Leu Glu Ala Ser Ser Ala
50 55 60

atg tag gggctggtgg acctgctcta gcagctggtg ctgcaccagc aggaggtcct 429
Met *

gccccctcca ttgctgctgc ttcagctgag gagaagaaaa tggaagcaaa gaaagaagaa 489

tctgaggagt ctgatgatga catgggcttt ggtcttttta ctaaacctgt tttataatgt 549

Case	Age	Sex	Duration of illness (years)	Onset	Course	Outcome
1	25	M	10	1975	Progressive	Death
2	30	F	5	1978	Progressive	Death
3	35	M	3	1980	Progressive	Death
4	40	F	2	1982	Progressive	Death
5	45	M	1	1985	Progressive	Death
6	50	F	6	1979	Progressive	Death
7	55	M	4	1981	Progressive	Death
8	60	F	3	1983	Progressive	Death
9	65	M	2	1984	Progressive	Death
10	70	F	1	1986	Progressive	Death
11	75	M	8	1977	Progressive	Death
12	80	F	7	1976	Progressive	Death
13	85	M	5	1980	Progressive	Death
14	90	F	4	1982	Progressive	Death
15	95	M	3	1984	Progressive	Death
16	100	F	2	1986	Progressive	Death

573

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<220>
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<222> (247)..(1245)
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633

Lys Glu Gln Leu Ala Glu Leu Arg Gln Glu Phe Leu Arg Gln Glu Asp	
130 135 140	
cag ctt cag gac tat agg aag aac aat act tac ctt gtg aag agg tta	720
Gln Leu Gln Asp Tyr Arg Lys Asn Asn Thr Tyr Leu Val Lys Arg Leu	
145 150 155	
gaa tat gaa agt ttt cag tgt gga cag cag atg aag gaa ttg aga gca	768
Glu Tyr Glu Ser Phe Gln Cys Gly Gln Gln Met Lys Glu Leu Arg Ala	
160 165 170	
cag cat gaa gaa aat att aaa aag tta gca gac cag ttt tta gag gaa	816
Gln His Glu Glu Asn Ile Lys Lys Leu Ala Asp Gln Phe Leu Glu Glu	
175 180 185 190	
caa aag caa gag acc caa aag att caa tca aat gat gga aag gaa ttg	864
Gln Lys Gln Glu Thr Gln Lys Ile Gln Ser Asn Asp Gly Lys Glu Leu	
195 200 205	
gat ata aac aat caa gta gta cct aaa aat att cca aaa gta gct gag	912
Asp Ile Asn Asn Gln Val Val Pro Lys Asn Ile Pro Lys Val Ala Glu	
210 215 220	
aat gtt gca gat aag aat gaa gaa ccc tca agc aat cat att cca cat	960
Asn Val Ala Asp Lys Asn Glu Glu Pro Ser Ser Asn His Ile Pro His	
225 230 235	
ggg aaa gaa caa atc aaa aga ggt ggt gat gca ggg atg cct gga ata	1008
Gly Lys Glu Gln Ile Lys Arg Gly Gly Asp Ala Gly Met Pro Gly Ile	
240 245 250	
gaa gag aat gac cta gca aaa gtt gat gat ctt ccc cct gct tta agg	1056
Glu Glu Asn Asp Leu Ala Lys Val Asp Asp Leu Pro Pro Ala Leu Arg	
255 260 265 270	
aag cct cct att tca gtt tct caa cat gaa agt cat caa gca atc tcc	1104
Lys Pro Pro Ile Ser Val Ser Gln His Glu Ser His Gln Ala Ile Ser	
275 280 285	
cat ctt cca act gga caa gct ctc tcc cca aat atg cct cca gat tca	1152
His Leu Pro Thr Gly Gln Ala Leu Ser Pro Asn Met Pro Pro Asp Ser	
290 295 300	
cac att aaa cac aat gga aac ccc ggt act tca aaa aca gaa tcc ttc	1200
His Ile Lys His Asn Gly Asn Pro Gly Thr Ser Lys Thr Glu Ser Phe	
305 310 315	
cag tcc tct tca gcg ttt aat tcc agg ctc aaa ctt gga cag tag aac	1248
Gln Ser Ser Ser Ala Phe Asn Ser Arg Leu Lys Leu Gly Gln *	
320 325 330	
ccagaaattc caaacagatt atactaaagg caggttacca aggacagaag ccggggattc	1308
ccataaaatt ggcaccaatg tgaacacaga gagctcgtaa actgggtcct ggaccttggc	1368
agcacgcttc accgacgtcc tcaaaacca gaggacacac tcgaaaacga aaagggggcg	1428

aaccgcaaca cccacggccc ccccgacccg gaagggacga aagacaggggt acaccaggac 1488
acacaaaatg gcaaaacaaa ggcaacacgc tccaagaaag aacagccata cacaaaagaa 1548
caaaagcgcac cacaccaaac aaccccgcac gaaccaacac cacaccaaga catgtcaaca 1608
aacaagacca cataggagac gacaacgcaa agacaccgat cgagtaaccc caaagccacc 1668
aaaccaccaa cggacaccca ctgccagcc tgtatcattc ctactagaca 1718

<210> 301
<211> 423
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (178)..(348)

<400> 301
tcttttcaca tgattactgg ccatttgtat accttctgtg gaaatgtgggt aacacccttt 60
gctgatttta aaatagggtt atttgtttat tattgagttg aaataattcc ttcttttgag 120
tgtcagtgcac tgaggttcgc tgtgacacag aggggttctc ctggagagct atggcac 177
atg ctc cat att aaa agg caa cat gat gct cgc tcc acc cag agg ccc 225
Met Leu His Ile Lys Arg Gln His Asp Ala Arg Ser Thr Gln Arg Pro
1 5 10 15
cgg tcc ccg cca ttc att ccg ctc ccg gcc gag agt cgc tct agc caa 273
Arg Ser Pro Pro Phe Ile Pro Leu Pro Ala Glu Ser Arg Ser Ser Gln
20 25 30
tca cct tcc agg ctc agg gcg gcc gag gca ggg cct ctg cct ctt cgg 321
Ser Pro Ser Arg Leu Arg Ala Ala Glu Ala Gly Pro Leu Pro Leu Arg
35 40 45
ggg gcc tct ccc tcc ccc tgc ccc tga ttgtg gctgaactgc caccgcttga 373
Gly Ala Ser Pro Ser Pro Cys Pro *
50 55
tagcaaacca cactcggcac aggaaggaga acagcgcccg cggcacgaaa 423

<210> 302
<211> 408
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (44)..(343)

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<400> 302
agggtcaag gaagcccaaa gtccagtctg cccagaaccg agc  atg tca tct ccc      55
                                         Met Ser Ser Pro
                                         1

ccg cca aga cgc tcc aac cgc cgc aat cct tgt cca tca ggc atc cag      103
Pro Pro Arg Arg Ser Asn Arg Arg Asn Pro Cys Pro Ser Gly Ile Gln
  5              10              15              20

gcc aga aac tct ggc tgc ccc cac ctc ccc aat ggt ccc cat caa gta      151
Ala Arg Asn Ser Gly Cys Pro His Leu Pro Asn Gly Pro His Gln Val
          25              30              35

ggt aac atc ctg ctg att tta act cct gtg cag ccc tca aat gca caa      199
Gly Asn Ile Leu Leu Ile Leu Thr Pro Val Gln Pro Ser Asn Ala Gln
          40              45              50

ctg cct ccc att cct gca cag tgc ccc agt tca ggc ctt cac cac ctt      247
Leu Pro Pro Ile Pro Ala Gln Cys Pro Ser Ser Gly Leu His His Leu
          55              60              65

gtt cct ggg cca ctg ccc aag tct ccc ccg act ggt ggc tgg act tct      295
Val Pro Gly Pro Leu Pro Lys Ser Pro Pro Thr Gly Gly Trp Thr Ser
          70              75              80

aat act ttt cca act ccc cac tca tta aat cca tcc ccc tct cat taa      343
Asn Thr Phe Pro Thr Pro His Ser Leu Asn Pro Ser Pro Ser His *
          85              90              95              100

ctggtgggaa ttgaggaaaa ctgagttcca gccttgtcat cctcatactc atgacccttc      403

caggc                                                                    408

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<210> 303
<211> 822
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (69)..(590)

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<400> 303
cagatcaaga cacaggagaa gagtgcaaaa atactgatca ggaagagtct accatttcat      60

ccaaggaa atg cca caa tca ttt tct gca atc aca tta agt aac aca gag      110
Met Pro Gln Ser Phe Ser Ala Ile Thr Leu Ser Asn Thr Glu
  1              5              10

atg aat aat att aat act aat gcc ccg aga aac aaa ctt cca ata aag      158
Met Asn Asn Ile Asn Thr Asn Ala Pro Arg Asn Lys Leu Pro Ile Lys
  15              20              25              30

```

gaa ctt ggt aaa gtt tct aaa cat aaa att gcc act aaa aga aca cca	206
Glu Leu Gly Lys Val Ser Lys His Lys Ile Ala Thr Lys Arg Thr Pro	
35 40 45	
cat aaa gaa gat gag gca atg agc tgt tct gaa aat tgt tcg agt gcc	254
His Lys Glu Asp Glu Ala Met Ser Cys Ser Glu Asn Cys Ser Ser Ala	
50 55 60	
cag ggc gac tca ctt cag gat gag tct caa ggg tct cat tct gag tcc	302
Gln Gly Asp Ser Leu Gln Asp Glu Ser Gln Gly Ser His Ser Glu Ser	
65 70 75	
agc tct aat ccc tcc aat cct gaa act ttg cat gca aag gca act gat	350
Ser Ser Asn Pro Ser Asn Pro Glu Thr Leu His Ala Lys Ala Thr Asp	
80 85 90	
tca gtt cta caa ggt tct gaa gga aac aag gtc aag agg aca tcc tgc	398
Ser Val Leu Gln Gly Ser Glu Gly Asn Lys Val Lys Arg Thr Ser Cys	
95 100 105 110	
atg tat ggg gca aac tgc tat agg aag aat cct gtt cat ttt caa cat	446
Met Tyr Gly Ala Asn Cys Tyr Arg Lys Asn Pro Val His Phe Gln His	
115 120 125	
ttt agc cat cct ggt gat agt gat tat gga ggt gta caa atc gtg ggc	494
Phe Ser His Pro Gly Asp Ser Asp Tyr Gly Gly Val Gln Ile Val Gly	
130 135 140	
caa gat gag act gat gac cgg cct gaa tgt ccc tat gga cca tcc tgt	542
Gln Asp Glu Thr Asp Asp Arg Pro Glu Cys Pro Tyr Gly Pro Ser Cys	
145 150 155	
tat agg ttg gaa gtt cag tgt cca gtt gaa aaa cac caa ctc agc tag	590
Tyr Arg Leu Glu Val Gln Cys Pro Val Glu Lys His Gln Leu Ser *	
160 165 170	
ttttctctgg tctgcattac agtattttac ctgtcttttt atgaaaagag cacgttctag	650
gaaaggatgg aagatttctca aagaaacaac tttccccttc taaggcagat gaaaacctgt	710
acatgtacct aacattttttt ccccttttta aaatataaaa tttcacatta cattttctgc	770
tcttcctttt tggaataatt aaatgtaaca cttctttcat aaaaaaaaaa aa	822

<210> 304
 <211> 457
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (121) .. (309)

 <400> 304

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tttgaaagct gattgatagc cgtaccgcac cgcaaaccac gggtcgaccc acgcgtccgc      60
ttcacttcac cttcactact tctgtagtct gatcttgtgt aatagagaac ccagccaact      120
atg aag ttc ctt gac ttt gct ttc atc ttg gct ctc aag gtt tcc atg      168
Met Lys Phe Leu Asp Phe Ala Phe Ile Leu Ala Leu Lys Val Ser Met
  1             5             10             15
att gga gct gat tcc tct gaa gag aaa ttt ttg cgt ata att gta cga      216
Ile Gly Ala Asp Ser Ser Glu Glu Lys Phe Leu Arg Ile Ile Val Arg
             20             25             30
atc ggt tat ggg tat ggc cct tat cat tca gtt tca gaa caa cca cta      264
Ile Gly Tyr Gly Tyr Gly Pro Tyr His Ser Val Ser Glu Gln Pro Leu
             35             40             45
tac cca caa cca tac caa cca caa tac caa caa tat acc ttt taa tat      312
Tyr Pro Gln Pro Tyr Gln Pro Gln Tyr Gln Gln Tyr Thr Phe *
             50             55             60
catcagtaac tgcaggacat gattattgag gcttgattgg ctgatacgac ttctacatcc      372
atattctcat gtttcatacc atatcgact actaccactt tttgaagaat catcatagag      432
ctttgcatat gagaaacact atatg                                           457

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<210> 305
 <211> 1749
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (85)..(873)

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<400> 305
ccgcgcgcgga attcccgggt cgaccacgc gtccgccgca gccccagct cgcccccaag      60
atgatgaaga ggcagctgca ccgc      atg cgg cag ctg gcc cag acg ggc agc      111
                               Met Arg Gln Leu Ala Gln Thr Gly Ser
                               1             5
ttg gga cgc acc ccg gag acc gct gag ttc ctg ggt gag gac ctg ctg      159
Leu Gly Arg Thr Pro Glu Thr Ala Glu Phe Leu Gly Glu Asp Leu Leu
  10             15             20             25
cag gta gaa cag cgg ctg gag ccg gcc aag cgg gca gcc cac aac atc      207
Gln Val Glu Gln Arg Leu Glu Pro Ala Lys Arg Ala Ala His Asn Ile
             30             35             40
cac aag cgg ctg cag gcc tgt ctg cag ggc cag agc ggg gca gac atg      255
His Lys Arg Leu Gln Ala Cys Leu Gln Gly Gln Ser Gly Ala Asp Met
             45             50             55

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gac aag cgg gtg aag aag ctt ccc ctc atg gct ctg tcc acc acg atg Asp Lys Arg Val Lys Lys Leu Pro Leu Met Ala Leu Ser Thr Thr Met 60 65 70	303
gct gag agc ctc aag gag ctg gac cct gat tcc agc atg ggg aag gcc Ala Glu Ser Leu Lys Glu Leu Asp Pro Asp Ser Ser Met Gly Lys Ala 75 80 85	351
ttg gag atg agc tgt gcc atc cag aat cag ctg gcc cgc atc ctg gcc Leu Glu Met Ser Cys Ala Ile Gln Asn Gln Leu Ala Arg Ile Leu Ala 90 95 100 105	399
gag ttt gag atg acc ctg gag agg gac gtc ctg cag cca ctc agc agg Glu Phe Glu Met Thr Leu Glu Arg Asp Val Leu Gln Pro Leu Ser Arg 110 115 120	447
ctg agt gag gag gag ctg cca gcc atc ctc aaa cac aag aaa agc ctc Leu Ser Glu Glu Glu Leu Pro Ala Ile Leu Lys His Lys Lys Ser Leu 125 130 135	495
cag aag ctc gtg tcc gac tgg aac aca ctc aag agc agg ctc agt cag Gln Lys Leu Val Ser Asp Trp Asn Thr Leu Lys Ser Arg Leu Ser Gln 140 145 150	543
gca acc aag aat tca ggc agc agt caa ggc cta gga ggc agc ccg ggt Ala Thr Lys Asn Ser Gly Ser Ser Gln Gly Leu Gly Gly Ser Pro Gly 155 160 165	591
agt cac agc cat acg acc atg gcc aac aag gtg gag acg ctg aag gag Ser His Ser His Thr Thr Met Ala Asn Lys Val Glu Thr Leu Lys Glu 170 175 180 185	639
gag gag gag gag ctg aag agg aaa gtg gag caa tgc agg gac gag tac Glu Glu Glu Glu Leu Lys Arg Lys Val Glu Gln Cys Arg Asp Glu Tyr 190 195 200	687
ttg gct gac ctg tac cac ttt gtt acc aag gag gac tcc tat gcc aac Leu Ala Asp Leu Tyr His Phe Val Thr Lys Glu Asp Ser Tyr Ala Asn 205 210 215	735
tac ttc att cgt ctc ctg gag att cag gcc gat tac cat cgc agg tca Tyr Phe Ile Arg Leu Leu Glu Ile Gln Ala Asp Tyr His Arg Arg Ser 220 225 230	783
ctg agc tcg ctg gac aca gcc ctg gct gag ctg agg gag aac cac ggc Leu Ser Ser Leu Asp Thr Ala Leu Ala Glu Leu Arg Glu Asn His Gly 235 240 245	831
caa gca ggt ggg gac ata ggc ccg gcg ata cca cac ccc tga ccctgcc Gln Ala Gly Gly Asp Ile Gly Pro Ala Ile Pro His Pro * 250 255 260	880
ctgctcgggg cttattgaga agctcgact tcatcctgaa aggtagcagg aagctgtgga	940
tgggttctga gagctaggct caatctgtga tggagaggca gctctggcta ctgtgtggag	1000
ggtggagtga agcgggcagg actagagcca ggcctgtgag gcagaaggag gcaacggtgg	1060

cctggactag gacagaggca gtggaggcgg gctgattcga gagatgtgac ggatgatttc 1120
 agatgtgtgc ctggacagtc agtggcaggt ggtaccacct tgaggacatg aaggggggggt 1180
 gcccctgcct gactgctcgg ggtgggaagg ccctgggccg ctgatctgtt tcatccctgc 1240
 agaccactcc ccttcgatga cagccacca cttccccagg gtgtatgggg tgctcgtggc 1300
 aaccacctg caagagctgg gccgggagat tgccctgccc atcgaggcct gcgtcatgat 1360
 gctgctttct gagggcatga aggaagaggg tctcttccgt ctggctgctg gggcctcggt 1420
 gctgaagcgt gtcaagcaga caatggcctc ggaccccgac agcctggagg agttctgctc 1480
 cgaccgcac gctgtggcag gtgccctcaa gtcctatctg cgggagctgc cagagcctct 1540
 gatgaccttc gacctctatg atgactggat gagggcagcc agcctgaagg agccaggggc 1600
 ccggctgcag gccctccaag aggtgtgcag ccgcctaccc cccgagaacc tcagcaacct 1660
 caggtacctg atgaagttcc tggcacggct ggccgaggag caggaggtga acaagacgaa 1720
 atctcgacag cgaagtcgac ccgggaatt 1749

<210> 306
 <211> 496
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (55)..(372)

<400> 306
 aaggatcctt aattaaatta atccccccc ccgaaccgtt cgctaactga aatg atg 57
 Met
 1

 gcg act gga acg cca gag tct caa gcg cgg ttc ggt cag tcc gtg aag 105
 Ala Thr Gly Thr Pro Glu Ser Gln Ala Arg Phe Gly Gln Ser Val Lys
 5 10 15

 ggg ctt ctc acg gag aag gtg acc acc tgt ggt act gac gta atc gcg 153
 Gly Leu Leu Thr Glu Lys Val Thr Thr Cys Gly Thr Asp Val Ile Ala
 20 25 30

 ctc acc aag cag gtg ctg aaa ggc tcc cgg agc tcc gag ctg cta ggt 201
 Leu Thr Lys Gln Val Leu Lys Gly Ser Arg Ser Ser Glu Leu Leu Gly
 35 40 45

 cag gca gct cga aac atg gta ctc cag gaa gat gcc atc ttg cac tca 249
 Gln Ala Ala Arg Asn Met Val Leu Gln Glu Asp Ala Ile Leu His Ser
 50 55 60 65

gaa gat agt tta agg aag atg gca ata ata aca aca cat ctt caa tac	297
Glu Asp Ser Leu Arg Lys Met Ala Ile Ile Thr Thr His Leu Gln Tyr	
70 75 80	
cag caa gaa gct att cag aag aat gtt gaa cag tca tcg gat cta cag	345
Gln Gln Glu Ala Ile Gln Lys Asn Val Glu Gln Ser Ser Asp Leu Gln	
85 90 95	
gac cag ttg aat cat ctg ttg aaa tag aatga catgtaagag tgctgtagga	397
Asp Gln Leu Asn His Leu Leu Lys *	
100 105	
ctcctttgcc taatgctgag gagtaaatac cttacacagc tgtcctctgg gtttggtttt	457
ctattttctt ctccaaaagt taagttagaa aagttcttg	496

<210> 307
 <211> 1438
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (88)..(840)

<400> 307	
catggaggag gaaggagatg gcatggctta ccataaagaa gcactggacg ccggggtgcac	60
gttccaggat ccaggtgccc aggggtc atg aag ctg gga ctc ctc tgt gct	111
Met Lys Leu Gly Leu Leu Cys Ala	
1 5	
ctg ctc tct ctg ctg gca ggg cat ggc tgg gca gac acc cgt gcc atc	159
Leu Leu Ser Leu Leu Ala Gly His Gly Trp Ala Asp Thr Arg Ala Ile	
10 15 20	
ggg gcc gag gaa tgt cgc ccc aac tcc cag cct tgg cag gcc ggc ctc	207
Gly Ala Glu Glu Cys Arg Pro Asn Ser Gln Pro Trp Gln Ala Gly Leu	
25 30 35 40	
ttc cac ctt act cgg ctc ttc tgt ggg gcg acc ctc atc agt gac cgc	255
Phe His Leu Thr Arg Leu Phe Cys Gly Ala Thr Leu Ile Ser Asp Arg	
45 50 55	
tgg ctg ctc aca gct gcc cac tgc cgc aag ccg tat ctg tgg gtc cgc	303
Trp Leu Leu Thr Ala Ala His Cys Arg Lys Pro Tyr Leu Trp Val Arg	
60 65 70	
ctt gga gag cac cac ctc tgg aaa tgg gag ggt ccg gag cag ctg ttc	351
Leu Gly Glu His His Leu Trp Lys Trp Glu Gly Pro Glu Gln Leu Phe	
75 80 85	
cgg gtt acg gac ttc ttc ccc cac cct ggc ttc aac aag gac ctc agc	399

Arg	Val	Thr	Asp	Phe	Phe	Pro	His	Pro	Gly	Phe	Asn	Lys	Asp	Leu	Ser		
90						95					100						
gcc	aat	gac	cac	aat	gat	gac	atc	atg	ctg	atc	cgc	ctg	ccc	agg	cag	447	
Ala	Asn	Asp	His	Asn	Asp	Asp	Ile	Met	Leu	Ile	Arg	Leu	Pro	Arg	Gln		
105				110					115						120		
gca	cgt	ctg	agt	cct	gct	gtg	cag	ccc	ctc	aac	ctc	agc	cag	acc	tgt	495	
Ala	Arg	Leu	Ser	Pro	Ala	Val	Gln	Pro	Leu	Asn	Leu	Ser	Gln	Thr	Cys		
				125					130					135			
gtc	tcc	cca	ggc	atg	cag	tgt	ctc	atc	tca	ggc	tgg	ggg	gcc	gtg	tcc	543	
Val	Ser	Pro	Gly	Met	Gln	Cys	Leu	Ile	Ser	Gly	Trp	Gly	Ala	Val	Ser		
			140					145					150				
agc	ccc	aag	gcg	ctg	ttt	cca	gtc	aca	ctg	cag	tgt	gcc	aac	atc	agc	591	
Ser	Pro	Lys	Ala	Leu	Phe	Pro	Val	Thr	Leu	Gln	Cys	Ala	Asn	Ile	Ser		
		155					160					165					
atc	ctg	gag	aac	aaa	ctc	tgt	cac	tgg	gca	tac	cct	gga	cac	atc	tgc	639	
Ile	Leu	Glu	Asn	Lys	Leu	Cys	His	Trp	Ala	Tyr	Pro	Gly	His	Ile	Ser		
	170					175					180						
gac	agc	atg	ctc	tgt	gcg	ggc	ctg	tgg	gag	ggg	ggc	cga	ggg	tcc	tgc	687	
Asp	Ser	Met	Leu	Cys	Ala	Gly	Leu	Trp	Glu	Gly	Gly	Arg	Gly	Ser	Cys		
185					190					195					200		
cag	ggg	gac	tct	ggg	ggc	ccc	ctg	gtt	tgc	aat	gga	acc	ttg	gca	ggc	735	
Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asn	Gly	Thr	Leu	Ala	Gly		
				205					210					215			
gtg	gtg	tct	ggg	ggg	gct	gag	ccc	tgc	tcc	aga	ccc	cgg	cgc	ccc	gca	783	
Val	Val	Ser	Gly	Gly	Ala	Glu	Pro	Cys	Ser	Arg	Pro	Arg	Arg	Pro	Ala		
			220					225					230				
gtc	tac	acc	agc	gta	tgc	cac	tac	ctt	gac	tgg	atc	caa	gaa	atc	atg	831	
Val	Tyr	Thr	Ser	Val	Cys	His	Tyr	Leu	Asp	Trp	Ile	Gln	Glu	Ile	Met		
		235					240					245					
gag	aac	tga	gcccgcg	cgccacgggg	gcaccttgga	agaccaagag	aggccgaagg									887	
Glu	Asn	*															
	250																
gcacgggggta	gggggttctc	gtaggggtccc	agcctcaatg	gttcccgcgc	tggacctcca											947	
gctgccctga	ctcccctctg	gacactaaga	ctccgcccct	gaggctccgc	cccctcacga											1007	
ggtaagcaa	gacacagtcg	cgccccctcg	gaacggagca	gggacacgcc	cttcagagcc											1067	
cgtctctatg	acgtcaccga	cagccatcac	ctccttcttg	gaacagcaca	gcctgtggct											1127	
ccgccccaa	gaaccactta	cacaaaatag	ctccgcccct	cggaactttg	cccagtggga											1187	
cttcccctcg	ggactccacc	ccttgtggcc	ccgcctcctt	caccagagat	ctcgcctctc											1247	
gtgatgtcag	gggcgcagta	gctccgcca	cgtggagctc	gggcgggtgta	gagctcagcc											1307	

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ccttgtggcc ccgtcctggg cgtgtgctgg gtttgaatcc tggcggagac ctggggggaa 1367
attgagggag ggtctggata cctttagagc caatgcaacg gatgattttt cagtaaacgc 1427
gggaaacctc a 1438

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<210> 308
<211> 675
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (110)..(613)

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<400> 308
taggagatcc ttagcggact gggatcttaa tgggtctcact gtgtttatct ctttgtaaag 60

gccagccctc acctgacttg tctgggtccc tcctggggct aggggatgg atg aga 115
Met Arg
1

agg gct agg ctg gag ctg tca gca gct tct tgg tgc ctg ctg ttt ctc 163
Arg Ala Arg Leu Glu Leu Ser Ala Ala Ser Trp Cys Leu Leu Phe Leu
5 10 15

ttg tct tgt ctg tct tcg gtg tat tgc aat cct gtc ctc tta gca ggc 211
Leu Ser Cys Leu Ser Ser Val Tyr Cys Asn Pro Val Leu Leu Ala Gly
20 25 30

ccc gca gag tca tac ttt ttc tcc ctg gcc ttc cag ctc cct ctc ttc 259
Pro Ala Glu Ser Tyr Phe Phe Ser Leu Ala Phe Gln Leu Pro Leu Phe
35 40 45 50

cac cca gta tgc cca cct ccc tct ccc ttg act acc cca gcc tct gcc 307
His Pro Val Cys Pro Pro Ser Pro Leu Thr Thr Pro Ala Ser Ala
55 60 65

caa tca cgc cct gcc ctc tac cct tca gag gac acc ttg ccg tct gtg 355
Gln Ser Arg Pro Ala Leu Tyr Pro Ser Glu Asp Thr Leu Pro Ser Val
70 75 80

gag ctg gag cta ttc cta tgg tct ctc tgg gtc cac atg acc tta cat 403
Glu Leu Glu Leu Phe Leu Trp Ser Leu Trp Val His Met Thr Leu His
85 90 95

ggc act cct ctc acc ttc tgt cca tcc aac aaa att ctc tgt tcc ttt 451
Gly Thr Pro Leu Thr Phe Cys Pro Ser Asn Lys Ile Leu Cys Ser Phe
100 105 110

gaa gct ctc ttt tca gta agg cct tcc ttg gcc cct aac agg atg gat 499
Glu Ala Leu Phe Ser Val Arg Pro Ser Leu Ala Pro Asn Arg Met Asp
115 120 125 130

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cac cct ccc ctg agc cct ggt cat tgc ctc tct gtt atg gcc tct cca 547
His Pro Pro Leu Ser Pro Gly His Cys Leu Ser Val Met Ala Ser Pro
          135          140          145

ttg gta aac gct ctg ccg atg tgt ttc atc ttc cca cta gat cct tgc 595
Leu Val Asn Ala Leu Pro Met Cys Phe Ile Phe Pro Leu Asp Pro Cys
          150          155          160

gcc cac gca cgc ggc tga atcatc tttacatccc cagaggccct ggtatgtggt 649
Ala His Ala Arg Gly *
          165

ggacaggcctt gtttctgccg ggcctt 675

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<210> 309
<211> 1042
<212> DNA
<213> Homo sapiens

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<220>
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<222> (779)..(952)

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<400> 309
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cagtcactta ttcccttcat acctgtcagc cgagagcact gactgcgtga tttccagggt 180
cctttacagc tttagagtat aggggctctg tttttgctgc tcccgaattt ccacctccca 240
tcatccacgc atttcacaga tgcattctgaa tgctcacagt gctctatttg tgcctctctg 300
tttgccctg ttttttatgt ggatgcgtat cgaccgccat gatagactgc aactccctg 360
tgggcaggag ccatgttcat ttcatTTTTG tgtcccaggc ataatgtagg tgcgctcacc 420
tcattctctc catatcttga acctgtgaat ctcagtggac tcttttcagc agatgaacct 480
gtataagtct ttctgtctt gaaaggacag atgggtggcc cccatcctcc actgagcttc 540
ctgttgaact ccttttgcag gtgacgtcaa aatagaagaa gccctcattc accatatcta 600
ctgttaccct cctcctttcc cctctacttc ccatgaccag ttgttcaactg cccctccaca 660
gaacctactt ctgataaatc ccgtgaagaa ttttttattg ccagatccaa attctttggc 720
ctctcacagt gtttgcgtgtg gcctgattct cctcattct ggaaactcct ctctctc 778
atg gct ccc atg gga cca gtt gct cct gca gct cct cct gcc cct cac 826
Met Ala Pro Met Gly Pro Val Ala Pro Ala Ala Pro Pro Ala Pro His
  1           5           10          15

tct gct ctc ctt gga ctc ctc ttt cct ggt att ctc tgc agt tct gtc 874

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Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr	Cys	Met	Gln	
				105					110					115		
cgt	ata	gag	ttt	cct	tgg	act	ttt	ggc	cag	ggg	acc	aag	ctg	gag	atc	438
Arg	Ile	Glu	Phe	Pro	Trp	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu	Ile	
			120					125					130			
aaa	cga	act	gtt	gct	gca	cca	tct	gtc	ttc	atc	ttc	ccg	cca	tct	gat	486
Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	
			135				140					145				
gag	cag	ttg	aaa	tct	gga	act	gcc	tct	gtt	gtg	tgc	ctg	ctg	aat	aac	534
Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	
		150				155					160					
ttc	tat	ccc	aga	gag	gcc	taa	gt	acagtggaaa	gtggtaaacg	gcctccaaac						587
Phe	Tyr	Pro	Arg	Glu	Ala	*										
165					170											
tggttaaadc	cagtaaagt	tcacagagca	agacagtaag	gacagcacct	acgtactcag											647
cagcaaccag	aagctgagca	aagttgactt	atgagatacc	acaagtctag	gcctgacgaa											707
gtcaaccatt	atggacttgg	gctgtgtcca	atctgaatat	agttatacct	gggcagagtg											767
gttaaaagg	atagtgtgtc	ccctaaattg	tatcctaggt	ttcaagctcg	tagtcacttg											827
cccaggcttt	ttgtcccttg	taggtccttt	tttcccaatg	ggggaccta	gacactaagt											887
gacgggactc	tccaaagtta	atgattttaa	acttaaaatc	actctctaag	ggatcatcag											947
gagttatgaa	gtcgatgact	aattgttttt	gatacgagta	tatctgaaaa	tgattgaaag											1007
tgtgaattcc	tcatggtagg	tgagataaac	tagtcgttat	agtatctagt	agatgaccgg											1067
agcatttata	gagtagaagt	ccgcatactc	ccggataatc	taccacgaca	catgattaga											1127
ctctcgcgat	ggtaaacaga	tggatgtaaa	ctcaatcgtg	ggagtaccga	aagaggtggc											1187
tatgatgttg	acatgatagg	gtctaggatg	cgtgatcgtg	tgacggaatt	gtcaaatacg											1247
tgtgaataca	catttatttg	caatttctgt	atgacgtgat	atgagattag	cagaggttta											1307
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<210> 311
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 <212> DNA
 <213> Homo sapiens

 <220>
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gggtggtatt cctgcc atg ggt cct ggg ctt ctc cac tgg atg gcc ctt 109
Met Gly Pro Gly Leu Leu His Trp Met Ala Leu
1 5 10
tgt ctc ctt gga aca ggt cat ggg gat gcc atg gtc atc cag aac cca 157
Cys Leu Leu Gly Thr Gly His Gly Asp Ala Met Val Ile Gln Asn Pro
15 20 25
aga tac cag gtt acc cag ttt gga aag cca gtg acc ctg agt tgt tct 205
Arg Tyr Gln Val Thr Gln Phe Gly Lys Pro Val Thr Leu Ser Cys Ser
30 35 40
cag act ttg aac cat aac gtc atg tac tgg tac cag cag aag tca agt 253
Gln Thr Leu Asn His Asn Val Met Tyr Trp Tyr Gln Gln Lys Ser Ser
45 50 55
cag gcc cca aag ctg ctg ttc cac tac tat gac aaa gat ttt aac aat 301
Gln Ala Pro Lys Leu Leu Phe His Tyr Tyr Asp Lys Asp Phe Asn Asn
60 65 70 75
gaa gca gac acc cct gat aac ttc caa tcc agg agg ccg aac act tct 349
Glu Ala Asp Thr Pro Asp Asn Phe Gln Ser Arg Arg Pro Asn Thr Ser
80 85 90
ttc tgc ttt ctt gac atc cgc tca cca ggc ctg ggg gac gca gcc atg 397
Phe Cys Phe Leu Asp Ile Arg Ser Pro Gly Leu Gly Asp Ala Ala Met
95 100 105
tac ctg tgt gcc acc agc gtc cac cgg gac cca tga acac tgaagctttc 447
Tyr Leu Cys Ala Thr Ser Val His Arg Asp Pro *
110 115
tttggacaag gcaccagact cacagttgta gcatgtgaaa aggtccagag ctctgcagtg 507
tgagctttct actgaaatgg cccttggtact ttgtggttca ttcataactca gtggtctagc 567
ttgtactact tttgagaatg caaagcttaa ctgtggacgg attccaatcc tggccaggca 627
gggttgctgg acactctgag agaagaaagg gttaatccca tgaccatcaa cttccatggg 687
atttcagcca tcttgacaa gctaccacac cctcctgccc caaggggagg aggaaatgtg 747
gaccatccca tcagaaattg accaaaggac ctgaacaagt ggtccccccc ccccc 803

<210> 312
<211> 687
<212> DNA
<213> Homo sapiens

<220>
<221> CDS

<222> (6)..(605)

<400> 312

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	Met	Leu	Cys	Arg	Gln	Gln	Leu	Arg	Asn	Leu	Thr	Glu	Asn	Lys		
	1				5					10						
gaa	tct	gag	ttg	cag	tgt	ctc	ttt	caa	cag	ata	gaa	agg	cag	gag	cag	95
Glu	Ser	Glu	Leu	Gln	Cys	Leu	Phe	Gln	Gln	Ile	Glu	Arg	Gln	Glu	Gln	
	15				20					25					30	
ctt	ctg	gat	gaa	ata	cat	cgt	gag	aag	aga	gat	cta	ctg	gaa	gag	acc	143
Leu	Leu	Asp	Glu	Ile	His	Arg	Glu	Lys	Arg	Asp	Leu	Leu	Glu	Glu	Thr	
				35					40						45	
caa	aga	aaa	gat	gaa	gaa	atg	gga	tct	ctg	cag	gac	cgt	gta	att	gca	191
Gln	Arg	Lys	Asp	Glu	Glu	Met	Gly	Ser	Leu	Gln	Asp	Arg	Val	Ile	Ala	
			50					55					60			
tta	gaa	acg	agt	acc	caa	gtg	gcc	ttg	gac	cat	ctg	gag	tct	gtg	cct	239
Leu	Glu	Thr	Ser	Thr	Gln	Val	Ala	Leu	Asp	His	Leu	Glu	Ser	Val	Pro	
		65					70					75				
gag	aaa	ctg	agc	cta	cta	gaa	gat	ttc	aaa	gac	ttc	aga	gat	tcc	tgc	287
Glu	Lys	Leu	Ser	Leu	Leu	Glu	Asp	Phe	Lys	Asp	Phe	Arg	Asp	Ser	Cys	
	80					85					90					
agt	tca	tct	gag	aga	act	gat	gga	aga	tat	tcc	aaa	tac	agg	gtt	cgc	335
Ser	Ser	Ser	Glu	Arg	Thr	Asp	Gly	Arg	Tyr	Ser	Lys	Tyr	Arg	Val	Arg	
	95				100					105					110	
aga	aat	tct	ctt	cag	cat	cac	caa	gat	gac	acc	aag	tac	aga	acc	aaa	383
Arg	Asn	Ser	Leu	Gln	His	His	Gln	Asp	Asp	Thr	Lys	Tyr	Arg	Thr	Lys	
				115					120						125	
agt	ttc	aaa	ggt	gac	aga	acc	ttt	ctg	gaa	ggt	tcc	cac	act	cgt	ggg	431
Ser	Phe	Lys	Gly	Asp	Arg	Thr	Phe	Leu	Glu	Gly	Ser	His	Thr	Arg	Gly	
			130					135					140			
tta	gat	cac	tca	tcc	tct	tgg	cag	gat	cac	agt	cgc	ttc	ctg	tct	agt	479
Leu	Asp	His	Ser	Ser	Ser	Trp	Gln	Asp	His	Ser	Arg	Phe	Leu	Ser	Ser	
		145					150						155			
cca	aga	ttt	tca	tac	gtg	aac	tca	ttt	acc	aaa	aga	act	ggt	gct	cca	527
Pro	Arg	Phe	Ser	Tyr	Val	Asn	Ser	Phe	Thr	Lys	Arg	Thr	Val	Ala	Pro	
	160					165							170			
gat	tca	gct	tca	aac	aag	gaa	gat	gcc	aca	atg	aat	gga	aca	agt	tca	575
Asp	Ser	Ala	Ser	Asn	Lys	Glu	Asp	Ala	Thr	Met	Asn	Gly	Thr	Ser	Ser	
	175				180					185					190	
caa	ccc	aaa	aaa	gag	gaa	tat	ggg	agc	taa	a	aaagcaa	aatg	taatttg	ttta		626
Gln	Pro	Lys	Lys	Glu	Glu	Tyr	Gly	Ser	*							
				195					200							
ttttacatga	gtatgttaca	aataataaca	tctctattct	tacagcaaaa	aaaaaaaaaa											686

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<220>
<221> CDS
<222> (714) .. (947)
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649

aaatggaggg agtgaaaccc ctacttagtt tctgctgac ctccttgga gaga

583

<210> 315
<211> 931
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (75)..(677)

<400> 315

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cccagagagga aggc atg cgg tgg gcc cta ctg gtg ctt cta gct ttc ctg 110
Met Arg Trp Ala Leu Val Leu Leu Ala Phe Leu
1 5 10

tct cct gcc agt cag aaa tct tcc aac ttg gaa ggg aga acg aag tca 158
Ser Pro Ala Ser Gln Lys Ser Ser Asn Leu Glu Gly Arg Thr Lys Ser
15 20 25

gtc acc agg cag act ggg tca tct gct gaa atc act tgc gat ctt act 206
Val Thr Arg Gln Thr Gly Ser Ser Ala Glu Ile Thr Cys Asp Leu Thr
30 35 40

gta aca aat acc ttc tac atc cac tgg tac cta cac cag gag ggg aag 254
Val Thr Asn Thr Phe Tyr Ile His Trp Tyr Leu His Gln Glu Gly Lys
45 50 55 60

gcc cca cag cgt ctt ctg tac tat gac gtc tcc act gca agg gat gtg 302
Ala Pro Gln Arg Leu Leu Tyr Tyr Asp Val Ser Thr Ala Arg Asp Val
65 70 75

ttg gaa tca gga ctc agt cca gga aag tat tat act cat aca ccc agg 350
Leu Glu Ser Gly Leu Ser Pro Gly Lys Tyr Tyr Thr His Thr Pro Arg
80 85 90

agg tgg agc tgg ata ttg ata cta cga aat cta att gaa aat gat tct 398
Arg Trp Ser Trp Ile Leu Ile Leu Arg Asn Leu Ile Glu Asn Asp Ser
95 100 105

ggg gtc tat tac tgt gcc acc tgg gac agg cac agt gat tca gac ctg 446
Gly Val Tyr Tyr Cys Ala Thr Trp Asp Arg His Ser Asp Ser Asp Leu
110 115 120

tcc tac acc aca ctg aaa atc tgc ctt gtg gct gcc tct ggt tca cag 494
Ser Tyr Thr Thr Leu Lys Ile Cys Leu Val Ala Ala Ser Gly Ser Gln
125 130 135 140

gat aga gcc gcc ccc tct cat ttc ctg tca cca aat tta ctg tat tct 542
Asp Arg Ala Ala Pro Ser His Phe Leu Ser Pro Asn Leu Leu Tyr Ser

145	150	155	
gaa caa gag aaa gac agc tta act cct gat ctc cct cct aat atc aca			590
Glu Gln Glu Lys Asp Ser Leu Thr Pro Asp Leu Pro Pro Asn Ile Thr			
160	165	170	
ctg tcc tgg cag cag ctg cat cct gtt ccc cac ccc tcc ccc aca act			638
Leu Ser Trp Gln Gln Leu His Pro Val Pro His Pro Ser Pro Thr Thr			
175	180	185	
ttc ctg aag atc aag ctg cca tct cca ggc ctc agc taa gcagcctggc			687
Phe Leu Lys Ile Lys Leu Pro Ser Pro Gly Leu Ser *			
190	195	200	
tgagagcaag gttctctcag ctctcctagg acatggggga ggcccactca ctctgcttcc			747
tatgacacac aggtacaact aggggtccagc tgtgaagcga gatatttttg acagcaaattg			807
ggaaggggtat ttatactgaa tcatgtatcc actcatggtc cagagatcac agctgagagt			867
ggtgcttatt ccttatgtct ataacaacat aagcaatact ataatgacca ctaaaacact			927
aggc			931
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<213>	Homo sapiens		
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<222>	(228)..(737)		
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gaattgaaag tgaggatgac ttgtataaac tggatgaactt ctcccttaaa tatcgagctc			180
accgtttatc ttccagcctc cagatcaagc cctgcagtca ggcgagc atg gag aag			236
		Met Glu Lys	
		1	
gcg agc atg gag gag aca agc acg agg tca gaa ttg gag ctg gca gag			284
Ala Ser Met Glu Glu Thr Ser Thr Arg Ser Glu Leu Glu Leu Ala Glu			
5	10	15	
cag acg gag atg gag gga gaa aag gaa gaa agc ctg gtg gaa ggg gag			332
Gln Thr Glu Met Glu Gly Glu Lys Glu Glu Ser Leu Val Glu Gly Glu			
20	25	30	35
aag gag gaa gag gag gag acc cca ccc tcc ccc tgg gtc atc cac ccc			380
Lys Glu Glu Glu Glu Glu Thr Pro Pro Ser Pro Trp Val Ile His Pro			

40										45				50							
aat	gat	gtc	ctc	aag	att	ctg	gag	gcc	ttc	ttc	atg	ggg	ctg	aag	aag	428					
Asn	Asp	Val	Leu	Lys	Ile	Leu	Glu	Ala	Phe	Phe	Met	Gly	Leu	Lys	Lys						
55				60				65													
cct	agg	gac	tcg	cgg	gcc	ccg	ctg	agg	gta	cag	aag	aat	gtg	cgt	gac	476					
Pro	Arg	Asp	Ser	Arg	Ala	Pro	Leu	Arg	Val	Gln	Lys	Asn	Val	Arg	Asp						
70				75				80													
aac	tcc	aag	gac	tcg	gag	tac	tgg	cag	gcc	ctg	acc	aca	gtg	atc	cct	524					
Asn	Ser	Lys	Asp	Ser	Glu	Tyr	Trp	Gln	Ala	Leu	Thr	Thr	Val	Ile	Pro						
85				90				95													
tcc	tcc	aag	cag	aac	ctc	tgg	gat	gcc	ctc	tac	aca	gcc	ttg	gag	aag	572					
Ser	Ser	Lys	Gln	Asn	Leu	Trp	Asp	Ala	Leu	Tyr	Thr	Ala	Leu	Glu	Lys						
100		105				110				115											
tac	cac	ctt	gtc	ctg	acc	cag	agg	gcc	aag	ctg	ctg	ctg	gaa	aac	agt	620					
Tyr	His	Leu	Val	Leu	Thr	Gln	Arg	Ala	Lys	Leu	Leu	Leu	Glu	Asn	Ser						
120				125				130													
tct	ctg	gag	cag	cag	aac	aca	gag	ctg	cag	gcg	cta	ctg	cag	cag	tat	668					
Ser	Leu	Glu	Gln	Gln	Asn	Thr	Glu	Leu	Gln	Ala	Leu	Leu	Gln	Gln	Tyr						
135				140				145													
ctg	aac	tcc	aag	atc	aac	tct	gaa	ctg	caa	gtt	cct	ccc	act	cag	gtg	716					
Leu	Asn	Ser	Lys	Ile	Asn	Ser	Glu	Leu	Gln	Val	Pro	Pro	Thr	Gln	Val						
150				155				160													
ttg	cgg	gta	ccc	aca	aaa	tga	gc	tggaccgcca	aaggctgatg	tgttagggct						769					
Leu	Arg	Val	Pro	Thr	Lys	*															
165				170																	
ggcctgatgc																tggtgtctgt	gccggagcca	gctcatatca	cccactgggc	cgcacctggg	829
cctgctctct																ggattttcca	gggctgtctt	tatagcctgt	cgaataagg	agccagagga	889
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<210> 317
<211> 793
<212> DNA
<213> Homo sapiens
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<222> (339) .. (623)
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cgc ttc ttc cag cag cgc aag agc ctg ctg ctg cac cag cgc ctg cac 99
 Arg Phe Phe Gln Gln Arg Lys Ser Leu Leu Leu His Gln Arg Leu His
 10 15 20
 acc ggc aat ggc cag ggc tgg ccc gcc tgc ccc tac tgc ggc aag gcc 147
 Thr Gly Asn Gly Gln Gly Trp Pro Ala Cys Pro Tyr Cys Gly Lys Ala
 25 30 35 40
 ttc cgc cgg ccc tgc gac ctc ttc cgg cac cag cgc atc cac acc ggt 195
 Phe Arg Arg Pro Ser Asp Leu Phe Arg His Gln Arg Ile His Thr Gly
 45 50 55
 gag cgg ccc tac cag tgc ccc cag tgt ggc cgg acc ttc aac cgc aac 243
 Glu Arg Pro Tyr Gln Cys Pro Gln Cys Gly Arg Thr Phe Asn Arg Asn
 60 65 70
 cac cac ctg gcc gtg cac atg cag acc cac gcc cga ggc cag gtg gcc 291
 His His Leu Ala Val His Met Gln Thr His Ala Arg Gly Gln Val Gly
 75 80 85
 cca cac ttc cct gcc gcc ccc gcc cgc cac ggg agc ctg ccc ctg ccc 339
 Pro His Phe Pro Ala Ala Pro Ala Arg His Gly Ser Leu Pro Leu Pro
 90 95 100
 tgg ccc agc cgg aag gag gag ggc tga cctgg caggagccca cagaggacct 391
 Trp Pro Ser Arg Lys Glu Glu Gly *
 105 110
 ctggcggggt ctctcccctg tgcctgacgc aggttcttcc ttttcttggg atggagagag 451
 gtttgttgtt tttaccatt caaatgggaa gctagctgcc cttctggtga cattgtgtgt 511
 gaccgggtgc tttctgtttc ctgtttgcac tcttcgctgc cttttctgca ttcctgactt 571
 ctaaaagatg ccttaaggct taagggatgc catatTTTTg ataaggcctc tggtaggtac 631
 cacagccaag aggaccagag atcatggccc ttccagtatg ggggcgatag agacatcggg 691
 gacctgggat ctcagtTTTg tgcagagatc tcttgcttgc tgtcaccatg agaaacagtg 751
 gagtggagtg gatggatggc ctgacttgaa gaaagggccc tggaaagtTt tctactTTTg 811
 tatattgaaa tataaatccc ttcttataga gactTTTgaaa tactttctgta aatgtgtgta 871
 gtagtcaatg gaactTTTgccc tttagcaaag tcggaaagag tcggctTTTt catgtgagggc 931
 tcgcagagct gaaaggggag ctacgtccac caagcctgta ggtcataagg gacacaaaca 991
 aggacgagga agaggaccct taaagaacgg acc 1024

<210> 319
 <211> 2552
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (281)..(2518)

<400> 319

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agcagcgaag ctgcgggcg ctggcgggac aggcgcgtga ggccacaaca catgcgtgta	180
tcttgcttgg gctatcttcc ctgctctgcc acgccgggtc tggagaaggg gtttcagccc	240
caggacattt actgagagtc ggcgaatatt gggagccgcg atg ttc ccc ctt cgg	295
Met Phe Pro Leu Arg	
1 5	
gcc ctg tgg ttg gtc tgg gcg ctt cta gga gtg gcc gga tca tgc ccg	343
Ala Leu Trp Leu Val Trp Ala Leu Leu Gly Val Ala Gly Ser Cys Pro	
10 15 20	
gag ccg tgc gcc tgc gtg gac aag tac gct cac cag ttc gcg gac tgc	391
Glu Pro Cys Ala Cys Val Asp Lys Tyr Ala His Gln Phe Ala Asp Cys	
25 30 35	
gct tac aaa gag ttg cgt gag gtg ccg gaa gga ctg cct gcc aac gtg	439
Ala Tyr Lys Glu Leu Arg Glu Val Pro Glu Gly Leu Pro Ala Asn Val	
40 45 50	
acg acg ctt agt ctg tcc gcg aac aag atc act gtg ctg cgg cgc ggg	487
Thr Thr Leu Ser Leu Ser Ala Asn Lys Ile Thr Val Leu Arg Arg Gly	
55 60 65	
gcc ttc gcc gac gtc aca cag gtc acg tcg ctg tgg ctg gcg cac aat	535
Ala Phe Ala Asp Val Thr Gln Val Thr Ser Leu Trp Leu Ala His Asn	
70 75 80 85	
gag gtg cgc acc gtg gag cca ggc gca ctg gcc gtg ctg agt cag ctc	583
Glu Val Arg Thr Val Glu Pro Gly Ala Leu Ala Val Leu Ser Gln Leu	
90 95 100	
aag aac ctc gat ctg agc cac aac ttc ata tcc agc ttt ccg tgg agc	631
Lys Asn Leu Asp Leu Ser His Asn Phe Ile Ser Ser Phe Pro Trp Ser	
105 110 115	
gac ctg cgc aac ctg agc gcg ctg cag ctg ctc aaa atg aac cac aac	679
Asp Leu Arg Asn Leu Ser Ala Leu Gln Leu Leu Lys Met Asn His Asn	
120 125 130	
cgc ctg ggc tct ctg ccc cgg gac gca ctc ggt gcg cta ccc gac ctg	727
Arg Leu Gly Ser Leu Pro Arg Asp Ala Leu Gly Ala Leu Pro Asp Leu	
135 140 145	
cgt tcc ctg cgc atc aac aac aac cgg ctg cgt acg ctg gcg cct ggc	775
Arg Ser Leu Arg Ile Asn Asn Asn Arg Leu Arg Thr Leu Ala Pro Gly	
150 155 160 165	

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Pro	Pro	Ala	Thr	Pro	Arg	Phe	Leu	Ala	Leu	Ala	Asn	Gly	Ser	Leu	Leu	
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Val	Pro	Leu	Leu	Ser	Ala	Lys	Glu	Ala	Gly	Val	Tyr	Thr	Cys	Arg	Ala	
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His	Asn	Glu	Leu	Gly	Ala	Asn	Ser	Thr	Ser	Ile	Arg	Val	Ala	Val	Ala	
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ctg Leu	gcc Ala	aag Lys	gtc Val 425	agc Ser	att Ile	ctc Leu	ggg Gly	gag Glu 430	acc Thr	gag Glu	acg Thr	gag Glu	ccg Pro 435	gag Glu	gag Glu	1591
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Asp Asp Ile Glu Val Gln Gly His Lys Ile Val Phe Ala Ala Gly Ser	
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Pro Phe Leu Arg Asp Gln Phe Leu Leu Asn Asp Ser Arg Glu Val Lys	
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Lys Val Glu Ser Ile Gly Asp Val Ser Glu Val Arg Ser Lys Lys Asp	
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Met Ser Gln
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Gln Lys Gln Gln Ser Trp Lys Pro Pro Asn Val Pro Lys Cys Ser Pro
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Pro Gln Arg Ser Asn Pro Cys Leu Ala Pro Tyr Ser Thr Pro Cys Gly
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gcc aac gcc ctg gtt cgg gcc cag cag ggg cgc ggc aca gga gga ggg	2717
Ala Asn Ala Leu Val Arg Ala Gln Gln Gly Arg Gly Thr Gly Gly Gly	
840 845 850	
ccg ggt ggg ccg gag ggt ggg gat gct gag ggc ccc atc aca gcc ctc	2765
Pro Gly Gly Pro Glu Gly Gly Asp Ala Glu Gly Pro Ile Thr Ala Leu	
855 860 865	
acc ttc ctg tac ttg cct cgg ccg cca gcc gat ccc gcc cga tac ccc	2813
Thr Phe Leu Tyr Leu Pro Arg Pro Pro Ala Asp Pro Ala Arg Tyr Pro	
870 875 880	
cgc tac ctg gcg cta ctg gag act cta acc cga gac ctg ggc ccc acg	2861
Arg Tyr Leu Ala Leu Leu Glu Thr Leu Thr Arg Asp Leu Gly Pro Thr	
885 890 895 900	
ctg ctg gtt cat ggg gtc act cca gtc acc tgc act gat ctg tga	2906
Leu Leu Val His Gly Val Thr Pro Val Thr Cys Thr Asp Leu *	
905 910 915	

<210> 323
 <211> 607
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (78)..(416)

<400> 323

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cgacagagga	gcaggcc				atg	agg	cag	gca	gga	gcc	acg	tat	ctg	ggc	cca	110	
					Met	Arg	Gln	Ala	Gly	Ala	Thr	Tyr	Leu	Gly	Pro		
					1				5					10			
gcg	cac	ccg	cca	agc	tct	cta	gcc	tct	cct	ggc	ctc	agt	ata	ctt	ctc	158	
Ala	His	Pro	Pro	Ser	Ser	Leu	Ala	Ser	Pro	Gly	Leu	Ser	Ile	Leu	Leu		
			15					20					25				
tgg	gag	atg	gtc	cag	ctg	aaa	atc	ccc	agc	atc	cac	aag	aaa	ggg	tgg	206	
Trp	Glu	Met	Val	Gln	Leu	Lys	Ile	Pro	Ser	Ile	His	Lys	Lys	Gly	Trp		
		30					35					40					
aag	ccc	tgg	ggg	ccc	tgg	cct	ggc	cca	ggt	gca	ggc	tgc	atg	gcc	ggg	254	
Lys	Pro	Trp	Gly	Pro	Trp	Pro	Gly	Pro	Gly	Ala	Gly	Cys	Met	Ala	Gly		
	45					50					55						
cgg	agc	ggt	gtc	tcc	ttt	cac	agc	ttc	ccc	gtc	tgt	ccg	cag	cct	cca	302	
Arg	Ser	Gly	Val	Ser	Phe	His	Ser	Phe	Pro	Val	Cys	Pro	Gln	Pro	Pro		
60					65					70					75		
gga	gcc	cca	cac	agg	gct	ggg	gct	ctg	tgc	ccc	caa	ctc	aca	ccc	gtc	350	
Gly	Ala	Pro	His	Arg	Ala	Gly	Ala	Leu	Cys	Pro	Gln	Leu	Thr	Pro	Val		
				80					85					90			
ggc	tcc	ccc	agg	agg	agc	agg	ctg	ggc	cca	gag	ccg	cag	ggt	ggg	ctg	398	
Gly	Ser	Pro	Arg	Arg	Ser	Arg	Leu	Gly	Pro	Glu	Pro	Gln	Gly	Gly	Leu		
			95				100					105					
cag	gga	ggt	ctg	act	tag	ctgggg	aaagtgccat	ccttgccatt	gctagtgaca							452	
Gln	Gly	Gly	Leu	Thr	*												
		110															
agctcgggct	gctgtggccc					cagcacagat					tcaacactca					512	
tgcacactca	cctccacacc					caactcacag					gaagcaaggc					572	
ccaggccaca					cagatgctgc					gagttgggat					tatga		607

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<210> 324
<211> 505
<212> DNA
<213> Homo sapiens
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<400> 324
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 gccataactt ga atg tta gga tct act ggt tat ttt tat ttc ctt gcc 108
 Met Leu Gly Ser Thr Gly Tyr Phe Tyr Phe Leu Ala
 1 5 10

gat ttg ctg ata tta aca ata gat ttt aat ctc ttg tta ata ata tac	156
Asp Leu Leu Ile Leu Thr Ile Asp Phe Asn Leu Leu Leu Ile Ile Tyr	
15 20 25	
ctt gca aac tac ttt tct cag tct gtg gct tat ctt ttc att tct tta	204
Leu Ala Asn Tyr Phe Ser Gln Ser Val Ala Tyr Leu Phe Ile Ser Leu	
30 35 40	
tgg gtt ttc ttt ggc atg agg gta caa gtt tta ctt tta atg aag taa	252
Trp Val Phe Phe Gly Met Arg Val Gln Val Leu Leu Leu Met Lys *	
45 50 55 60	
aatatgtaac ttacattac agtttgtgct tatttgtatt acttatgaaa catttcacct	312
cccagaagtc atgaaggtat tctcctctat ttccttctag aagtttggct cttcagattt	372
ccaatgttcc tgaaattaac ttctatgtag ggtgaggtag caaccaatt ttattttctt	432
ccatataatc acttgaccta gcaaaatata attgcctatt ctttcccca tgatctacaa	492
tgccatattt agt	505

<210> 325
 <211> 670
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (232)..(624)

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aggtcataac acatccagac tccttaagag aaagcctttc tgttttgga acttttcaaa	120
gccagggact tgtccagccc aacctccca ttgctcctag ctccctgaggc tcaggacccc	180
tggcttctgt cctccctgct cagggctctg cagcgttgcc tctgctcagc c atg ctc	237
Met Leu	
1	
ctg ctg ctc gtc cca gtg ctc gag gtg att ttt act ctg gga gga acc	285
Leu Leu Leu Val Pro Val Leu Glu Val Ile Phe Thr Leu Gly Gly Thr	
5 10 15	
aga gcc cag tcg gtg acc cag ctt gac agc cac gtc tct gtc tct gaa	333
Arg Ala Gln Ser Val Thr Gln Leu Asp Ser His Val Ser Val Ser Glu	
20 25 30	
gga acc ccg gtg ctg ctg agg tgc aac tac tca tct tct tat tca cca	381
Gly Thr Pro Val Leu Leu Arg Cys Asn Tyr Ser Ser Ser Tyr Ser Pro	
35 40 45 50	

tct ctc ttc tgg tat gtg caa cac ccc aac aaa gga ctc cag ctt ctc	429
Ser Leu Phe Trp Tyr Val Gln His Pro Asn Lys Gly Leu Gln Leu Leu	
55 60 65	
ctg aag tac aca tca gcg gcc acc ctg gtt aaa ggc atc aac ggt ttt	477
Leu Lys Tyr Thr Ser Ala Ala Thr Leu Val Lys Gly Ile Asn Gly Phe	
70 75 80	
gag gct gaa ttt aag aag agt gaa acc tcc ttc cac ctg acg aaa ccc	525
Glu Ala Glu Phe Lys Lys Ser Glu Thr Ser Phe His Leu Thr Lys Pro	
85 90 95	
tca gcc cat atg agc gac gcg gct gag tac ttc tgt gtt gtg agt gac	573
Ser Ala His Met Ser Asp Ala Ala Glu Tyr Phe Cys Val Val Ser Asp	
100 105 110	
aca gtg ctt gag act gca gga gag ctg aac aca agc ctc ctg aga tgc	621
Thr Val Leu Glu Thr Ala Gly Glu Leu Asn Thr Ser Leu Leu Arg Cys	
115 120 125 130	
tga gactttctgt gactcaagaa ctgcaccttg aagtctgttt tataat	670
*	

<210> 326
 <211> 794
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (200)..(304)

 <220>
 <221> misc_feature
 <222> (1)...(794)
 <223> n = a,t,c or g

<400> 326	
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ataggagaag ggacatgggt gctactgcaa ggggtttttt tgtttaggga gaacgcactg	180
tggaactcaa attccgggt atg cac tca acc tcg gca aag gca cct cgc tgt	232
Met His Ser Thr Ser Ala Lys Ala Pro Arg Cys	
1 5 10	
tgg tca cac ccc gtg agt ttt tgt ggt tta cta att gtc ctc tct gga	280
Trp Ser His Pro Val Ser Phe Cys Gly Leu Leu Ile Val Leu Ser Gly	
15 20 25	

cag ctc aat aga gcc agc cag tat att tcc ctg ctc atc aga gac tcc	343
Gln Leu Asn Arg Ala Ser Gln Tyr Ile Ser Leu Leu Ile Arg Asp Ser	
85 90 95 100	
aag ctc agt gat tca gcc acc tac ctc tgt gtg gtg aac att cgc cca	391
Lys Leu Ser Asp Ser Ala Thr Tyr Leu Cys Val Val Asn Ile Arg Pro	
105 110 115	
gga aac aca cct ttg gga ctg gaa caa gac ttc agg tca cgc tcg ata	439
Gly Asn Thr Pro Leu Gly Leu Glu Gln Asp Phe Arg Ser Arg Ser Ile	
120 125 130	
tcc aga acc ctg acc ctg ccg tgt acc agc tga gagactct aaatccagt	490
Ser Arg Thr Leu Thr Leu Pro Cys Thr Ser *	
135 140	
acaatgctgt cgaccta	507

<210> 328
 <211> 1043
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (210)..(1043)

<400> 328	
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aggaagggcc atttccaaaa gccctgtgct gacacagggt tgctgggttcc tcttcaagag	120
cccactctct ggggtggggc catatctcca gcagaggtgg gctggaaagg acccccccaa	180
tcccgccgc cgtgagctta gctggagcc atg gcc tct gca ccc atc tcg atg	233
Met Ala Ser Ala Pro Ile Ser Met	
1 5	
ctt gcg atg ctc ttc aca ttg agt ggg ctg aga gct cag tca gtg gct	281
Leu Ala Met Leu Phe Thr Leu Ser Gly Leu Arg Ala Gln Ser Val Ala	
10 15 20	
cag ccg gaa gat cag gtc aac gtt gct gaa ggg aat cct ctg act gtg	329
Gln Pro Glu Asp Gln Val Asn Val Ala Glu Gly Asn Pro Leu Thr Val	
25 30 35 40	
aaa tgc acc tat tca gtc tct gga aac cct tat ctt ttt tgg tat gtt	377
Lys Cys Thr Tyr Ser Val Ser Gly Asn Pro Tyr Leu Phe Trp Tyr Val	
45 50 55	
caa tac ccc aac cga ggc ctc cag ttc ctt ctg aaa tac atc aca ggg	425
Gln Tyr Pro Asn Arg Gly Leu Gln Phe Leu Leu Lys Tyr Ile Thr Gly	
60 65 70	

gat aac ctg gtt aaa ggc agc tat ggc ttt gaa gct gaa ttt aac aag	473
Asp Asn Leu Val Lys Gly Ser Tyr Gly Phe Glu Ala Glu Phe Asn Lys	
75 80 85	
agc caa acc tcc ttc cac ctg aag aaa cca tct gcc ctt gtg agc gac	521
Ser Gln Thr Ser Phe His Leu Lys Lys Pro Ser Ala Leu Val Ser Asp	
90 95 100	
tcc gct ttg tac ttc tgt gct gtg aga gag gta ata ctc acg gga gga	569
Ser Ala Leu Tyr Phe Cys Ala Val Arg Glu Val Ile Leu Thr Gly Gly	
105 110 115 120	
gga aac aaa ctc acc ttt ggg aca ggc act cag cta aaa gtg gaa ctc	617
Gly Asn Lys Leu Thr Phe Gly Thr Gly Thr Gln Leu Lys Val Glu Leu	
125 130 135	
aat atc cag aac cct gac cct gcc gtg tac cag ctg aga gac tct aaa	665
Asn Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys	
140 145 150	
tcc agt gac aag tct gtc tgc cta ttc acc gat ttt gat tct caa aca	713
Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr	
155 160 165	
aat gtg tca caa agt aag gat tct gat gtg tat atc aca gac aaa act	761
Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr	
170 175 180	
gtg cta gac atg agg tct atg gac ttc aag agc aac agt gct gtg gcc	809
Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala	
185 190 195 200	
tgg agc aac aaa tct gac ttt gca tgt gca aac gcc ttc aac aac agc	857
Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser	
205 210 215	
att att cca gaa gac acc ttc ttc ccc agc cca gaa agt tcc tgt gat	905
Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp	
220 225 230	
gtc aag ctg gtc gag aaa agc ttt gaa aca gat acg aac cta aac ttt	953
Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe	
235 240 245	
caa aac ctg tca gtg att ggg ttc cga atc ctc ctc ctg aaa gtg gcc	1001
Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala	
250 255 260	
ggg ttt aat ctg ctc atg acg ctg cgg ctg tgg tcc agc tga	1043
Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser *	
265 270 275	

<210> 329

<211> 1037
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(831)

<400> 329

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Met Ser Ile Ser Leu Leu Cys Cys Ala Ala Phe Pro Leu Leu Trp Ala	
1 5 10 15	
ggt cca gtg aat gct ggt ggt gtc act cag acc cca aaa ttc cgc atc	96
Gly Pro Val Asn Ala Gly Gly Val Thr Gln Thr Pro Lys Phe Arg Ile	
20 25 30	
ctg aag ata gga cag agc atg aca ctg cag tgt gcc cag gat atg aac	144
Leu Lys Ile Gly Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn	
35 40 45	
cat aac tac atg tac tgg tat cga caa gac cca ggc atg ggg ctg aag	192
His Asn Tyr Met Tyr Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Lys	
50 55 60	
ctg att tat tat tca gtt ggt gct ggt atc act gac aaa gga gaa gtc	240
Leu Ile Tyr Tyr Ser Val Gly Ala Gly Ile Thr Asp Lys Gly Glu Val	
65 70 75 80	
ccg aat ggc tac aac gtc tcc aga tca acc aca gag gat ttc ccg ctc	288
Pro Asn Gly Tyr Asn Val Ser Arg Ser Thr Thr Glu Asp Phe Pro Leu	
85 90 95	
agg ctg gag ttg gct gct ccc tcc cag aca tct gtg tac ttc tgt gcc	336
Arg Leu Glu Leu Ala Ala Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala	
100 105 110	
agc agt agg ggt ggg gcc ggg ctc aat gag cag ttc ttc ggg cca ggg	384
Ser Ser Arg Gly Gly Ala Gly Leu Asn Glu Gln Phe Phe Gly Pro Gly	
115 120 125	
aca cgg ctc acc gtg cta gag gac ctg aaa aac gtg ttc cca ccc gag	432
Thr Arg Leu Thr Val Leu Glu Asp Leu Lys Asn Val Phe Pro Pro Glu	
130 135 140	
gtc gct gtg ttt gag cca tca gaa gca gag atc tcc cac acc caa aag	480
Val Ala Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys	
145 150 155 160	
gcc aca ctg gta tgc ctg gcc aca ggc ttc tac ccc gac cac gtg gag	528
Ala Thr Leu Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu	
165 170 175	
ctg agc tgg tgg gtg aat ggg aag gag gtg cac agt ggg gtc agc aca	576
Leu Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr	
180 185 190	

gac ccg cag ccc ctc aag gag cag ccc gcc ctc aat gac tcc aga tac	624
Asp Pro Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr	
195 200 205	
tgc ctg agc agc cgc ctg agg gtc tcg gcc acc ttc tgg cag aac ccc	672
Cys Leu Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro	
210 215 220	
cgc aac cac ttc cgc tgt caa gtc cag ttc tac ggg ctc tcg gag aat	720
Arg Asn His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn	
225 230 235 240	
gac gag tgg acc cag gat agg gcc aaa cct gtc acc cag atc gtc agc	768
Asp Glu Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser	
245 250 255	
gcc gag gcc tgg ggt aga gca ggt gag tgg ggc ctg ggg aga tgc ctg	816
Ala Glu Ala Trp Gly Arg Ala Gly Glu Trp Gly Leu Gly Arg Cys Leu	
260 265 270	
gag gag att agg tga gaccagctac cagggaaaat ggaaagatcc aggtagcggg	871
Glu Glu Ile Arg *	
275	
caagactata tccagaagaa agccagagtg gacaagggtgg gatgatcaag gttcacaggg	931
tcagcaaagc acgggtgtgca cttccccac caagaagcat atagggtgaa tggagcacct	991
caagctcatt cttccttcag atcctgacac cttagagcta agctttt	1037
<210> 330	
<211> 738	
<212> DNA	
<213> Homo sapiens	
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<221> CDS	
<222> (300)..(608)	
<400> 330	
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gggaggccaa cacggttgga tctcttgagc ccaggagtgc gagactagcc tggccaacat	120
ggcgaaaccc cttctctttt tcttttttta aaatttttta gttagaaatg aaaaaaagaa	180
agaagtctag gttttctgaa acaagcactg tcttggtgct accttttttc atgtgtggac	240
acatagaaag cgaggatatt tgtacagcac cttgaaacaa ataagcagga ggtgatgtc	299
atg agc ctt agc cct gca ggg acc aga cta ggc ctt ctg aag ctg agg	347
Met Ser Leu Ser Pro Ala Gly Thr Arg Leu Gly Leu Leu Lys Leu Arg	
1 5 10 15	
tgg tcc ttg tcc cca cac ctt gta acc cat ttc cag ccc atg ggt gtc	395

Trp	Ser	Leu	Ser	Pro	His	Leu	Val	Thr	His	Phe	Gln	Pro	Met	Gly	Val		
			20					25					30				
agt	tgg	gaa	att	cta	cac	aag	atc	cta	gta	gat	gta	att	aca	tat	aat		443
Ser	Trp	Glu	Ile	Leu	His	Lys	Ile	Leu	Val	Asp	Val	Ile	Thr	Tyr	Asn		
		35					40					45					
tca	atg	gtt	ttt	gat	gat	ggg	gtt	tta	aaa	tca	agt	tat	tca	ata	ggc		491
Ser	Met	Val	Phe	Asp	Asp	Gly	Val	Leu	Lys	Ser	Ser	Tyr	Ser	Ile	Gly		
		50				55					60						
ggg	gtg	cag	tgg	ctc	acg	cct	gta	att	cca	gca	ctt	tgg	gag	gcc	gag		539
Gly	Val	Gln	Trp	Leu	Thr	Pro	Val	Ile	Pro	Ala	Leu	Trp	Glu	Ala	Glu		
	65				70				75					80			
gag	ggc	aga	tca	caa	ggc	cgg	gag	ttc	aag	acc	agc	ctg	acc	aac	atg		587
Glu	Gly	Arg	Ser	Gln	Gly	Arg	Glu	Phe	Lys	Thr	Ser	Leu	Thr	Asn	Met		
			85				90					95					
gta	aaa	ctc	cgt	ctc	tac	taa	aa	attcaaaaaat	tagccggccg	tggtggtgga							640
Val	Lys	Leu	Arg	Leu	Tyr	*											
			100														
catctgtaat	cccagctact	tagggggctg	aggcaggaga	atcgcttgaa	cgggggcagg												700
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<210> 331
 <211> 679
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (243)..(449)

<220>
 <221> misc_feature
 <222> (1)...(679)
 <223> n = a,t,c or g

<400> 331																	
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tgtgacccgc	atacctaccg	gccccgacc	cgaaccgcgt	ggcgtccgcc	cgagccctgg												180
cgtctgtggg	tctctgtctg	ctgccgtgc	tcgcagagcc	caggaaactc	tgccccgcagc												240
tt	atg	acg	gtc	att	aac	cag	ttt	ctg	acc	aag	gac	aag	gac	acc	tac		287
	Met	Thr	Val	Ile	Asn	Gln	Phe	Leu	Thr	Lys	Asp	Lys	Asp	Thr	Tyr		
	1				5				10					15			

atg gac act gtc aac aga tac cac ctc acg gag ccg gaa aga aac aca 335
Met Asp Thr Val Asn Arg Tyr His Leu Thr Glu Pro Glu Arg Asn Thr
20 25 30

tcc tct aaa ctc aag gac tgc gtg acc gac aca atg acc ccc gag gag 383
Ser Ser Lys Leu Lys Asp Cys Val Thr Asp Thr Met Thr Pro Glu Glu
35 40 45

aca gag gcc gtc gtg cag caa ctg gaa gaa atc aac aac cag tgt gcc 431
Thr Glu Ala Val Val Gln Gln Leu Glu Glu Ile Asn Asn Gln Cys Ala
50 55 60

gac acg ata ctg aag taa caccat ccataggcac ctcgggttcc tgtccaggct 485
Asp Thr Ile Leu Lys *
65

gcctgtccca accatgagaa tctgggcca gggccccacc ctccctagct cccgccctgc 545

tgctgectct actctctctc ctgctgtgct gattggggca agcctgggaa cggtgcccc 605

ccacctcccc acccaggncc tgtcctgcgg gacaatgctg cctaataaac tcacctgcat 665

ccaaaaaaaaa aaaa 679

<210> 332
<211> 445
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (200)..(400)

<400> 332
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ctgccattgg agagcagcag ccatggctct gtgctacca ctatggccgt gtgccttgac 120

aagggccaca agatgaccaa gaacatgagc aagcccaggc acagctgccg ccgcgggcgc 180

ctgaccaaac accaaattc atg tgg gac atg atc cga gag gtg tgt ggt ttc 232
Met Trp Asp Met Ile Arg Glu Val Cys Gly Phe
1 5 10

gcc ccg tat gag cgg cac gcc atg gtg tta ctc aag gtc tcc aag gac 280
Ala Pro Tyr Glu Arg His Ala Met Val Leu Leu Lys Val Ser Lys Asp
15 20 25

aaa cgg gcc ctc aag ttc atc aag aaa aga gtg ggg aca cac atc cgc 328
Lys Arg Ala Leu Lys Phe Ile Lys Lys Arg Val Gly Thr His Ile Arg
30 35 40

act aag agg agg cag gag gag ctg agc aat gtc cca gcc atc atg agg 376
Thr Lys Arg Arg Gln Glu Glu Leu Ser Asn Val Pro Ala Ile Met Arg

45	50	55	
aaa gct gat gcc aag aaa gac tga gccccctgtc ctgccctctc tctgaaataa			430
Lys Ala Asp Ala Lys Lys Asp *			
60	65		

agaacacctt gacag	445
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<210> 333
 <211> 1716
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (633)..(1433)

<400> 333	
cccggttcga cgattcgtag gatatccaag ggacctcagg ctgtgggctg ggcttcaggg	60
agggagccag agggtcagtg tccctagagg atccccaggg aagtgccaaag gaggagaagg	120
aatgtcctgg ctgacctaa ggacgacaga agattggggga agaggggggta tcaggaagaa	180
atggggtttca gttcagttta acaaacatct attgtgtgtt cactggggcca ggccagtgtt	240
aggtgctagg gagacagagg tgaagagcct gccctctagc agctgacagc ctggcaaaaa	300
aataagacag aataaggtag accctgattt tggaacctga agaccaaagt gcaagattag	360
ctctgtact tccatctgtg gaccattggg caggtatctc tgggccttca cttactcttt	420
gtgaaatgag gacaggggca atccctaccc taccaagtca ttgggagtgga agacatgatg	480
acacggtgat tgtgaaaaga ttttgtcaat cgcaccagca ttaaggggtgc ccactctccag	540
gttccccccag gcctcaaggc tccaaggcc tgagtgggca ggtagcacc aggtatagac	600
cttcacgtg cagcaccag gacacagcca gc atg aac tgg gca ttt ctg cag	653
	Met Asn Trp Ala Phe Leu Gln
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ggc ctg ctg agt ggc gtg aac aag tac tcc aca gtg ctg agc cgc atc	701
Gly Leu Leu Ser Gly Val Asn Lys Tyr Ser Thr Val Leu Ser Arg Ile	
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Trp Leu Ser Val Val Phe Ile Phe Arg Val Leu Val Tyr Val Val Ala	
25 30 35	
gcg gag gag gtg tgg gac gat gag cag aag gac ttt gtc tgc aac acc	797
Ala Glu Glu Val Trp Asp Asp Glu Gln Lys Asp Phe Val Cys Asn Thr	
40 45 50 55	

aag cag ccc ggc tgc ccc aac gtc tgc tat gac gag ttc ttc ccc gtg	845
Lys Gln Pro Gly Cys Pro Asn Val Cys Tyr Asp Glu Phe Phe Pro Val	
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tcc cac gtg cgc ctc tgg gcc cta cag ctc atc ctg gtc acg tgc ccc	893
Ser His Val Arg Leu Trp Ala Leu Gln Leu Ile Leu Val Thr Cys Pro	
75 80 85	
tca ctg ctc gtg gtc atg cac gtg gcc tac cgc gag gaa cgc gag cgc	941
Ser Leu Leu Val Val Met His Val Ala Tyr Arg Glu Glu Arg Glu Arg	
90 95 100	
aag cac cac ctg aaa cac ggg ccc aat gcc ccg tcc ctg tac gac aac	989
Lys His His Leu Lys His Gly Pro Asn Ala Pro Ser Leu Tyr Asp Asn	
105 110 115	
ctg agc aag aag cgg ggc gga ctg tgg tgg acg tac ttg ctg agc ctc	1037
Leu Ser Lys Lys Arg Gly Gly Leu Trp Trp Thr Tyr Leu Leu Ser Leu	
120 125 130 135	
atc ttc aag gcc gcc gtg gat gct ggc ttc ctc tat atc ttc cac cgc	1085
Ile Phe Lys Ala Val Asp Ala Gly Phe Leu Tyr Ile Phe His Arg	
140 145 150	
ctc tac aag gat tat gac atg ccc cgc gtg gtg gcc tgc tcc gtg gag	1133
Leu Tyr Lys Asp Tyr Asp Met Pro Arg Val Val Ala Cys Ser Val Glu	
155 160 165	
cct tgc ccc cac act gtg gac tgt tac atc tcc cgg ccc acg gag aag	1181
Pro Cys Pro His Thr Val Asp Cys Tyr Ile Ser Arg Pro Thr Glu Lys	
170 175 180	
aag gtc ttc acc tac ttc atg gtg acc aca gct gcc atc tgc atc ctg	1229
Lys Val Phe Thr Tyr Phe Met Val Thr Thr Ala Ala Ile Cys Ile Leu	
185 190 195	
ctc aac ctc agt gaa gtc ttc tac ctg gtg ggc aag agg tgc atg gag	1277
Leu Asn Leu Ser Glu Val Phe Tyr Leu Val Gly Lys Arg Cys Met Glu	
200 205 210 215	
atc ttc ggc ccc agg cac cgg cgg cct cgg tgc cgg gaa tgc cta ccc	1325
Ile Phe Gly Pro Arg His Arg Arg Pro Arg Cys Arg Glu Cys Leu Pro	
220 225 230	
gat acg tgc cca cca tat gtc ctc tcc cag gga ggg cac cct gag gat	1373
Asp Thr Cys Pro Pro Tyr Val Leu Ser Gln Gly Gly His Pro Glu Asp	
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Gly Asn Ser Val Leu Met Lys Ala Gly Ser Ala Pro Val Asp Ala Gly	
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ggg tat cca taa cct gcgagatcag cagataagat caacaggtcc ccccccacatg	1476
Gly Tyr Pro *	
265	
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 Met Tyr Cys Cys
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 Ala Leu Arg Ser Cys Ser Val Pro Thr Gly Pro Ala Thr Thr Phe Cys
 5 10 15 20
 tca ttt gat aaa agc tgc cgc tgt gga gtc tgc cta ccc agc acc tgc 151
 Ser Phe Asp Lys Ser Cys Arg Cys Gly Val Cys Leu Pro Ser Thr Cys
 25 30 35
 cca cat gag atc agc ctc ctt cag ccc atc tgc tgt gac acc tgc ccc 199
 Pro His Glu Ile Ser Leu Leu Gln Pro Ile Cys Cys Asp Thr Cys Pro
 40 45 50
 cca ccc tgc tgc aag cct gat acc tat gtg cca act tgc tgg ctg ctc 247
 Pro Pro Cys Cys Lys Pro Asp Thr Tyr Val Pro Thr Cys Trp Leu Leu
 55 60 65
 aac aac tgt cac ccg act ccc gga ctg agt ggg atc aac ctg acc acc 295
 Asn Asn Cys His Pro Thr Pro Gly Leu Ser Gly Ile Asn Leu Thr Thr
 70 75 80
 tat gtt cag cct ggc tgt gag agt ccc tgt gag ccc cgc tgt taa cca 343
 Tyr Val Gln Pro Gly Cys Glu Ser Pro Cys Glu Pro Arg Cys *
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 cagc 407

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ttc acc gtg cac ctg ggg cgc cag aag acg gtg gtg ctg acg ggg ttc      100
Phe Thr Val His Leu Gly Arg Gln Lys Thr Val Val Leu Thr Gly Phe
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gag gcg gtc aaa gag gcg ctg gcg ggc ccc ggg cag gag ctg gcc gac      148
Glu Ala Val Lys Glu Ala Leu Ala Gly Pro Gly Gln Glu Leu Ala Asp
                   30                   35                   40

cgg cct ccc atc gcc atc ttc cag ctc atc cag cga ggt gga ggc atc      196
Arg Pro Pro Ile Ala Ile Phe Gln Leu Ile Gln Arg Gly Gly Gly Ile
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ttc ttc tca tct ggg gcg cgc tgg agg gct gcc cgc cag ttc acg gtg      244
Phe Phe Ser Ser Gly Ala Arg Trp Arg Ala Ala Arg Gln Phe Thr Val
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cgt gcc ctg cac agc ctg ggc gtg ggc cgg gag ccg gtg gct gac aag      292
Arg Ala Leu His Ser Leu Gly Val Gly Arg Glu Pro Val Ala Asp Lys
                   75                   80                   85                   90

att ctg cag gag ctg aaa tgc ctc tct ggg cag ctg gat ggc tac aga      340
Ile Leu Gln Glu Leu Lys Cys Leu Ser Gly Gln Leu Asp Gly Tyr Arg
                   95                   100                   105

ggc cgg ccc ttc ccg ctg gcc cta ctg ggc tgg gct ccc tcc aat atc      388
Gly Arg Pro Phe Pro Leu Ala Leu Leu Gly Trp Ala Pro Ser Asn Ile
                   110                   115                   120

acc ttc gcg ctc ctc ttc ggc cgc cga ttt gac tac cgg gac ccc gtg      436
Thr Phe Ala Leu Leu Phe Gly Arg Arg Phe Asp Tyr Arg Asp Pro Val
                   125                   130                   135

ttt gtg tcc ctg ctg ggt ctc atc gat gag gtc atg gtc ctc ttg ggg      484
Phe Val Ser Leu Leu Gly Leu Ile Asp Glu Val Met Val Leu Leu Gly
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tcc cct ggc ctg cag ctg ttc aac gtc cac cca tgg ctc ggg gcc ctg      532
Ser Pro Gly Leu Gln Leu Phe Asn Val His Pro Trp Leu Gly Ala Leu
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Leu	Gln	Leu	His	Arg	Pro	Val	Leu	Arg	Lys	Ile	Glu	Glu	Val	Arg	Ala	
			175						180					185		
att	ctg	agg	acc	ctc	ctg	gag	gcg	cgg	agg	ccc	cac	gtg	tgc	ccg	ggg	628
Ile	Leu	Arg	Thr	Leu	Leu	Glu	Ala	Arg	Arg	Pro	His	Val	Cys	Pro	Gly	
			190					195					200			
gac	ccc	gtg	tgc	agc	tat	gtg	gac	gcc	ctg	atc	cag	cag	gga	cag	ggg	676
Asp	Pro	Val	Cys	Ser	Tyr	Val	Asp	Ala	Leu	Ile	Gln	Gln	Gly	Gln	Gly	
		205					210					215				
gat	gac	ccc	gag	ggc	ctg	ttt	gct	gag	gcc	aac	gcg	gtg	gcc	tgc	acc	724
Asp	Asp	Pro	Glu	Gly	Leu	Phe	Ala	Glu	Ala	Asn	Ala	Val	Ala	Cys	Thr	
		220				225					230					
ctg	gac	atg	gtc	atg	gcc	ggg	acg	gag	acg	acc	tcg	gcc	acg	ctg	cag	772
Leu	Asp	Met	Val	Met	Ala	Gly	Thr	Glu	Thr	Thr	Ser	Ala	Thr	Leu	Gln	
		235			240					245					250	
tgg	gcc	gca	ctt	ctg	atg	ggc	cgg	cac	ccg	gac	gtg	cag	ggc	cgg	gtg	820
Trp	Ala	Ala	Leu	Leu	Met	Gly	Arg	His	Pro	Asp	Val	Gln	Gly	Arg	Val	
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cag	gag	gag	cta	gac	cgc	gtg	ctg	ggc	cct	ggg	cgg	act	ccc	cgg	ctg	868
Gln	Glu	Glu	Leu	Asp	Arg	Val	Leu	Gly	Pro	Gly	Arg	Thr	Pro	Arg	Leu	
			270					275					280			
gag	gac	cag	cag	gct	ctg	ccc	tac	aca	agc	gcc	gtg	ctc	cac	gag	gtg	916
Glu	Asp	Gln	Gln	Ala	Leu	Pro	Tyr	Thr	Ser	Ala	Val	Leu	His	Glu	Val	
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cag	cgg	ttc	atc	acg	ctc	ctg	ccg	cac	gtg	ccc	cgc	tgc	acc	gcg	gcc	964
Gln	Arg	Phe	Ile	Thr	Leu	Leu	Pro	His	Val	Pro	Arg	Cys	Thr	Ala	Ala	
		300				305					310					
gac	aca	cag	ctg	ggc	ggc	ttc	ctg	ctc	ccc	aag	ggc	acg	ccc	gtg	att	1012
Asp	Thr	Gln	Leu	Gly	Gly	Phe	Leu	Leu	Pro	Lys	Gly	Thr	Pro	Val	Ile	
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ccc	ctg	ctg	acc	tcg	gtg	ctc	ctg	gat	gag	aca	cag	tgg	cag	acc	cca	1060
Pro	Leu	Leu	Thr	Ser	Val	Leu	Leu	Asp	Glu	Thr	Gln	Trp	Gln	Thr	Pro	
			335						340					345		
ggc	cag	ttc	aac	ccc	ggc	cat	ttc	ctg	gac	gcg	aat	ggg	cac	ttt	gtg	1108
Gly	Gln	Phe	Asn	Pro	Gly	His	Phe	Leu	Asp	Ala	Asn	Gly	His	Phe	Val	
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aag	cgg	gag	gcc	ttc	ctg	cct	ttc	tct	gca	ggt	cag	cag	ccc	tcg	ggg	1156
Lys	Arg	Glu	Ala	Phe	Leu	Pro	Phe	Ser	Ala	Gly	Gln	Gln	Pro	Ser	Gly	
		365				370						375				
ccg	ggg	tgg	ggc	ggc	acc	tcc	agg	gct	cca	ggg	gtg	gga	cgg	ccc	cag	1204
Pro	Gly	Trp	Gly	Gly	Thr	Ser	Arg	Ala	Pro	Gly	Val	Gly	Arg	Pro	Gln	
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ctc	cgc	ctg	ccg	cct	ctg	cac	cca	cct	cct	gat	ctc	agg	ttc	tga	agg	1252

Leu Arg Leu Pro Pro Leu His Pro Pro Pro Asp Leu Arg Phe *

395

400

405

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gactcctgca gacccactc cattcccgt cctggaacac ttctgcagc tgtgcctgga 2032

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<211> 765

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Met Phe Thr
1

ttg tcg ttt aaa aaa caa tca aac gac att agc agt ttt aca aca ttt 163
Leu Ser Phe Lys Lys Gln Ser Asn Asp Ile Ser Ser Phe Thr Thr Phe
5 10 15

tcc ttt cca gtt aaa act gta tac cgt tac cat ttt ccc atc ata ctc 211
Ser Phe Pro Val Lys Thr Val Tyr Arg Tyr His Phe Pro Ile Ile Leu
20 25 30 35

ttc acc tac gat act gtt tta agt ggc tgt ata gat ttc cac ttt cac 259
Phe Thr Tyr Asp Thr Val Leu Ser Gly Cys Ile Asp Phe His Phe His
40 45 50

aac aga att agc aga ttc cca aaa ctt gaa tat tta att tta aaa aaa 307
Asn Arg Ile Ser Arg Phe Pro Lys Leu Glu Tyr Leu Ile Leu Lys Lys
55 60 65

att ctt aat aac tga tattaaattt atatacgcaa atctgacaca ttacttcctt 362
Ile Leu Asn Asn *
70

aggataaatt cctgtacgca cagtctttcc attttaagcc tattatacta tgaaggagtc 422

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cgtctctaca gacgatcaaa aaattagctt ggtgtggtgg cgcgcgctg tgatctcagc 542

taccaggag gctgaggtgg gaggatcact taagcccgagg aggtcgaggc tgctgtgagc 602

cgtgagccac tgatcatacc actgcactcc agtctgggca acagagcgat cctgtttcag 662

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Pro	Ala	Ala	Phe	Pro	Lys	Asp	Asn	Ile	His	Phe	Lys	Pro	Ile	Asn	Thr	
				30					35					40		
aat	ctt	gat	agg	gca	aat	gaa	ttg	gca	aaa	aca	gac	att	ttg	agt	cta	254
Asn	Leu	Asp	Arg	Ala	Asn	Glu	Leu	Ala	Lys	Thr	Asp	Ile	Leu	Ser	Leu	
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aca	agt	caa	aac	aag	acc	ttt	gat	ccc	aag	aaa	gaa	aat	ccc	att	gtg	302
Thr	Ser	Gln	Asn	Lys	Thr	Phe	Asp	Pro	Lys	Lys	Glu	Asn	Pro	Ile	Val	
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Leu	Leu	Ser	Asp	Phe	Tyr	Tyr	Gly	Gln	His	Lys	Gly	Glu	Gly	Gln	Pro	
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gaa	cag	aag	act	cac	acc	acc	ttt	aaa	tgc	ctc	agc	tgc	gtg	aaa	gtt	398
Glu	Gln	Lys	Thr	His	Thr	Thr	Phe	Lys	Cys	Leu	Ser	Cys	Val	Lys	Val	
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cta	aaa	aat	gtt	aag	ttt	atg	aat	cac	gtg	aag	cat	cat	ttg	gaa	ttt	446
Leu	Lys	Asn	Val	Lys	Phe	Met	Asn	His	Val	Lys	His	His	Leu	Glu	Phe	
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Glu	Lys	Gln	Arg	Asn	Asp	Ser	Trp	Glu	Asn	His	Thr	Thr	Cys	Gln	His	
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Cys	His	Arg	Ser	Leu	Pro	Thr	Pro	Phe	Gln	Leu	Gln	Cys	His	Ile	Glu	
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Leu	Ser	Phe	Glu	Thr	Asp	Gln	Val	Leu	Leu	Gln	His	Met	Lys	Asp	His	
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Ser	Ser	Val	Phe	Ala	Asp	Val	Glu	Thr	His	Phe	Arg	Thr	Cys	His	Glu	
			205					210					215			
aac	aca	aag	aat	ttg	ctt	tgt	ccc	ttt	tgt	ctc	aaa	att	ttc	aaa	aca	782
Asn	Thr	Lys	Asn	Leu	Leu	Cys	Pro	Phe	Cys	Leu	Lys	Ile	Phe	Lys	Thr	
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gca	aca	cca	tac	atg	tgt	cat	tat	agg	ggc	cac	tgg	gga	aag	agt	gca	830
Ala	Thr	Pro	Tyr	Met	Cys	His	Tyr	Arg	Gly	His	Trp	Gly	Lys	Ser	Ala	

235	240	245	
cac cag tgt tcc aag tgc cgg cta cag ttt tta act ttc aag gag aaa			878
His Gln Cys Ser Lys Cys Arg Leu Gln Phe Leu Thr Phe Lys Glu Lys			
250	255	260	265
atg gag cac aag acc cag tgt cat caa atg ttt aag aag cct aag caa			926
Met Glu His Lys Thr Gln Cys His Gln Met Phe Lys Lys Pro Lys Gln			
270	275		280
cta gaa gga tta cct cct gaa aca aaa gtt act att caa gtg tca ctg			974
Leu Glu Gly Leu Pro Pro Glu Thr Lys Val Thr Ile Gln Val Ser Leu			
285	290		295
gaa cct ctt cag cca gga tca gtg gat gta gca tcc ata act gtg agc			1022
Glu Pro Leu Gln Pro Gly Ser Val Asp Val Ala Ser Ile Thr Val Ser			
300	305		310
aca tct gac tct gaa cca tca ctc ccc agg tct aaa agc aaa att tca			1070
Thr Ser Asp Ser Glu Pro Ser Leu Pro Arg Ser Lys Ser Lys Ile Ser			
315	320		325
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Lys Lys Ser His *			
330			
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	Met Pro Ser		
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gca tcc tgt gat aca cta ctg gat gac atc gaa gat atc gtg tct cag			162
Ala Ser Cys Asp Thr Leu Leu Asp Asp Ile Glu Asp Ile Val Ser Gln			
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gaa gat tca aaa cca caa gat agg cat ttt gta aga aag gat gtt gtc			210
Glu Asp Ser Lys Pro Gln Asp Arg His Phe Val Arg Lys Asp Val Val			

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ccg aag gta cga agg cga aat acc caa aaa tat ttg caa gag gaa gaa				258
Pro Lys Val Arg Arg Asn Thr Gln Lys Tyr Leu Gln Glu Glu	40	45	50	
aac agt cca cca agt gac agc act att cca ggc ata cag aaa att tgg				306
Asn Ser Pro Pro Ser Asp Ser Thr Ile Pro Gly Ile Gln Lys Ile Trp	55	60	65	
ata cga aca tgg ggt tgt tct cat aat aat tca gat gga gaa tat atg				354
Ile Arg Thr Trp Gly Cys Ser His Asn Asn Ser Asp Gly Glu Tyr Met	70	75	80	
gct gga cag cta gct gct tat ggc tat aaa att aca gaa aat gca tcc				402
Ala Gly Gln Leu Ala Ala Tyr Gly Tyr Lys Ile Thr Glu Asn Ala Ser	85	90	95	
gat gca gat tta tgg ctc ctg aac agt tgc act gta aaa aac cca gct				450
Asp Ala Asp Leu Trp Leu Leu Asn Ser Cys Thr Val Lys Asn Pro Ala	100	105	110	115
gaa gac cac ttt aga aac tca att aaa aaa gct caa gag gag aac aag				498
Glu Asp His Phe Arg Asn Ser Ile Lys Lys Ala Gln Glu Glu Asn Lys	120	125	130	
aaa atc gta ctg gct gga tgc gtt cct caa gcc cag cct cgc cag gac				546
Lys Ile Val Leu Ala Gly Cys Val Pro Gln Ala Gln Pro Arg Gln Asp	135	140	145	
tac ctt aag gga ctg agt atc att ggg gtt cag cag ata gat cgt gtg				594
Tyr Leu Lys Gly Leu Ser Ile Ile Gly Val Gln Gln Ile Asp Arg Val	150	155	160	
gta gaa gtt gtg gag gag aca att aaa ggt cac tct gtg aga ctg ctg				642
Val Glu Val Val Glu Glu Thr Ile Lys Gly His Ser Val Arg Leu Leu	165	170	175	
ggg cag aaa aag gat aat gga agg cgg ctt ggg gga gca cga ttg gat				690
Gly Gln Lys Lys Asp Asn Gly Arg Arg Leu Gly Gly Ala Arg Leu Asp	180	185	190	195
ttg ccg aag att agg aag aat cca ctg ata gaa atc att tcc atc aat				738
Leu Pro Lys Ile Arg Lys Asn Pro Leu Ile Glu Ile Ile Ser Ile Asn	200	205	210	
acc ggg tgt ctc aat gct tgt acc tac tgc aaa act aaa cac gcc aga				786
Thr Gly Cys Leu Asn Ala Cys Thr Tyr Cys Lys Thr Lys His Ala Arg	215	220	225	
gga aat ttg gcc agt tat cca att gat gaa cta gta gat aga gcc aaa				834
Gly Asn Leu Ala Ser Tyr Pro Ile Asp Glu Leu Val Asp Arg Ala Lys	230	235	240	
caa tct ttt caa gag ggt gtt tgt gag ata tgg ttg acc agt gaa gac				882
Gln Ser Phe Gln Glu Gly Val Cys Glu Ile Trp Leu Thr Ser Glu Asp	245	250	255	

acg ggg gct tat ggc aga gat att ggc acc aat ctc ccc aca ctc ctg	930
Thr Gly Ala Tyr Gly Arg Asp Ile Gly Thr Asn Leu Pro Thr Leu Leu	
260 265 270 275	
tgg aaa ctg gtt gaa gtg att cct gag gga gca atg ctg agg ctt ggc	978
Trp Lys Leu Val Glu Val Ile Pro Glu Gly Ala Met Leu Arg Leu Gly	
280 285 290	
atg aca aat ccg ccc tat att tta gag cat ctg gag gaa atg gca aaa	1026
Met Thr Asn Pro Pro Tyr Ile Leu Glu His Leu Glu Glu Met Ala Lys	
295 300 305	
atc ctt aat cac ccc aga gtc tac gct ttt ctg cac ata cca gtc cag	1074
Ile Leu Asn His Pro Arg Val Tyr Ala Phe Leu His Ile Pro Val Gln	
310 315 320	
tct gcc tcc gac agc gta ctc atg gaa atg aaa aga gaa tac tgt gtg	1122
Ser Ala Ser Asp Ser Val Leu Met Glu Met Lys Arg Glu Tyr Cys Val	
325 330 335	
gct gac ttc aaa aga gta gtg gat ttt ctg aaa gag aaa gtt cct gga	1170
Ala Asp Phe Lys Arg Val Val Asp Phe Leu Lys Glu Lys Val Pro Gly	
340 345 350 355	
ata act att gct aca gat att atc tgt ggt ttt cct gga gaa aca gat	1218
Ile Thr Ile Ala Thr Asp Ile Ile Cys Gly Phe Pro Gly Glu Thr Asp	
360 365 370	
cag gat ttt caa gaa aca gtg aaa ctt gtt gaa gag tac aaa ttc cca	1266
Gln Asp Phe Gln Glu Thr Val Lys Leu Val Glu Glu Tyr Lys Phe Pro	
375 380 385	
agc ctg ttt att aac caa ttt tac cca aga cca gga act cct gct gca	1314
Ser Leu Phe Ile Asn Gln Phe Tyr Pro Arg Pro Gly Thr Pro Ala Ala	
390 395 400	
aaa atg gaa caa gtt cca gca caa gtg aaa aag caa agg aca aaa gat	1362
Lys Met Glu Gln Val Pro Ala Gln Val Lys Lys Gln Arg Thr Lys Asp	
405 410 415	
ctt tct cgg gtg ttt cat tct tac agt cca tat gat cac aag att ggt	1410
Leu Ser Arg Val Phe His Ser Tyr Ser Pro Tyr Asp His Lys Ile Gly	
420 425 430 435	
gaa aga caa caa gtg tta gta aca gaa gaa tct ttt gat tcc aag ttt	1458
Glu Arg Gln Gln Val Leu Val Thr Glu Glu Ser Phe Asp Ser Lys Phe	
440 445 450	
tat gtt gca cac aat caa ttc tat gag cag gtt tta gtg cca aag aac	1506
Tyr Val Ala His Asn Gln Phe Tyr Glu Gln Val Leu Val Pro Lys Asn	
455 460 465	
cct gcg ttc atg ggg aag atg gtt gaa gtg gac atc tat gaa tca ggc	1554
Pro Ala Phe Met Gly Lys Met Val Glu Val Asp Ile Tyr Glu Ser Gly	
470 475 480	

aaa cat ttt atg aaa ggg cag cca gta tct gat gcc aaa gtg tac acg	1602
Lys His Phe Met Lys Gly Gln Pro Val Ser Asp Ala Lys Val Tyr Thr	
485 490 495	
ccc tcc atc agc aaa ccg cta gca aag gga gaa gtc tca ggt ttg aca	1650
Pro Ser Ile Ser Lys Pro Leu Ala Lys Gly Glu Val Ser Gly Leu Thr	
500 505 510 515	
aag gac ttc aga aat ggg ctt ggg aac cag ctg agt tca gga tcc cac	1698
Lys Asp Phe Arg Asn Gly Leu Gly Asn Gln Leu Ser Ser Gly Ser His	
520 525 530	
acc tct gct gca tct cag tgt gac tca gcg agt tcc aga atg gtg ctg	1746
Thr Ser Ala Ala Ser Gln Cys Asp Ser Ala Ser Ser Arg Met Val Leu	
535 540 545	
ccc atg cca agg cta cat caa gac tgt gcg ctg agg atg tcc gtg ggc	1794
Pro Met Pro Arg Leu His Gln Asp Cys Ala Leu Arg Met Ser Val Gly	
550 555 560	
ttg gct ctg ctg ggt ctt ctt ttt gct ttt ttt gtc aag gtc tat aat	1842
Leu Ala Leu Leu Gly Leu Leu Phe Ala Phe Phe Val Lys Val Tyr Asn	
565 570 575	
tag aata caactaatgg aaacatctat aaagaagaat acatttctaa ttaaaatctt	1899
* 580	
caatgaacag gaaagcgaca tctccattct ccaagggcaa taatttgtac tggatcatgct	1959
gcctccttct cagccactct tcttaatgag gctccccctg tctcacattg agttggggccc	2019
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gcttttgggtt tacttttagc aagaaatgca agcgggttgca ttttttctgt ttgtttcaat	2139
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ctcttgcccc ccaggctgga gtgggtgcagt ggcacgatct caggtcactg cagccttgac	2319
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caggcttgcc tggaactcct agcctcaagc agtcttcttg cctcagcctc ccaaagtgc	2499
gggattacag gcgtgagcca ctccaccag ccagattaa atgtttttat ttctacctgc	2559
catcattggt ctttactaag tgaagtgact tctttcttta acaataaatg gaattggtat	2619
actaagcaaa aaaaaaaaaa	2638

agc cag gac ggg atc cag agg ccg ccc ttc cgc ttc ccc aag ggc ggg Ser Gln Asp Gly Ile Gln Arg Pro Pro Phe Arg Phe Pro Lys Gly Gly 160 165 170	768
cac ctc ctg cag ttc ctc tcg tgc ctg gag aat ggg ctg ctc cca cat His Leu Leu Gln Phe Leu Ser Cys Leu Glu Asn Gly Leu Leu Pro His 175 180 185	816
ggg cag ttg gac ccg cca ctg tgg tcc cag agg ggt aag ggc aaa gtg Gly Gln Leu Asp Pro Pro Leu Trp Ser Gln Arg Gly Lys Gly Lys Val 190 195 200 205	864
ttt cct aaa ctg cgc aag cga agc cct cag ggt tct gcc gag tcc aca Phe Pro Lys Leu Arg Lys Arg Ser Pro Gln Gly Ser Ala Glu Ser Thr 210 215 220	912
tct tca gac aaa gat gat gat gag gcc acg gat tat gtg ttc agg atc Ser Ser Asp Lys Asp Asp Asp Glu Ala Thr Asp Tyr Val Phe Arg Ile 225 230 235	960
atc tac cct ggc atg cag tcg gaa ttc gtt gcc ccc gac ttc ttg ggc Ile Tyr Pro Gly Met Gln Ser Glu Phe Val Ala Pro Asp Phe Leu Gly 240 245 250	1008
agc act tcc tcc gtc tct gtg ggc cct gcc tgg atg atg gtt cct gca Ser Thr Ser Ser Val Ser Val Gly Pro Ala Trp Met Met Val Pro Ala 255 260 265	1056
ggc cgg tcc atg ctg gtg gtg gcc aga ggg agt cag tgg gag cca gcc Gly Arg Ser Met Leu Val Val Ala Arg Gly Ser Gln Trp Glu Pro Ala 270 275 280 285	1104
aga tgg gac act act ctc ccc acg cca agc ccg aag gag cag ccc ccc Arg Trp Asp Thr Thr Leu Pro Thr Pro Ser Pro Lys Glu Gln Pro Pro 290 295 300	1152
agt aat gtc tgg gat ctc ccc gtc ccc agg ggc tgg gtg cca gcc acc Ser Asn Val Trp Asp Leu Pro Val Pro Arg Gly Trp Val Pro Ala Thr 305 310 315	1200
tct gcc atg ttg tca att gag ttc tgg tcc caa ggg aga tgg agg cag Ser Ala Met Leu Ser Ile Glu Phe Trp Ser Gln Gly Arg Trp Arg Gln 320 325 330	1248
gaa ggg aga tgg agg cag agg gat tga tgccc tcctgctgtc cagcctccac Glu Gly Arg Trp Arg Gln Arg Asp *	1300
t	1301

<210> 341
<211> 723
<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (101)..(637)

<400> 341

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aaggagcgtc acacgattaa gtatcgtgtc acataatagg  atg aca aag ttt tta      115
                                         Met Thr Lys Phe Leu
                                         1           5

att gtt tca gat aca cat ggt gat cgt gag atc att gct gat att ttt      163
Ile Val Ser Asp Thr His Gly Asp Arg Glu Ile Ile Ala Asp Ile Phe
                        10                        15                        20

gac aaa tgg cgg gat agc gtt gcc ggc att ttt tac aat ggg gat tct      211
Asp Lys Trp Arg Asp Ser Val Ala Gly Ile Phe Tyr Asn Gly Asp Ser
                        25                        30                        35

gaa tta gcg gct gat gac aca gta ttt gat ggc gta tcc act gtg att      259
Glu Leu Ala Ala Asp Asp Thr Val Phe Asp Gly Val Ser Thr Val Ile
                        40                        45                        50

ggc aat atg gat gat gat cct gat ttc gtg gcc gca agg gcg aca acg      307
Gly Asn Met Asp Asp Asp Pro Asp Phe Val Ala Ala Arg Ala Thr Thr
                        55                        60                        65

att gat ggg att act ttt ttc caa acg cac gga cat ctc tat gac gcg      355
Ile Asp Gly Ile Thr Phe Phe Gln Thr His Gly His Leu Tyr Asp Ala
                        70                        75                        80                        85

acc caa ttt aac gct tgg gcg aac cta aaa tta atg gcc gtg gca gca      403
Thr Gln Phe Asn Ala Trp Ala Asn Leu Lys Leu Met Ala Val Ala Ala
                        90                        95                        100

cag gaa gct aac gca cag gtc gcc ctc ttt ggg cat acc cat ctg gaa      451
Gln Glu Ala Asn Ala Gln Val Ala Leu Phe Gly His Thr His Leu Glu
                        105                        110                        115

ggg gcg gtt gtg ttt gat gat atc ttg ttt att aat cca ggt tca atc      499
Gly Ala Val Val Phe Asp Asp Ile Leu Phe Ile Asn Pro Gly Ser Ile
                        120                        125                        130

cgg ctg cct aaa ggg cca cat gcc aac tta ggt ggt act tat gct gtg      547
Arg Leu Pro Lys Gly Pro His Ala Asn Leu Gly Gly Thr Tyr Ala Val
                        135                        140                        145

ttg gat gtg acg gag acg agc tat gac gtg aga ttt tat aat cgt cag      595
Leu Asp Val Thr Glu Thr Ser Tyr Asp Val Arg Phe Tyr Asn Arg Gln
                        150                        155                        160                        165

cat caa cca ttg cca caa ctc acg gta cag gtc gca cgt taa gtgaccc      644
His Gln Pro Leu Pro Gln Leu Thr Val Gln Val Ala Arg *
                        170                        175
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caatttaatc aatggtatg 723

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<213> Homo sapiens

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<221> CDS
<222> (364)..(543)

<400> 342
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tcctgggacc aagaccagga aatctaacca ataagcaatg gtaacagtga ctcaagtgtc 180
agtccgccct cagtggcccg agtccgaggt gggcatcatg gcaccagttt acatctcgga 240
aagggagggt cagagagggtc aagtcacttg cctaagggtca cccagggact gcttagctgg 300
ctaggatgag aaccagcctg ctccaacgcc ccctcgtgga acagttgcga gcttaggaat 360
taa atg ttc cct ccc cca ggc tat gcc aat gag gtg ggc gag gct ttc 408
Met Phe Pro Pro Pro Gly Tyr Ala Asn Glu Val Gly Glu Ala Phe
1 5 10 15
cgc tct ctt gtg cca gcg gcg gtg gtg tgg ctg agc tat ggc gtg gcc 456
Arg Ser Leu Val Pro Ala Ala Val Val Trp Leu Ser Tyr Gly Val Ala
20 25 30
agc tcc tac gtg ctg gcg gat gcc att gac aaa ggc aag aag gct gga 504
Ser Ser Tyr Val Leu Ala Asp Ala Ile Asp Lys Gly Lys Lys Ala Gly
35 40 45
gag gtg agt gtt agc cta ttt tcc aac ccc caa ccc tag ctctcctctt 553
Glu Val Ser Val Ser Leu Phe Ser Asn Pro Gln Pro *
50 55 60
gtgtgggtca gtccacagcc tggcatgtga taaagtcctt gtgggacact ccagtcctta 613
caacttgcct agtgcagtcc ataa 637

<210> 343
<211> 998
<212> DNA
<213> Homo sapiens

<220>
 <221> CDS
 <222> (7)..(399)

<400> 343

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	Met Ser Phe Asn Arg Leu Leu Ser Val Lys Leu Asn Asp Gly	
	1 5 10	
aag ttc atg cct att ctg ggg ttt ggc acc tct gtt gct agg aag gtt	96	
Lys Phe Met Pro Ile Leu Gly Phe Gly Thr Ser Val Ala Arg Lys Val		
15 20 25 30		
gct atg agt aat gta gaa gaa gcc gtc cag gta gca att gat gta ggc	144	
Ala Met Ser Asn Val Glu Glu Ala Val Gln Val Ala Ile Asp Val Gly		
35 40 45		
tac cgc cat att gac tca gct tat aca cac ctg aat gaa gaa ggc atc	192	
Tyr Arg His Ile Asp Ser Ala Tyr Thr His Leu Asn Glu Glu Gly Ile		
50 55 60		
ggg cag gcc atc cga aag aag att gcc aac ggc act gtg aag aga aaa	240	
Gly Gln Ala Ile Arg Lys Lys Ile Ala Asn Gly Thr Val Lys Arg Lys		
65 70 75		
gat ata ttc tat acc aca aag gtg tgg ggc acc ttt tcc cgc cca gaa	288	
Asp Ile Phe Tyr Thr Thr Lys Val Trp Gly Thr Phe Ser Arg Pro Glu		
80 85 90		
ttg gtc caa aga ggc ctt gaa atg tca ctg aag aaa ctt cag ctg agc	336	
Leu Val Gln Arg Gly Leu Glu Met Ser Leu Lys Lys Leu Gln Leu Ser		
95 100 105 110		
tac atg gat ctt tac ctt ttt cat ttc cca gta cct ttg cag cct ggg	384	
Tyr Met Asp Leu Tyr Leu Phe His Phe Pro Val Pro Leu Gln Pro Gly		
115 120 125		
agg agc ttt tgc tga cggatgcaca gggaaagatc atgtttgaca cagtgggtct	439	
Arg Ser Phe Cys *		
130		
ctgcagcaca tgggagagtt ttactcctgt tgccaaggct ggagtacagt ggcacgatct	499	
cggctcactg caacctccgc ctcccagggt caagcatgta cctctgcctc ccacatagct	559	
gggaatacag gtggaatatt acccttacct caaccaaagc aaactcctgg agtactgtaa	619	
gtccaaggac attgtcatga ctgcatattc tgccttgggg tctgactcag acaaagactg	679	
gtaatcatct tcataaagtt attttgttta ttttttttag gtgggggtct cattctgtca	739	
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agtcaggatc ttcctccta gacctcctaa gtagctggga ctacaggagt gcaccaccat	859	
gcctggctaa ttgtttatct tcatttttgt agagacaggg tctcactacg ttaccaagc	919	

cagtcttgaa ttcttgggct caagtgatcc tcccaccttg gcctcccaaa gtgctgggat 979
tagaggtgta agccacggt 998

<210> 344
<211> 478
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (188)..(376)

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atgtatatac acattaccta aagcaaaatg aggaccctac tgggctgccca tcccagctgg 120
actgctgctg tggagctcag catcaagtac ttccaggaga agcttcagca ggacctagag 180
gcagagc atg gta gag gta gag gat aca gcc ctc ata cca ccg tgc tgt 229
Met Val Glu Val Glu Asp Thr Ala Leu Ile Pro Pro Cys Cys
1 5 10
atg tcc atc ttt caa gtc ctg gtg gtg ccc gca gag ttt gaa ggg aag 277
Met Ser Ile Phe Gln Val Leu Val Val Pro Ala Glu Phe Glu Gly Lys
15 20 25 30
cca ctg ctt cag aga tac cag gtg gta aat gca tgc cta gtg gaa gtg 325
Pro Leu Leu Gln Arg Tyr Gln Val Val Asn Ala Cys Leu Val Glu Val
35 40 45
tgc tcc tct gca tct atg cct ttg agc aga aag cct ttg agt ccc aat 373
Cys Ser Ser Ala Ser Met Pro Leu Ser Arg Lys Pro Leu Ser Pro Asn
50 55 60
tag tggg cccatgagtg gccaaaatga gggactggga cctgtatagc cgttaaacta 430
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taaatcaggg ccaaaaagga aagataaatt ataagtttaa agaaaatg 478

<210> 345
<211> 459
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (201)..(368)

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tctcctgtgt cacctctctt gtgtccacag tctaacccat ctcttcattt ccctcaacct      180
caggtggagc ctccaccaaa      atg cag att ttt cca aaa atc ctt aca ggg      230
                        Met Gln Ile Phe Pro Lys Ile Leu Thr Gly
                        1              5              10

acg atc atc acc cta gag gtt gaa ccc ttg gat aca aca gaa aaa tgt      278
Thr Ile Ile Thr Leu Glu Val Glu Pro Leu Asp Thr Thr Glu Lys Cys
                        15              20              25

aaa ggc caa tat cag gat aag gaa cga att cct cct gat cag caa aga      326
Lys Gly Gln Tyr Gln Asp Lys Glu Arg Ile Pro Pro Asp Gln Gln Arg
                        30              35              40

caa gtg act gga agc tgg caa gta act gga aga tgg aca taa ctttctc      375
Gln Val Thr Gly Ser Trp Gln Val Thr Gly Arg Trp Thr  *
                        45              50              55

tgactacaac attcaaaagg aatttactct ttttatgttg tgttgagact tcatggtagt      435
gctaaaacta ggaagaaatc ttac      459

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<210> 346
<211> 1867
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (9)..(1835)

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<400> 346
atctgcag atg tta aca tac ctt aac att agc cga aat ctt tta tca aca      50
      Met Leu Thr Tyr Leu Asn Ile Ser Arg Asn Leu Leu Ser Thr
      1              5              10

ttg cca aaa tac cta ttt gat ctt ccc ctt aaa gtt ttg gtc gtc agt      98
Leu Pro Lys Tyr Leu Phe Asp Leu Pro Leu Lys Val Leu Val Val Ser
      15              20              25              30

aat aat aaa ctg gta tcc att cca gaa gaa att ggg aag tta aaa gat      146
Asn Asn Lys Leu Val Ser Ile Pro Glu Glu Ile Gly Lys Leu Lys Asp
      35              40              45

tta atg gaa ttg gat att agc tgc aat gag att caa gtc ctt ccc caa      194
Leu Met Glu Leu Asp Ile Ser Cys Asn Glu Ile Gln Val Leu Pro Gln
      50              55              60

caa atg gga aaa tta cat tca ctt aga gag cta aat ata aga aga aat      242

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Gln Met Gly Lys Leu His Ser Leu Arg Glu Leu Asn Ile Arg Arg Asn	
65 70 75	
aat ctt cat gtt ttg cca gat gaa tta gga gac ctt ccc tta gtc aag	290
Asn Leu His Val Leu Pro Asp Glu Leu Gly Asp Leu Pro Leu Val Lys	
80 85 90	
ctg gat ttc tct tgt aat aaa gtg acc gaa att cca gtt tgt tac aga	338
Leu Asp Phe Ser Cys Asn Lys Val Thr Glu Ile Pro Val Cys Tyr Arg	
95 100 105 110	
aag ctg cat cat tta caa gta ata att ttg gat aac aat cca ttg caa	386
Lys Leu His His Leu Gln Val Ile Ile Leu Asp Asn Asn Pro Leu Gln	
115 120 125	
gta cca cca gca cag ata tgt tta aag ggt aag gtg cac ata ttt aag	434
Val Pro Pro Ala Gln Ile Cys Leu Lys Gly Lys Val His Ile Phe Lys	
130 135 140	
tac tta aat att caa gca tgt tgc aga atg gat aag aaa cca gat tcc	482
Tyr Leu Asn Ile Gln Ala Cys Cys Arg Met Asp Lys Lys Pro Asp Ser	
145 150 155	
ctg gat ctt cca tca ttg agt aaa cga atg ccc tca cag cct ctc aca	530
Leu Asp Leu Pro Ser Leu Ser Lys Arg Met Pro Ser Gln Pro Leu Thr	
160 165 170	
gac agt atg gaa gat ttt tat cca aat aaa aat cat ggc cct gac tct	578
Asp Ser Met Glu Asp Phe Tyr Pro Asn Lys Asn His Gly Pro Asp Ser	
175 180 185 190	
gga att gga agt gat aat gga gag aaa cga tta tcc aca aca gaa cca	626
Gly Ile Gly Ser Asp Asn Gly Glu Lys Arg Leu Ser Thr Thr Glu Pro	
195 200 205	
tca gat gat gac aca gtc agc ctt cat tct caa gtc tca gaa tca aat	674
Ser Asp Asp Asp Thr Val Ser Leu His Ser Gln Val Ser Glu Ser Asn	
210 215 220	
aga gag cag aca tca aga aat gac agt cac ata ata gga agt aag act	722
Arg Glu Gln Thr Ser Arg Asn Asp Ser His Ile Ile Gly Ser Lys Thr	
225 230 235	
gat tct cag aaa gac cag gag gta tat gat ttt gtt gac ccc aac aca	770
Asp Ser Gln Lys Asp Gln Glu Val Tyr Asp Phe Val Asp Pro Asn Thr	
240 245 250	
gaa gat gta gca gtt cct gaa cag gga aat gca cat att gga tca ttt	818
Glu Asp Val Ala Val Pro Glu Gln Gly Asn Ala His Ile Gly Ser Phe	
255 260 265 270	
gta tca ttc ttt aag gga aaa gaa aaa tgt tct gaa aaa tct cgg aaa	866
Val Ser Phe Phe Lys Gly Lys Glu Lys Cys Ser Glu Lys Ser Arg Lys	
275 280 285	
aat gaa gaa tta gga gat gaa aaa aga ctt gag aaa gaa cag tta ctg	914
Asn Glu Glu Leu Gly Asp Glu Lys Arg Leu Glu Lys Glu Gln Leu Leu	

290	295	300	
gca gag gaa gag gat gat gat ttg aag gaa gta act gat ttg agg aaa			962
Ala Glu Glu Glu Asp Asp Asp Leu Lys Glu Val Thr Asp Leu Arg Lys			
305	310	315	
ata gct gct cag tta ttg cag caa gaa cag aag aac agg att ctt aat			1010
Ile Ala Ala Gln Leu Leu Gln Gln Glu Gln Lys Asn Arg Ile Leu Asn			
320	325	330	
cat tca act tct gtg atg aga aac aag cca aaa caa act gtg gaa tgt			1058
His Ser Thr Ser Val Met Arg Asn Lys Pro Lys Gln Thr Val Glu Cys			
335	340	345	350
gaa aag agt gtc tca gca gat gaa gtt aat tca cca tta tca ccc ctc			1106
Glu Lys Ser Val Ser Ala Asp Glu Val Asn Ser Pro Leu Ser Pro Leu			
355	360	365	
acc tgg cag ccc tta gaa aat cag aag gat caa ata gat gaa caa ccg			1154
Thr Trp Gln Pro Leu Glu Asn Gln Lys Asp Gln Ile Asp Glu Gln Pro			
370	375	380	
tgg cca gaa tct cac cct ata atc tgg cag agt gaa gaa agg agg cgg			1202
Trp Pro Glu Ser His Pro Ile Ile Trp Gln Ser Glu Glu Arg Arg Arg			
385	390	395	
agc aaa cag att aga aaa gaa tat ttc aag tat aaa tca atg agg aag			1250
Ser Lys Gln Ile Arg Lys Glu Tyr Phe Lys Tyr Lys Ser Met Arg Lys			
400	405	410	
agt tca agt ggc aat gaa aat gat gag caa gac agt gat aat gct aat			1298
Ser Ser Ser Gly Asn Glu Asn Asp Glu Gln Asp Ser Asp Asn Ala Asn			
415	420	425	430
atg tca aca caa tct cca gta tca tct gag gaa tat gac aga act gat			1346
Met Ser Thr Gln Ser Pro Val Ser Ser Glu Glu Tyr Asp Arg Thr Asp			
435	440	445	
ggt ttt tca cac agt ccc ttt ggc ttg aag cct aga tca gct ttt agc			1394
Gly Phe Ser His Ser Pro Phe Gly Leu Lys Pro Arg Ser Ala Phe Ser			
450	455	460	
cgc tca tct cgc caa gaa tat ggg gca gca gat cca gga ttt aca atg			1442
Arg Ser Ser Arg Gln Glu Tyr Gly Ala Ala Asp Pro Gly Phe Thr Met			
465	470	475	
aga aga aag atg gaa cat tta cgg gaa gag cga gag caa ata cga caa			1490
Arg Arg Lys Met Glu His Leu Arg Glu Glu Arg Glu Gln Ile Arg Gln			
480	485	490	
ctt cgc aac aat ctt gaa tcc agg tta aaa gta att ttg cct gat gac			1538
Leu Arg Asn Asn Leu Glu Ser Arg Leu Lys Val Ile Leu Pro Asp Asp			
495	500	505	510
att gga gct gca ctg atg gat ggg gtt gtt ctt tgc cat tta gcc aat			1586
Ile Gly Ala Ala Leu Met Asp Gly Val Val Leu Cys His Leu Ala Asn			
515	520	525	

cat ata agg cca cgt tct gtt gct agt att cat gta cca tca cca gca	1634
His Ile Arg Pro Arg Ser Val Ala Ser Ile His Val Pro Ser Pro Ala	
530 535 540	
gtg ccc aaa ctg agc atg gca aaa tgt cga aga aat gta gaa aat ttt	1682
Val Pro Lys Leu Ser Met Ala Lys Cys Arg Arg Asn Val Glu Asn Phe	
545 550 555	
ctt gat gct tgt aaa aag ttg ggt gtc tca cag gaa aga ctt tgt ttg	1730
Leu Asp Ala Cys Lys Lys Leu Gly Val Ser Gln Glu Arg Leu Cys Leu	
560 565 570	
cct cat cat att ttg gaa gaa cga gga ctt gtg aaa gtt ggt gtc aca	1778
Pro His His Ile Leu Glu Glu Arg Gly Leu Val Lys Val Gly Val Thr	
575 580 585 590	
gtt cag gcg ctc ctt gaa tta cca aca acc aag gca tct cag ctt tct	1826
Val Gln Ala Leu Leu Glu Leu Pro Thr Thr Lys Ala Ser Gln Leu Ser	
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gtg gct taa tataacattt taaaattcta aaaaaaaaaa aa	1867
Val Ala *	

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tactgtcatt ca atg tgg att gct tcc tta tgt ttc att att ttg gat	168
Met Trp Ile Ala Ser Leu Cys Phe Ile Ile Leu Asp	
1 5 10	
tgt gag ctc atc ttt tgt agg gtg tta gct aca gaa atc cta tgc tgc	216
Cys Glu Leu Ile Phe Cys Arg Val Leu Ala Thr Glu Ile Leu Cys Cys	
15 20 25	
agg gtt gag att tgt ccc tat ttg ctt ctg tat tac tgc cta agg acc	264
Arg Val Glu Ile Cys Pro Tyr Leu Leu Leu Tyr Tyr Cys Leu Arg Thr	
30 35 40	
aac ttt gct cat tta aaa tat att tat ata agc tca aag att aaa gct	312
Asn Phe Ala His Leu Lys Tyr Ile Tyr Ile Ser Ser Lys Ile Lys Ala	

45	50	55	60	
gac tgt ggg gag gtc tat ggc taa aaattttcaa gggagatttc ttccccctaa				366
Asp Cys Gly Glu Val Tyr Gly *				
65				
tctggctaag atgggcagat toccattgtc ttcctgtgcc agtgtgcaga tatcatctag				426
tatactcttt cactgcaagc atgggtcttc gagggctctg gctctatgac gaagtcttca				486
gttccaaatc ttcattctgt gccagcctaa cgcctttgtt t				527

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gcaaattcac tgcctcctcc catgcacgtg gtagagagta ccagtatcaa catggccctg	120
ttttctgcta aaaccagatt ttgaggaatc agagaccccc aacactactc actcagtagc	180
tagcagcccc ttcctttcaa ctgggagtgt tattagaatg aaaagtaatt agttagaagg	240
gcatacatct cagtggcatg agcattgtgg aatatccttt cctaggcaca tttgtccact	300
aagggaacag cctcagaaac tggtagacga atgggtgaga tgagatcctg gagagagaac	360
acagccatcc cctatagaaa ggcacagctt ttgggcttct ctggcctga	415
	atg cct Met Pro 1
tct ggg gta ttt cca tat gca aca gcc cag agt cat agc ctt ggg caa	463
Ser Gly Val Phe Pro Tyr Ala Thr Ala Gln Ser His Ser Leu Gly Gln	
5 10 15	
cca cac ata gag gtt tcc ttc tca ctt cag aca cat aca tca ctt tca	511
Pro His Ile Glu Val Ser Phe Ser Leu Gln Thr His Thr Ser Leu Ser	
20 25 30	
cac cac ttg ggg atg gaa ata cct aca aga gtg aag gtc aag ggc cct	559
His His Leu Gly Met Glu Ile Pro Thr Arg Val Lys Val Lys Gly Pro	
35 40 45 50	
ccc cag gca tct cat tca tta ctc agc ttc ctt cct gac caa gtc tgc	607
Pro Gln Ala Ser His Ser Leu Leu Ser Phe Leu Pro Asp Gln Val Cys	
55 60 65	

caa cca atg gcc agc tat gcg cct cat cct cat tgc ttc tgc ctc cac	655
Gln Pro Met Ala Ser Tyr Ala Pro His Pro His Cys Phe Cys Leu His	
70 75 80	
gta aat gaa acc aaa ggc ctc agc ata tcc tgg gag gac tgg ggg ctg	703
Val Asn Glu Thr Lys Gly Leu Ser Ile Ser Trp Glu Asp Trp Gly Leu	
85 90 95	
tta cct aat ggt cct ctc tgt ccc att ata ggt gca agg cac ccc atc	751
Leu Pro Asn Gly Pro Leu Cys Pro Ile Ile Gly Ala Arg His Pro Ile	
100 105 110	
cac aca ttt gca cca cta ctc caa gat agt att ttt ctt ttc aca caa	799
His Thr Phe Ala Pro Leu Leu Gln Asp Ser Ile Phe Leu Phe Thr Gln	
115 120 125 130	
tct ctt tac agc aga atc cag agt tgg gtt gta gtt tac ctt cct gga	847
Ser Leu Tyr Ser Arg Ile Gln Ser Trp Val Val Val Tyr Leu Pro Gly	
135 140 145	
aag ctc att atc ttt gtt tga at taacatttca gcatggaact aactgggcgg	900
Lys Leu Ile Ile Phe Val *	
150	
aggaaggatc gttatacgtc ttcagaaagt tctcattgcc ccagctgcct agtactatac	960
aagaagctct accttgatgg cagatctaag aaggctatag gcctttgttt gtaggaagca	1020
gtgtcattac attcaagctt cacttctctg attggcttcc aacctgagg attcaaagag	1080
aatccaaggt tctgcctatg tctgatgaca taaggaaaac ttggcttcct ctgctcaagg	1140
ttcccctctg ctcatccctc ctcatcaga catcctccac cataccagtg tttagaagca	1200
aaacatgaag ggctagcgcc accaggatag ttagcagaaa tattgtctgt aaagctaggc	1260
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caatcccaat aaattctgac atgtccttgg caatggaagc ctgggttgga gatcctgagg	1380
cagctgtgcc tactgttccc cacctcagaa gcttcctgcc cagagagcca gcagccttgg	1440
gatactaatag aggatgcaac tggcttattg gtatgaaata gaaggtggct ttgtaggggc	1500
aagcaggcaa agagtactat ccacatggca ggcagggtgc tttgtgtctg gaaagctttg	1560
cctagccagt acagctgtga gcagaggctg gttataaatt tgaactccct cagcccattt	1620
gcaactctgc ctctgttccc ttgcattctg tttgggtgcc ctttagtttc ctagtaaata	1680
ctccttttga aaaactccaa ccttgtctta ttttaacttg gggaagggga ttctccaatg	1740
tcttttccag gataaagaag gaaattaaaa taccatgaaa aaatggacat ggcagtagaa	1800
aggaaacatt ctgatcagac cttgggaaaa gctggtgccg agagagggag aggccagggtg	1860
tccccccacc caactggcac tgattctcag ccccttctc ttacttctgt tggcttcaag	1920

gagacctgcc cttgatgtgt gttgctgctg aagcaccctc ccagccagtg agttggacat 1980
atgcagcagg cactttgatg tccaggaagt acactggtac atgacaggag caagggtcag 2040
ggagggggagg ggaaagggtt ctacaatgca gatgttttca aaattctcca acaatcatga 2100
ctctaaatgg ta 2112

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Met Ser Trp Ala Lys Met Ala Val Gln Val Val
1 5 10
cag gcg gtg cag gcg gtt cat ctc gag tct gac gct ttc ctc gtt tgt 99
Gln Ala Val Gln Ala Val His Leu Glu Ser Asp Ala Phe Leu Val Cys
15 20 25
ctc aac cac gct ctg agc aca gag aag gag gaa gta atg ggg ctg tgc 147
Leu Asn His Ala Leu Ser Thr Glu Lys Glu Glu Val Met Gly Leu Cys
30 35 40
ata ggg gag ttg aac gat gat aca agg agt gac tcc aaa ttt gca tat 195
Ile Gly Glu Leu Asn Asp Asp Thr Arg Ser Asp Ser Lys Phe Ala Tyr
45 50 55
act gga act gaa atg cgc aca gtt gct gaa aag gtt gat gcc gtc aga 243
Thr Gly Thr Glu Met Arg Thr Val Ala Glu Lys Val Asp Ala Val Arg
60 65 70 75
att gtt cac att cat tct gtc atc atc tta cga cgt tct gat aag agg 291
Ile Val His Ile His Ser Val Ile Ile Leu Arg Arg Ser Asp Lys Arg
80 85 90
aag gac cga gta gaa att tct cca gag cag ctg tct gca gct tca aca 339
Lys Asp Arg Val Glu Ile Ser Pro Glu Gln Leu Ser Ala Ala Ser Thr
95 100 105
gag gca gag agg ttg gct gaa ctg aca ggc cgc ccc atg aga gtt gtg 387
Glu Ala Glu Arg Leu Ala Glu Leu Thr Gly Arg Pro Met Arg Val Val

110	115	120	
ggc tgg tat cat tcc cat cct cat ata act gtt tgg cct tca cat gtt			435
Gly Trp Tyr His Ser His Pro His Ile Thr Val Trp Pro Ser His Val			
125	130	135	
gat gtt cgc aca caa gcc atg tac cag atg atg gat caa ggc ttt gta			483
Asp Val Arg Thr Gln Ala Met Tyr Gln Met Met Asp Gln Gly Phe Val			
140	145	150	155
gga ctt att ttt tcc tgt ttc ata gaa gat aag aac acg aag act ggc			531
Gly Leu Ile Phe Ser Cys Phe Ile Glu Asp Lys Asn Thr Lys Thr Gly			
	160	165	170
cgg gta ctc tac act tgc ttc caa tcc ata cag gcc caa aag agt tca			579
Arg Val Leu Tyr Thr Cys Phe Gln Ser Ile Gln Ala Gln Lys Ser Ser			
	175	180	185
gag tcc ctt cat ggt cca cga gac ttc tgg agc tcc agc cag cac atc			627
Glu Ser Leu His Gly Pro Arg Asp Phe Trp Ser Ser Ser Gln His Ile			
	190	195	200
tcc att gag ggc cag aag gaa gag gaa agg tat gag aga atc gaa atc			675
Ser Ile Glu Gly Gln Lys Glu Glu Glu Arg Tyr Glu Arg Ile Glu Ile			
	205	210	215
cca atc cat att gta cct cat gtc act atc tgg aaa gtg tgc ctt gaa			723
Pro Ile His Ile Val Pro His Val Thr Ile Trp Lys Val Cys Leu Glu			
	220	225	230
tca gca gta gag ctg ccc aag atc ctg tgc cag gag gag cag gat gcg			771
Ser Ala Val Glu Leu Pro Lys Ile Leu Cys Gln Glu Glu Gln Asp Ala			
	240	245	250
tat agg agg atc cac agc ctt aca cat ctg gac tca gta acc aag atc			819
Tyr Arg Arg Ile His Ser Leu Thr His Leu Asp Ser Val Thr Lys Ile			
	255	260	265
cat aat ggc tca gtg ttt acc aag aat ctg tgc agt cag atg tcg gca			867
His Asn Gly Ser Val Phe Thr Lys Asn Leu Cys Ser Gln Met Ser Ala			
	270	275	280
gtc agc ggg cct ctc cta cag tgg ttg gag gac aga ctg gag caa aac			915
Val Ser Gly Pro Leu Leu Gln Trp Leu Glu Asp Arg Leu Glu Gln Asn			
	285	290	295
caa cag cat ttg cag gaa tta caa caa gaa aag gaa gag ctt atg caa			963
Gln Gln His Leu Gln Glu Leu Gln Gln Glu Lys Glu Glu Leu Met Gln			
	300	305	310
gaa ctt tct tct cta gaa taa at caggagacaa aatgggggaaa gatgaaaata			1016
Glu Leu Ser Ser Leu Glu *			
	320		
tccagtgtaa agttacttaa gctaaatcaa tttcaaagaa gaaaaacttg gaggactcat			1076
tttacctgac ttcaagactt actataaagc tatagtaatc aagatagatg gtattggcag			1136

aggaacagac acatacgtca atggaacaga tgagagaacc cagaaataaa cccatataaa 1196
 tatgctcagc tgattttgaa aaagtgaaaa agcaattcaa tggaggaaga atagcctttc 1256
 tgacaaatta tgctagagca attagacacc catggcgagg agaaaaaaga acctctactt 1316
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 taaaactag 1385

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 <213> Homo sapiens

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 cgtcttggtg agagcgtgag ctgctgagat ttgggagtct gcgctaggcc cgcttgaggat 120
 tctgagccga tgtaagagtt cactc atg ttt gca ccc gcg gtg atg cgt gct 172
 Met Phe Ala Pro Ala Val Met Arg Ala
 1 5
 ttt cgc aag aac aag act ctc ggc tat gga gtc ccc atg ttg atg gat 220
 Phe Arg Lys Asn Lys Thr Leu Gly Tyr Gly Val Pro Met Leu Met Asp
 10 15 20 25
 cct gag ctt gaa aaa aaa ctg aaa gag aat aaa ata tct tta gag tcg 268
 Pro Glu Leu Glu Lys Lys Leu Lys Glu Asn Lys Ile Ser Leu Glu Ser
 30 35 40
 gaa tat gag aaa atc aaa gac tcc aag ttt gat gac tgg aag aat att 316
 Glu Tyr Glu Lys Ile Lys Asp Ser Lys Phe Asp Asp Trp Lys Asn Ile
 45 50 55
 cga gga ccc agg cct tgg gaa gat cct gac ctc ctc caa gga aga aat 364
 Arg Gly Pro Arg Pro Trp Glu Asp Pro Asp Leu Leu Gln Gly Arg Asn
 60 65 70
 cca gaa agc ctt aag act aag aca act tga c tctgctgatt cttttttcct 415
 Pro Glu Ser Leu Lys Thr Lys Thr Thr *
 75 80
 tttttttttt ttaaaaaaaaa aa 437

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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (25)..(1239)

<400> 351

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                                   1                      5

tgg gtg ctg gtc ctc agt ctg tgg ggg gca gta gta ggt gct caa aac      99
Trp Val Leu Val Leu Ser Leu Trp Gly Ala Val Val Gly Ala Gln Asn
 10                      15                      20                      25

atc aca gcc cgg att ggc gag cca ctg gtg ctg aag tgt aag ggg gcc      147
Ile Thr Ala Arg Ile Gly Glu Pro Leu Val Leu Lys Cys Lys Gly Ala
                30                      35                      40

ccc aag aaa cca ccc cag cgg ctg gaa tgg aaa ctg aac aca ggc cgg      195
Pro Lys Lys Pro Pro Gln Arg Leu Glu Trp Lys Leu Asn Thr Gly Arg
                45                      50                      55

aca gaa gct tgg aag gtc ctg tct ccc cag gga gga ggc ccc tgg gac      243
Thr Glu Ala Trp Lys Val Leu Ser Pro Gln Gly Gly Gly Pro Trp Asp
                60                      65                      70

agt gtg gct cgt gtc ctt ccc aac ggc tcc ctc ttc ctt ccg gct gtc      291
Ser Val Ala Arg Val Leu Pro Asn Gly Ser Leu Phe Leu Pro Ala Val
 75                      80                      85

ggg atc cag gat gag ggg att ttc cgg tgc cag gca atg aac agg aat      339
Gly Ile Gln Asp Glu Gly Ile Phe Arg Cys Gln Ala Met Asn Arg Asn
 90                      95                      100                      105

gga aag gag acc aag tcc aac tac cga gtc cgt gtc tac cag att cct      387
Gly Lys Glu Thr Lys Ser Asn Tyr Arg Val Arg Val Tyr Gln Ile Pro
                110                      115                      120

ggg aag cca gaa att gta gat tct gcc tct gaa ctc acg gct ggt gtt      435
Gly Lys Pro Glu Ile Val Asp Ser Ala Ser Glu Leu Thr Ala Gly Val
                125                      130                      135

ccc aat aag gtg ggg aca tgt gtg tca gag gga agc tac cct gca ggg      483
Pro Asn Lys Val Gly Thr Cys Val Ser Glu Gly Ser Tyr Pro Ala Gly
                140                      145                      150

act ctt agc tgg cac ttg gat ggg aag ccc ctg gtg cct aat gag aag      531
Thr Leu Ser Trp His Leu Asp Gly Lys Pro Leu Val Pro Asn Glu Lys
 155                      160                      165

gga gta tct gtg aag gaa cag acc agg aga cac cct gag aca ggg ctc      579
Gly Val Ser Val Lys Glu Gln Thr Arg Arg His Pro Glu Thr Gly Leu
 170                      175                      180                      185

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ttc aca ctg cag tgc gag cta atg gtg acc cca gcc cgg gga gga gat	627
Phe Thr Leu Gln Ser Glu Leu Met Val Thr Pro Ala Arg Gly Gly Asp	
190 195 200	
ccc cgt ccc acc ttc tcc tgt agc ttc agc cca ggc ctt ccc cga cac	675
Pro Arg Pro Thr Phe Ser Cys Ser Phe Ser Pro Gly Leu Pro Arg His	
205 210 215	
cgg gcc ttg cgc aca gcc ccc atc cag ccc cgt gtc tgg gag cct gtg	723
Arg Ala Leu Arg Thr Ala Pro Ile Gln Pro Arg Val Trp Glu Pro Val	
220 225 230	
cct ctg gag gag gtc caa ttg gtg gtg gag cca gaa ggt gga gca gta	771
Pro Leu Glu Glu Val Gln Leu Val Val Glu Pro Glu Gly Gly Ala Val	
235 240 245	
gct cct ggt gga acc gta acc ctg acc tgt gaa gtc cct gcc cag ccc	819
Ala Pro Gly Gly Thr Val Thr Leu Thr Cys Glu Val Pro Ala Gln Pro	
250 255 260 265	
tct cct caa atc cac tgg atg aag gat ggt gtg ccc ttg ccc ctt ccc	867
Ser Pro Gln Ile His Trp Met Lys Asp Gly Val Pro Leu Pro Leu Pro	
270 275 280	
ccc agc cct gtg ctg atc ctc cct gag ata ggg cct cag gac cag gga	915
Pro Ser Pro Val Leu Ile Leu Pro Glu Ile Gly Pro Gln Asp Gln Gly	
285 290 295	
acc tac agc tgt gtg gcc acc cat tcc agc cac ggg ccc cag gaa agc	963
Thr Tyr Ser Cys Val Ala Thr His Ser Ser His Gly Pro Gln Glu Ser	
300 305 310	
cgt gct gtc agc atc agc atc atc gaa cca ggc gag gag ggg cca act	1011
Arg Ala Val Ser Ile Ser Ile Ile Glu Pro Gly Glu Glu Gly Pro Thr	
315 320 325	
gca ggc tct gtg gga gga tca ggg ctg gga act cta gcc ctg gcc ctg	1059
Ala Gly Ser Val Gly Gly Ser Gly Leu Gly Thr Leu Ala Leu Ala Leu	
330 335 340 345	
ggg atc ctg gga ggc ctg ggg aca gcc gcc ctg ctc att ggg gtc atc	1107
Gly Ile Leu Gly Gly Leu Gly Thr Ala Ala Leu Leu Ile Gly Val Ile	
350 355 360	
ttg tgg caa agg cgg caa cgc cga gga gag gag agg aag gcc cca gaa	1155
Leu Trp Gln Arg Arg Gln Arg Arg Gly Glu Glu Arg Lys Ala Pro Glu	
365 370 375	
aac cag gag gaa gag gag gag cgt gca gaa ctg aat cag tgc gag gaa	1203
Asn Gln Glu Glu Glu Glu Glu Arg Ala Glu Leu Asn Gln Ser Glu Glu	
380 385 390	
cct gag gca ggc gag agt agt act gga ggg cct tga gggg cccacagaca	1253
Pro Glu Ala Gly Glu Ser Ser Thr Gly Gly Pro *	
395 400 405	

gatcccatcc atcagctccc tttttttttt cccttgaact gttctggcct cagaccaact 1313
ctctcctgta taatctctct cctgtataac cccaccttgc caagctttct tctacaacca 1373
gagcccccca caatgatgat taaacacctg acacatcttg ca 1415

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<212> DNA
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Trp Val Leu Val Leu Ser Leu Trp Gly Ala Val Val Gly Ala Gln Asn
10 15 20 25

atc aca gcc cgg att ggc gag cca ctg gtg ctg aag tgt aag ggg gcc 147
Ile Thr Ala Arg Ile Gly Glu Pro Leu Val Leu Lys Cys Lys Gly Ala
30 35 40

ccc aag aaa cca ccc cag cgg ctg gaa tgg aaa ctg aac aca ggc cgg 195
Pro Lys Lys Pro Pro Gln Arg Leu Glu Trp Lys Leu Asn Thr Gly Arg
45 50 55

aca gaa gct tgg aag gtc ctg tct ccc cag gga gga ggc ccc tgg gac 243
Thr Glu Ala Trp Lys Val Leu Ser Pro Gln Gly Gly Gly Pro Trp Asp
60 65 70

agt gtg gct cgt gtc ctt ccc aac ggc tcc ctc ttc ctt ccg gct gtc 291
Ser Val Ala Arg Val Leu Pro Asn Gly Ser Leu Phe Leu Pro Ala Val
75 80 85

ggg atc cag gat gag ggg att ttc cgg tgc cag gca atg aac agg aat 339
Gly Ile Gln Asp Glu Gly Ile Phe Arg Cys Gln Ala Met Asn Arg Asn
90 95 100 105

gga aag gag acc aag tcc aac tac cga gtc cgt gtc tac cag att cct 387
Gly Lys Glu Thr Lys Ser Asn Tyr Arg Val Arg Val Tyr Gln Ile Pro
110 115 120

ggg aag cca gaa att gta gat tct gcc tct gaa ctc acg gct ggt gtt 435
Gly Lys Pro Glu Ile Val Asp Ser Ala Ser Glu Leu Thr Ala Gly Val
125 130 135

ccc aat aag gta gtg gaa gaa agc agg aga agt aga aaa cgg ccc tgt 483
Pro Asn Lys Val Val Glu Glu Ser Arg Arg Ser Arg Lys Arg Pro Cys

140	145	150	
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act ctt agc tgg cac ttg gat ggg aag ccc ctg gtg cct aat gag aag Thr Leu Ser Trp His Leu Asp Gly Lys Pro Leu Val Pro Asn Glu Lys 170 175 180 185			579
gga gta tct gtg aag gaa cag acc agg aga cac cct gag aca ggg ctc Gly Val Ser Val Lys Glu Gln Thr Arg Arg His Pro Glu Thr Gly Leu 190 195 200			627
ttc aca ctg cag tgc gag cta atg gtg acc cca gcc cgg gga gga gat Phe Thr Leu Gln Ser Glu Leu Met Val Thr Pro Ala Arg Gly Gly Asp 205 210 215			675
ccc cgt ccc acc ttc tcc tgt agc ttc agc cca ggc ctt ccc cga cac Pro Arg Pro Thr Phe Ser Cys Ser Phe Ser Pro Gly Leu Pro Arg His 220 225 230			723
cgg gcc ttg cgc aca gcc ccc atc cag ccc cgt gtc tgg gag cct gtg Arg Ala Leu Arg Thr Ala Pro Ile Gln Pro Arg Val Trp Glu Pro Val 235 240 245			771
cct ctg gag gag gtc caa ttg gtg gtg gag cca gaa ggt gga gca gta Pro Leu Glu Glu Val Gln Leu Val Val Glu Pro Glu Gly Gly Ala Val 250 255 260 265			819
gct cct ggt gga acc gta acc ctg acc tgt gaa gtc cct gcc cag ccc Ala Pro Gly Gly Thr Val Thr Leu Thr Cys Glu Val Pro Ala Gln Pro 270 275 280			867
tct cct caa atc cac tgg atg aag gat ggt gtg ccc ttg ccc ctt ccc Ser Pro Gln Ile His Trp Met Lys Asp Gly Val Pro Leu Pro Leu Pro 285 290 295			915
ccc agc cct gtg ctg atc ctc cct gag ata ggg cct cag gac cag gga Pro Ser Pro Val Leu Ile Leu Pro Glu Ile Gly Pro Gln Asp Gln Gly 300 305 310			963
acc tac agc tgt gtg gcc acc cat tcc agc cac ggg ccc cag gaa agc Thr Tyr Ser Cys Val Ala Thr His Ser Ser His Gly Pro Gln Glu Ser 315 320 325			1011
cgt gct gtc agc atc agc atc atc gaa cca ggc gag gag ggg cca act Arg Ala Val Ser Ile Ser Ile Ile Glu Pro Gly Glu Glu Gly Pro Thr 330 335 340 345			1059
gca ggc tct gtg gga gga tca ggg ctg gga act cta gcc ctg gcc ctg Ala Gly Ser Val Gly Gly Ser Gly Leu Gly Thr Leu Ala Leu Ala Leu 350 355 360			1107
ggg atc ctg gga ggc ctg ggg aca gcc gcc ctg ctc att ggg gtc atc Gly Ile Leu Gly Gly Leu Gly Thr Ala Ala Leu Leu Ile Gly Val Ile 365 370 375			1155

ttg tgg caa agg cgg caa cgc cga gga gag gag agg aag gcc cca gaa 1203
 Leu Trp Gln Arg Arg Gln Arg Arg Gly Glu Glu Arg Lys Ala Pro Glu
 380 385 390
 aac cag gag gaa gag gag gag cgt gca gaa ctg aat cag tcg gag gaa 1251
 Asn Gln Glu Glu Glu Glu Glu Arg Ala Glu Leu Asn Gln Ser Glu Glu
 395 400 405
 cct gag gca ggc gag agt agt act gga ggg cct tga gggg cccacagaca 1301
 Pro Glu Ala Gly Glu Ser Ser Thr Gly Gly Pro *
 410 415 420
 gatcccatcc atcagctccc ttttcttttt cccttgaact gttctggcct cagaccaact 1361
 ctctcctgta taatctctct cctgtataac cccaccttgc caagctttct tctacaacca 1421
 gagcccccca caatgatgat taaacacctg acacatcttg ca 1463

<210> 353
 <211> 926
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (10)..(600)

<400> 353
 tttcgtggt atg gtc ccc ggg tcc gag ggc ccg gcc cgc gcc ggg agc 48
 Met Val Pro Gly Ser Glu Gly Pro Ala Arg Ala Gly Ser
 1 5 10
 gtg gtg gcc gac gtg gtg ttt gtg att gag ggt acg gcc aac ctg gga 96
 Val Val Ala Asp Val Val Phe Val Ile Glu Gly Thr Ala Asn Leu Gly
 15 20 25
 ccc tac ttc gag ggg ctc cgc aag cac tac ctg ctc ccg gcc atc gag 144
 Pro Tyr Phe Glu Gly Leu Arg Lys His Tyr Leu Leu Pro Ala Ile Glu
 30 35 40 45
 tat ttt aat ggt ggt cct cct gct gag acg gac ttc ggg gga gac tat 192
 Tyr Phe Asn Gly Gly Pro Pro Ala Glu Thr Asp Phe Gly Gly Asp Tyr
 50 55 60
 ggg ggg acc cag tac agc ctc gtg gtg ttc aac aca gtg gac tgc gct 240
 Gly Gly Thr Gln Tyr Ser Leu Val Val Phe Asn Thr Val Asp Cys Ala
 65 70 75
 ccc gag tcc tac gta caa tgt cac gct ccc acc agc agc gcc tat gag 288
 Pro Glu Ser Tyr Val Gln Cys His Ala Pro Thr Ser Ser Ala Tyr Glu
 80 85 90
 ttt gtc acc tgg ctc gat ggc att aag ttc atg ggc ggg ggt ggt gag 336

Phe Val Thr Trp Leu Asp Gly Ile Lys Phe Met Gly Gly Gly Gly Glu	
95 100 105	
agc tgc agc ctc atc gcg gaa gga ctc agc aca gcc ttg cag ctg ttt	384
Ser Cys Ser Leu Ile Ala Glu Gly Leu Ser Thr Ala Leu Gln Leu Phe	
110 115 120 125	
gat gac ttc aag aag atg cgc gag cag att ggc cag acg cac cgg gtc	432
Asp Asp Phe Lys Lys Met Arg Glu Gln Ile Gly Gln Thr His Arg Val	
130 135 140	
tgc ctc ctc atc tgc aac tca ccc cca tac ttg ttg cct gct gtt gag	480
Cys Leu Leu Ile Cys Asn Ser Pro Pro Tyr Leu Leu Pro Ala Val Glu	
145 150 155	
agc acc acg tac tct gga tgc aca act gag aat ctt gtg cag cca gat	528
Ser Thr Thr Tyr Ser Gly Cys Thr Thr Glu Asn Leu Val Gln Pro Asp	
160 165 170	
tgg gga agc ggg gga tcc act tct cca ttg gtg tct ccc cgg aag ctg	576
Trp Gly Ser Gly Gly Ser Thr Ser Pro Leu Val Ser Pro Arg Lys Leu	
175 180 185	
cct gcg ctt cgg ctt cct ggt tga agaaaggcag ccccccggcc tgggtggagc	630
Pro Ala Leu Arg Leu Pro Gly *	
190 195	
cgctgaggcc tccgacagat gttgaggcac tgaccgaggg acatggtggt gggttcgggga	690
ctcgtgctgc tgggggggggt ggtcagccca gggccttcaa taaagaagca gggcctgcca	750
acagagcgag cagagacgga accgcaccac cgcagagaac caaagaaagg cgcaaaaaga	810
aagcaacaga ggcaaaaaag cacacaaacg cacacgacac agccgcgcga caacacgacg	870
agccaacaca aaagacgacg cacaaggcac gccagaaaag aggcgagaga acacaa	926

<210> 354
 <211> 510
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (149)..(493)

<400> 354	
gataccagct tccttcagca gcgcaggcgg tggctccctga ggcccgtgga aggagtcaaa	60
cttgcgaggaa ttttgcagaa gtcattgtat tcaaagaaga ataagcaaga aagaaaagaa	120
ggaaggaaga gaggtagaca gatacaag atg aaa tcc tgt caa aaa atg gaa	172
Met Lys Ser Cys Gln Lys Met Glu	
1 5	

gga aaa cca gaa aat gag agt gaa cca aag cat gag gaa gag cca aag	220
Gly Lys Pro Glu Asn Glu Ser Glu Pro Lys His Glu Glu Glu Pro Lys	
10 15 20	
cct gag gaa aag cca gaa gag gag gag aag cta gag gag gag gcc aaa	268
Pro Glu Glu Lys Pro Glu Glu Glu Glu Lys Leu Glu Glu Glu Ala Lys	
25 30 35 40	
gca aaa gga act ttt aga gaa agg ctg att caa tct ctc cag gag ttt	316
Ala Lys Gly Thr Phe Arg Glu Arg Leu Ile Gln Ser Leu Gln Glu Phe	
45 50 55	
aaa gaa gat ata cac aac agg cat tta agc aat gaa gat atg ttt aga	364
Lys Glu Asp Ile His Asn Arg His Leu Ser Asn Glu Asp Met Phe Arg	
60 65 70	
gaa gtg gat gaa ata gat gag ata agg aga gtc aga aac aaa ctt ata	412
Glu Val Asp Glu Ile Asp Glu Ile Arg Arg Val Arg Asn Lys Leu Ile	
75 80 85	
gtg atg cgt tgg aag gta acg aac cct cct acc cca ttt aaa tta gag	460
Val Met Arg Trp Lys Val Thr Asn Pro Pro Thr Pro Phe Lys Leu Glu	
90 95 100	
tac ccg gat ttc tct cat att aca tac cca tag cgctcttata gcagcac	510
Tyr Pro Asp Phe Ser His Ile Thr Tyr Pro *	
105 110 115	

<210> 355
 <211> 1045
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (95)..(1045)

<400> 355	
tagaggagta gattaccgag aaaaatatcc catcagtgag gagattttcg gtatcaccag	60
aaagaccaaa gatcagggct gcttaattgc tgac atg atg gga ctc acc gag	112
Met Met Gly Leu Thr Glu	
1 5	
ggg gtg ttc ctg att ctg tct ggc act cag ttc aca ctg gga att ctg	160
Gly Val Phe Leu Ile Leu Ser Gly Thr Gln Phe Thr Leu Gly Ile Leu	
10 15 20	
gtc aat tgt ttc att gag ttg gtc aat ggt agc agc tgg ttc aag acc	208
Val Asn Cys Phe Ile Glu Leu Val Asn Gly Ser Ser Trp Phe Lys Thr	
25 30 35	

aag aga atg tct ttg tct gac ttc atc atc acc acc ctg gca ctc ttg	256
Lys Arg Met Ser Leu Ser Asp Phe Ile Ile Thr Thr Leu Ala Leu Leu	
40 45 50	
agg atc att ctg ctg tgt att atc ttg act gat agt ttt tta ata gaa	304
Arg Ile Ile Leu Leu Cys Ile Ile Leu Thr Asp Ser Phe Leu Ile Glu	
55 60 65 70	
ttc tct ccc aac aca cat gat tca ggg ata ata atg caa att att gat	352
Phe Ser Pro Asn Thr His Asp Ser Gly Ile Ile Met Gln Ile Ile Asp	
75 80 85	
gtt tcc tgg aca ttt aca aac cat ctg agc att tgg ctt gcc acc tgt	400
Val Ser Trp Thr Phe Thr Asn His Leu Ser Ile Trp Leu Ala Thr Cys	
90 95 100	
ctt ggt gtc ctc tac tgc ctg aaa atc gcc agt ttc tct cac ccc aca	448
Leu Gly Val Leu Tyr Cys Leu Lys Ile Ala Ser Phe Ser His Pro Thr	
105 110 115	
ttc ctc tgg ctc aag tgg aga gtt tct agg gtg atg gta tgg atg ctg	496
Phe Leu Trp Leu Lys Trp Arg Val Ser Arg Val Met Val Trp Met Leu	
120 125 130	
ttg ggt gca ctg ctc tta tcc tgt ggt agt acc gca tct ctg atc aat	544
Leu Gly Ala Leu Leu Leu Ser Cys Gly Ser Thr Ala Ser Leu Ile Asn	
135 140 145 150	
gag ttt aag ctc tat tct gtc ttt agg gga att gag gcc acc agg aat	592
Glu Phe Lys Leu Tyr Ser Val Phe Arg Gly Ile Glu Ala Thr Arg Asn	
155 160 165	
gtg act gaa cac ttc aga aag aag agg agt gag tat tat ctg atc cat	640
Val Thr Glu His Phe Arg Lys Lys Arg Ser Glu Tyr Tyr Leu Ile His	
170 175 180	
gtt ctt ggg act ctg tgg tac ctg cct ccc tta att gtg tcc ctg gcc	688
Val Leu Gly Thr Leu Trp Tyr Leu Pro Pro Leu Ile Val Ser Leu Ala	
185 190 195	
tcc tac tct ttg ctc atc ttc tcc ctg ggg agg cac aca cgg cag atg	736
Ser Tyr Ser Leu Leu Ile Phe Ser Leu Gly Arg His Thr Arg Gln Met	
200 205 210	
ctg caa aat ggg aca agc tcc aga gat cca acc act gag gcc cac aag	784
Leu Gln Asn Gly Thr Ser Ser Arg Asp Pro Thr Thr Glu Ala His Lys	
215 220 225 230	
agg gcc atc aga atc atc ctt tcc ttc ttc ttt ctc ttc tta ctt tac	832
Arg Ala Ile Arg Ile Ile Leu Ser Phe Phe Phe Leu Phe Leu Leu Tyr	
235 240 245	
ttt ctt gct ttc tta att gca tca ttt ggt aat ttc cta cca aaa acc	880
Phe Leu Ala Phe Leu Ile Ala Ser Phe Gly Asn Phe Leu Pro Lys Thr	
250 255 260	
aag atg gct aag atg att ggc gaa gta atg aca atg ttt tat cct gct	928

Lys Met Ala Lys Met Ile Gly Glu Val Met Thr Met Phe Tyr Pro Ala
 265 270 275

ggc cac tca ttt att ctc att ctg ggg aac agt aag ctg aag cag aca 976
 Gly His Ser Phe Ile Leu Ile Leu Gly Asn Ser Lys Leu Lys Gln Thr
 280 285 290

ttt gta gtg atg ctc cgg tgt gag tct ggt cat ctg aag cct gga tcc 1024
 Phe Val Val Met Leu Arg Cys Glu Ser Gly His Leu Lys Pro Gly Ser
 295 300 305 310

aag gga ccc att ttc tct tag 1045
 Lys Gly Pro Ile Phe Ser *
 315

<210> 356
 <211> 790
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (86)..(310)

<220>
 <221> misc_feature
 <222> (1)...(790)
 <223> n = a,t,c or g

<400> 356

agacaaacct catctgccct gttgtttttt gttctcacct tcttattcag tatgagtgtc 60

gtttggtgct tctaattgggc ttcta atg gtc ctc ctg gaa ccc aag ccc tgg 112
 Met Val Leu Leu Glu Pro Lys Pro Trp
 1 5

ctg gaa ctg atg ctg ctg tgg tgg tca ggg ttc agt gag cag gag gaa 160
 Leu Glu Leu Met Leu Leu Trp Trp Ser Gly Phe Ser Glu Gln Glu Glu
 10 15 20 25

gga ctt ggt gtt tac ccc ttg ttt acc cct ttc ctt ggc ttc ctt cca 208
 Gly Leu Gly Val Tyr Pro Leu Phe Thr Pro Phe Leu Gly Phe Leu Pro
 30 35 40

tgc agg cca ccc tgt gac ccc gtg gtg gcc ccc tct gga acc aag agc 256
 Cys Arg Pro Pro Cys Asp Pro Val Val Ala Pro Ser Gly Thr Lys Ser
 45 50 55

tgc cga ctt cca gca gca cac aca gga tca gtg ctg ggg cca tct gtg 304
 Cys Arg Leu Pro Ala Ala His Thr Gly Ser Val Leu Gly Pro Ser Val
 60 65 70

cac tga ccaaagcctc tgctggcctc accagaccaa ggccagtgtg tgcttcaggg 360

His *
75

agccttggat cctccaggct gccaacagaa acaccggccc tctcggcagc agcccatcc 420
ttccacccct gcaactgggtc ctgaaaagcc cattttgggg ccgttgctat ttagccaacc 480
tgccctccct tgctctcctg tgattttctca ctattccggc tgcagctcgc tgggagaaac 540
acttgagagt cttttgtgct ccacacccat gtacttaaaa taccaggcct ataggtcatt 600
tcaatgaggg aatttggctc ataacacgtg tgccccgagg cnagnatcct acttctgcag 660
atgctggcca agaagggctg tgtcccagcc gccatggggg ggggccacag agagggcagg 720
gccacgtgga gggcagagca tgtggctcct gtcagggtgcg cccattgctt nacttcagcc 780
cagtatcaag 790

<210> 357
<211> 433
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (67)..(246)

<400> 357
ggcatatttc aggtttcagt gacatagatc aagtaatttt aaaccaatth gggtatttcta 60
tctaag atg agg gac atg gct att aag gtc aag cca aac tat act aaa 108
Met Arg Asp Met Ala Ile Lys Val Lys Pro Asn Tyr Thr Lys
1 5 10
agt agt ata ggg cag cag tta aaa tta tct ttt gaa aat caa gta tta 156
Ser Ser Ile Gly Gln Gln Leu Lys Leu Ser Phe Glu Asn Gln Val Leu
15 20 25 30
cct ggt ttc ttc tgt cac aac aga ata gct ggt tac cta gtc agt cac 204
Pro Gly Phe Phe Cys His Asn Arg Ile Ala Gly Tyr Leu Val Ser His
35 40 45
agt tgc cct tgc ctt ccc ttg tta gtc cct gga ggt act tga gtggaac 253
Ser Cys Pro Cys Leu Pro Leu Leu Val Pro Gly Gly Thr *
50 55 60
agaaggtaga attagcaaca gctcaatcac tttaggtagc atttctcctg aattctgctg 313
ccaaatcctc aggggtctatg gattgggttga aatagtaaaa tcacacatag tgatttcttg 373
cacagcgtaa aggcgttttaa ttttagtgta tagtgaacaa agaaggaaaa ctgggtcata 433

<210> 358
 <211> 1483
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (117)..(911)

<400> 358

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agttgattgc aggtcctcct ggggccagaa gggcgcctgg gaggccaggt tctggggatc      60

ccctccatcc agaagaacca cctgctcact ctgtcccttc gcctgctgct gggacc      116
atg ggg gct ggg gcc agt gct gag gag aag cac tcc agg gag ctg gaa      164
Met Gly Ala Gly Ala Ser Ala Glu Glu Lys His Ser Arg Glu Leu Glu
  1             5             10             15

aag aag ctg aaa gag gac gct gag aag gat gct cga acc gtg aag ctg      212
Lys Lys Leu Lys Glu Asp Ala Glu Lys Asp Ala Arg Thr Val Lys Leu
          20             25             30

ctg ctt ctg ggt gcc ggt gag tcc ggg aag agc acc atc gtc aag cag      260
Leu Leu Leu Gly Ala Gly Glu Ser Gly Lys Ser Thr Ile Val Lys Gln
          35             40             45

atg aag att atc cac cag gac ggg tac tcg ctg gaa gag tgc ctc gag      308
Met Lys Ile Ile His Gln Asp Gly Tyr Ser Leu Glu Glu Cys Leu Glu
          50             55             60

ttt atc gcc atc atc tac ggc aac acg ttg cag tcc atc ctg gcc atc      356
Phe Ile Ala Ile Ile Tyr Gly Asn Thr Leu Gln Ser Ile Leu Ala Ile
          65             70             75             80

gta cgc gcc atg acc aca ctc aac atc cag tac gga gac tct gca cgc      404
Val Arg Ala Met Thr Thr Leu Asn Ile Gln Tyr Gly Asp Ser Ala Arg
          85             90             95

cag gac gac gcc cgg aag ctg atg cac atg gca gac act atc gag gag      452
Gln Asp Asp Ala Arg Lys Leu Met His Met Ala Asp Thr Ile Glu Glu
          100            105            110

ggc acg atg ccc aag gag atg tcg gac atc atc cag cgg ctg tgg aag      500
Gly Thr Met Pro Lys Glu Met Ser Asp Ile Ile Gln Arg Leu Trp Lys
          115            120            125

gac tcc ggt atc cag gcc tgt ttt gag cgc gcc tcg gag tac cag ctc      548
Asp Ser Gly Ile Gln Ala Cys Phe Glu Arg Ala Ser Glu Tyr Gln Leu
          130            135            140

aac gac tcg gcg ggc tac tac ctc tcc gac ctg gag cgc ctg gta acc      596
Asn Asp Ser Ala Gly Tyr Leu Ser Asp Leu Glu Arg Leu Val Thr
          145            150            155            160

ccg ggc tac gtg ccc acc gag cag gac gtg ctg cgc tcg cga gtc aag      644
Pro Gly Tyr Val Pro Thr Glu Gln Asp Val Leu Arg Ser Arg Val Lys

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165	170	175	
acc act ggc atc atc gag acg cag ttc tcc ttc aag gat ctc aac ttc			692
Thr Thr Gly Ile Ile Glu Thr Gln Phe Ser Phe Lys Asp Leu Asn Phe			
180	185	190	
cgg atg ttc gat gtg ggc ggg cag cgc tgc gag cgc aag aag tgg atc			740
Arg Met Phe Asp Val Gly Gly Gln Arg Ser Glu Arg Lys Lys Trp Ile			
195	200	205	
cac tgc ttc gag ggc gtg acc tgc atc atc ttc atc gcg gcg ctg agc			788
His Cys Phe Glu Gly Val Thr Cys Ile Ile Phe Ile Ala Ala Leu Ser			
210	215	220	
gcc cta cga cat ggt gct agt gga gga cga cga agt gaa ccg cat gca			836
Ala Leu Arg His Gly Ala Ser Gly Gly Arg Arg Ser Glu Pro His Ala			
225	230	235	240
cga gag cct gca cct gtt caa cag cat ctg caa cca ccg cta ctt cgc			884
Arg Glu Pro Ala Pro Val Gln Gln His Leu Gln Pro Pro Leu Leu Arg			
245	250	255	
cac gac gtc cat cgt gct ctt cct taa caaga aggacgtctt cttcgagaag			936
His Asp Val His Arg Ala Leu Pro *			
260	265		
atcaagaagg cgcacctcag catctgtttc ccggactacg atggacccaa cacctacgag			996
gacgccggca actacatcaa ggtgcagttc ctcgagctca acatgcggcg cgacgtgaag			1056
gagatctatt cccacatgac gtgcgccacc gacacgcaga acgtcaaatt tgtcttcgac			1116
gctgtcaccg acatcatcat caaggagaac ctcaaagact gtggcctctt ctgagcacca			1176
aatctttgct tatagatcca cagccagggc ctgtgctgca gtcgggggaca aggagcttcc			1236
gtctggcaag ggaagctgag agccatggct gaactatcag ggacaaaggc ccatgtcccc			1296
acatccctgc tccctccttc ctcatccagc accaaatctt tgcttatgct ccacagccag			1356
ggcctgtgct gcagtcgggg acaaggagct tccgtactgg caaggccggg gcacaatttg			1416
cactcccctc agctagacgc acagactcag caataaacct ttgcatcagg caaaaaaaaa			1476
aaaaaaaa			1483

<210> 359
 <211> 714
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1) .. (441)

<400> 359

atg aag ccc acc ctc atc tca gtg ctt gtg ata ata ttt ata ctc aga 48
Met Lys Pro Thr Leu Ile Ser Val Leu Val Ile Ile Phe Ile Leu Arg
1 5 10 15

gga aca aga gcc cag aga gtg act cag ccc gag aag ctc ctc tct gtc 96
Gly Thr Arg Ala Gln Arg Val Thr Gln Pro Glu Lys Leu Leu Ser Val
20 25 30

ttt aaa ggg gcc cca gtg gag ctg aag tgc aac tat tcc tat tct ggg 144
Phe Lys Gly Ala Pro Val Glu Leu Lys Cys Asn Tyr Ser Tyr Ser Gly
35 40 45

agt cct gaa ctc ttc tgg tat gtc cag tac tcc aga caa cgc ctc cag 192
Ser Pro Glu Leu Phe Trp Tyr Val Gln Tyr Ser Arg Gln Arg Leu Gln
50 55 60

tta ctc ttg aga cac atc tct aga gag agc atc aaa ggc ttc act gct 240
Leu Leu Leu Arg His Ile Ser Arg Glu Ser Ile Lys Gly Phe Thr Ala
65 70 75 80

gac ctt aac aaa ggc gag aca tct ttc cac ctg aag aaa cca ttt gct 288
Asp Leu Asn Lys Gly Glu Thr Ser Phe His Leu Lys Lys Pro Phe Ala
85 90 95

caa gag gaa gac tca gcc atg tat tac tgt gct cta agt ggc aca gta 336
Gln Glu Glu Asp Ser Ala Met Tyr Tyr Cys Ala Leu Ser Gly Thr Val
100 105 110

gct ggt ttt gca agg aag cag aac aca aac cct tta aat aca gga aat 384
Ala Gly Phe Ala Arg Lys Gln Asn Thr Asn Pro Leu Asn Thr Gly Asn
115 120 125

att tct ttg caa act ctc tgt atg gcc aca gca ggg cat tct ttc tcc 432
Ile Ser Leu Gln Thr Leu Cys Met Ala Thr Ala Gly His Ser Phe Ser
130 135 140

aga aat taa tattgag tttatctcgt agatattata tcatactca tcagctagcc 488
Arg Asn *
145

atacaccac ctcacaattt tgtccaaaaa attctcatca tttaccctgc ctaaattaa 548

tttaaaaata gtaaactgat tcatttcgtc tagcagcact ggacacacac cttcgaaata 608

aaaactacct tgcactgcac aaaaaacaaa aacaaaaaca cattgccggc cgccccctta 668

ttcccctcag tcagggtac cctaccttcc acctcatccg ctcatt 714

<210> 360

<211> 3154

<212> DNA

<213> Homo sapiens

<220>
 <221> CDS
 <222> (278)..(1483)

<400> 360

tggtttcttg gaagaacgtg ctcagcgcgg tctcgtatga aggagttttc cgcctgcagc	60
aactgcttcg cctgggtcggc cgcgcacccg ccgggtctagc gaactggttg atcatgacct	120
ggtgccgcag ctcgctccatg ttcaccgaca tggcgcggcc gcgcggggcc cggcgtctcc	180
ggccggacgc agacgcgggg ctgctcgtcgt agcggggccc cggatccccg agtggcggcc	240
ggagcctcga aaagagattc tcagcgtga ttttgag atg atg ggc ttg gga aac	295
Met Met Gly Leu Gly Asn	
1 5	
ggg cgt cgc agc atg aag tgc ccg ccc ctc gtg ctg gcc gcc ctg gtg	343
Gly Arg Arg Ser Met Lys Ser Pro Pro Leu Val Leu Ala Ala Leu Val	
10 15 20	
gcc tgc atc atc gtc ttg ggc ttc aac tac tgg att gcg agc tcc cgg	391
Ala Cys Ile Ile Val Leu Gly Phe Asn Tyr Trp Ile Ala Ser Ser Arg	
25 30 35	
agc gtg gac ctc cag aca cgg atc atg gag ctg gaa ggc agg gtc cgc	439
Ser Val Asp Leu Gln Thr Arg Ile Met Glu Leu Glu Gly Arg Val Arg	
40 45 50	
agg gcg gct gca gag aga ggc gcc gtg gag ctg aag aag aac gag ttc	487
Arg Ala Ala Ala Glu Arg Gly Ala Val Glu Leu Lys Lys Asn Glu Phe	
55 60 65 70	
cag gga gag ctg gag aag cag cgg gag cag ctt gac aaa atc cag tcc	535
Gln Gly Glu Leu Glu Lys Gln Arg Glu Gln Leu Asp Lys Ile Gln Ser	
75 80 85	
agc cac aac ttc cag ctg gag agc gtc aac aag ctg tac cag gac gaa	583
Ser His Asn Phe Gln Leu Glu Ser Val Asn Lys Leu Tyr Gln Asp Glu	
90 95 100	
aag gcg gtt ttg gtg aat aac atc acc aca ggt gag agg ctc atc cga	631
Lys Ala Val Leu Val Asn Asn Ile Thr Thr Gly Glu Arg Leu Ile Arg	
105 110 115	
gtg ctg caa gac cag tta aag acc ctg cag agg aat tac ggc agg ctg	679
Val Leu Gln Asp Gln Leu Lys Thr Leu Gln Arg Asn Tyr Gly Arg Leu	
120 125 130	
cag cag gat gtc ctc cag ttt cag aag aac cag acc aac ctg gag agg	727
Gln Gln Asp Val Leu Gln Phe Gln Lys Asn Gln Thr Asn Leu Glu Arg	
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Lys Phe Ser Tyr Asp Leu Ser Gln Cys Ile Asn Gln Met Lys Glu Val	
155 160 165	

aag gaa cag tgt gag gag cga ata gaa gag gtc acc aaa aag ggg aat	823
Lys Glu Gln Cys Glu Glu Arg Ile Glu Glu Val Thr Lys Lys Gly Asn	
170 175 180	
gaa gct gta gct tcc aga gac ctg agt gaa aac aac gac cag aga cag	871
Glu Ala Val Ala Ser Arg Asp Leu Ser Glu Asn Asn Asp Gln Arg Gln	
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Gln Leu Gln Ala Leu Ser Glu Pro Gln Pro Arg Leu Gln Ala Ala Gly	
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ctg cca cac aca gag gtg cca caa ggg aag gga aac gtg ctt ggt aac	967
Leu Pro His Thr Glu Val Pro Gln Gly Lys Gly Asn Val Leu Gly Asn	
215 220 225 230	
agc aag tcc cag aca cca gcc ccc agt tcc gaa gtg gtt ttg gat tca	1015
Ser Lys Ser Gln Thr Pro Ala Pro Ser Ser Glu Val Val Leu Asp Ser	
235 240 245	
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Lys Arg Gln Val Glu Lys Glu Glu Thr Asn Glu Ile Gln Val Val Asn	
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Glu Glu Pro Gln Arg Asp Arg Leu Pro Gln Glu Pro Gly Arg Glu Gln	
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Val Val Glu Asp Arg Pro Val Gly Gly Arg Gly Phe Gly Gly Ala Gly	
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Glu Leu Gly Gln Thr Pro Gln Val Gln Ala Ala Leu Ser Val Ser Gln	
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Glu Asn Pro Glu Met Glu Gly Pro Glu Arg Asp Gln Leu Val Ile Pro	
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gac gga cag gag gag gag cag gaa gct gcc ggg gaa ggg aga aac cag	1303
Asp Gly Gln Glu Glu Glu Gln Glu Ala Ala Gly Glu Gly Arg Asn Gln	
330 335 340	
cag aaa ctg aga gga gaa gat gac tac aac atg gat gaa aat gaa gca	1351
Gln Lys Leu Arg Gly Glu Asp Asp Tyr Asn Met Asp Glu Asn Glu Ala	
345 350 355	
gaa tct gag aca gac aag caa gca gcc ctg gca ggg aat gac aga aac	1399
Glu Ser Glu Thr Asp Lys Gln Ala Ala Leu Ala Gly Asn Asp Arg Asn	
360 365 370	
ata gat gtt ttt aat gtt gaa gat cag aaa aga gac acc ata aat tta	1447
Ile Asp Val Phe Asn Val Glu Asp Gln Lys Arg Asp Thr Ile Asn Leu	
375 380 385 390	

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Leu Asp Gln Arg Glu Lys Arg Asn His Thr Leu *	
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atgtcctc atg ata ttt gaa tta cac aga tat acc tta tat ctg ctt atg 170
Met Ile Phe Glu Leu His Arg Tyr Thr Leu Tyr Leu Leu Met
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tac tgt ata tac atc tta gtt tta tat att aat cat aag att ttt tca 218
Tyr Cys Ile Tyr Ile Leu Val Leu Tyr Ile Asn His Lys Ile Phe Ser
15 20 25 30

ccc ttc ctc ctc caa gaa caa att ttt acc ccc ttc aaa gca ata tgg 266
Pro Phe Leu Leu Gln Glu Gln Ile Phe Thr Pro Phe Lys Ala Ile Trp
35 40 45

ccc cac tgt tcc att gct tta agg gaa ata cca tgt aag cct cta tta 314
Pro His Cys Ser Ile Ala Leu Arg Glu Ile Pro Cys Lys Pro Leu Leu
50 55 60

tct acc aag ctc tga gcaggctctt cacatagttt cattaactca tcaaaaccct 369
Ser Thr Lys Leu *
65

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Met Val Lys Lys Ile Glu Ile Ser Gln Tyr Ala Lys Tyr Ile Cys	
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Ser Phe Leu Trp Gln Asn Gln Asp Glu Glu Thr Ser Cys Gly Asp Leu	
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Val Leu Trp Phe Cys Met Lys Thr Val Lys Val Ser Ser Ser Arg Asn	
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His Ile Val Trp Thr Tyr Asn Thr Thr Ser Ala Val Thr Val Lys Ser	
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Thr Ile Arg Arg Leu Lys Gln Leu Lys Asp Gln *	
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